

OM of: TGFB3P to: EST:* out_format : pfs

Date: Oct 30, 2001 9:11 AM

About: Results were produced by the GenCore software, version 4.5,
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Command line parameters:

-MODEL=frame+p2n.model -DEV=xlh
-Q=/cgn2-1/USPTO.spool/DUFFY097/runat_29102001_162247_25239/app_query.fasta_1.159
-DB=EST -Qfmt=fastap -SURFIX=rst -GAPOP=12.000 -GAPEXT=4.000
-MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000 -FGAPOP=4.500
-CGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500 -FGAPOP=6.000
-FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500 -DELOP=6.000
-DELEXT=7.000 -START=1 -MATRIX=blotsum62 -TRANS=human40.cdi
-LIST=100 -DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0
-ALIGN=100 -MOD=LOCAL -OUTFMT=pfs -NORM=ext -MINLEN=0
-MAXLEN=2000000000 -USER=DUFFY097 -CGCN1_1_3535 -ICPU=3
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -NO_XLPXY -WAIT
-THREADS=1

Search information block:

Query: TGFB3P

Query length: 113

Database: EST:*

Database sequences: 10228115

Database length: 43145454

Search time (sec): 1008.120000

score.list:

Sequence	Strd Orig	Zscore	EScore	Len	Documentation
gb_est46:AW412139	+ 633.00	1272.89	8.8e-62	645	! AW412139 uq46g03.y1 NCI_CGAP_M
gb_est47:BG175423	+ 633.00	1270.49	1.2e-61	812	! BG175423 602337778F1 NCI_CGAP_M
gb_est20:AI433146	+ 633.00	1268.70	1.5e-61	964	! AI433146 AI532438 LFI_NFL001.NH
gb_est29:AL532438	+ 611.00	1230.72	2.0e-59	503	! BF542567 UI-R-C3-sm-a-12-0-UI.NH
gb_est83:BF101203	+ 605.00	1205.08	5.3e-58	1820	! BF101203 601754782F1 NCI_CGAP
gb_est50:AW670561	+ 535.00	1076.61	7.5e-51	477	! AW670561 114847 MARC LP1G Sus s
gb_est82:BF042894	+ 535.00	1075.81	8.4e-51	515	! BF042894 BP250019B10B3 Soares s
gb_est89:BF542567	+ 530.00	1066.57	2.7e-50	471	! BF542567 UI-R-AFI-aq4-f-07-0-UI
gb_est18:BF044612	+ 530.00	1065.66	3.1e-50	514	! BF044612 EST370126 MAGE resequ
gb_est96:BG067564	+ 530.00	1063.90	3.8e-50	608	! BG067564 H3055G07-3 NIA Mouse
gb_est18:AI323791	+ 530.00	1062.72	4.5e-50	681	! AI323791 mm47e08.x1 Strateg
gb_est76:BE575698	+ 532.00	1050.88	2.0e-49	445	! BE575698 dc62d10.x1 NICHD XGC H
gb_est49:AW600944	+ 519.00	1047.71	3.1e-49	336	! AW600944 RC1-BN0014-210100-012
gb_est13:AA915041	+ 510.00	1024.06	6.4e-48	560	! AA915041 AW600944 UI-R-AFI-aq4-f-07-0-UI
gb_est98:BG244370	+ 506.00	1010.23	3.8e-47	966	! BG244370 602356090F1 NCI_CGAP_M
gb_est53:AW919738	+ 503.00	1010.79	3.5e-47	510	! AW919738 EST351042 Rat gene ind
gb_est22:AI599959	+ 503.00	1010.41	3.7e-47	529	! AI599959 EST351662 Normalized r
gb_est18:AI323392	+ 503.00	1009.58	4.1e-47	573	! AI323392 mj35f01.x1 Soares mous
gb_est101:BG518882	+ 503.00	1007.18	5.6e-47	721	! BG518882 602578182F1 NCI_CGAP_M
gb_est53:AW580556	+ 500.00	1004.79	7.5e-47	505	! AW580556 EST370126 MAGE resequ
gb_est75:BE464068	+ 500.00	1003.56	8.8e-47	568	! BE464068 hx84h02.x1 NCI_CGAP_ki
gb_est27:AI951831	+ 500.00	1003.03	9.5e-47	598	! AI951831 wx38b08.x1 NCI_CGAP_P
gb_est91:BF126995	+ 500.00	1002.99	9.5e-47	600	! BF126995 y1lsc03.y1 Human Lens
gb_est16:AI31171	+ 500.00	1000.99	1.2e-46	727	! AI31171 qcl5c11.x1 Soares_feta
gb_est18:AI323037	+ 498.00	1001.32	1.2e-46	477	! AI323037 mj35f01.x1 Soares mous
gb_est49:AW600952	+ 496.00	1001.25	1.2e-46	325	! AW600952 RC1-BN0014-210100-012
gb_est42:AW073988	+ 494.00	991.28	4.3e-46	572	! AW073988 xb6a06.x1 NCI_CGAP_G
gb_est16:AI089904	+ 492.00	989.04	5.7e-46	480	! AI089904 q1a6a08.x1 NCI_CGAP_B
gb_est47:BG152491	+ 492.00	985.94	8.5e-46	646	! BG152491 xx75d02.x1 NCI_CGAP_Ly
gb_est16:AI148173	+ 491.00	981.87	1.4e-45	785	! AI148173 q556d01.x1 NCI_CGAP_B
gb_est85:BF287476	+ 490.00	983.96	1.1e-45	529	! BF287476 EST452067 Rat Gene Ind
gb_est1:AA000733	+ 488.00	982.03	1.4e-45	431	! AA000733 mg35b06.r1 Soares mous
gb_est24:AI743724	+ 487.00	973.83	4.0e-45	778	! AI743724 w53b06.x1 Soares_NSF
gb_est77:BE645704	+ 486.00	976.96	2.7e-45	474	! BE645704 7e74h10.x1 NCI_CGAP_P
gb_est27:AI919139	+ 485.00	972.66	4.7e-45	589	! AI919139 wu38g03.x1 Soares_Die
gb_est52:AW823286	+ 481.00	966.04	1.1e-44	509	! AW823286 ur71c12.y1 NCI_CGAP_M
gb_est14:W160533	+ 481.00	965.31	1.2e-44	546	! W160533 wh88b09.x1 NCI_CGAP_C
gb_est10:W45844	+ 480.00	964.67	1.3e-44	478	! W45844 mc77e02.r1 Soares mous
gb_est49:AW627667	+ 471.00	946.62	1.3e-43	466	! AW627667 hb89h10.x1 NCI_CGAP_G
gb_est97:BG180040	+ 468.00	941.33	2.6e-43	431	! BG180040 602329596F1 NIH_MGC_91

gb_est26:AI927187	- 463.00	928.09	1.4e-42	578	! AI927187 wo88c02.x1 NCI_CGAP
gb_est20:AI430179	- 451.00	909.94	1.4e-41	317	! AI430179 me44c04.y1 Soares m
gb_est20:AI433146	- 448.00	898.97	5.9e-41	505	! AI433146 ti33a11.x1 NCI_CGAP
gb_est30:AU016729	- 447.00	895.56	9.2e-41	576	! AU016729 AU016729 Mouse two-
gb_est10:AA657145	- 438.00	878.12	8.6e-40	530	! AA657145 vr76d03.r1 Barstead
gb_est20:AI434956	- 438.00	877.41	9.4e-40	567	! AI434956 ti46f04.x1 NCI_CGAP
gb_est96:BG058804	- 437.50	876.54	1.0e-39	559	! BG058804 na1f0g09.x1 Soares
gb_est102:BG540633	- 437.00	870.68	2.2e-39	889	! BG540633 602570520F1 NIH_MGC
gb_est103:C86748	- 433.00	866.84	3.6e-39	599	! C86748 C86748 Mouse fertiliz
gb_99s4:CN503XHH	- 433.00	859.69	9.1e-39	1168	! AL265022 Tetraodon nigrovir
gb_est103:C86879	- 432.00	864.91	4.7e-39	583	! C86879 C86879 Mouse fertiliz
gb_est103:BF682484	- 428.50	852.20	2.4e-38	996	! BF682484 602117568F1 Soares
gb_est91:BF682484	- 426.00	855.62	1.5e-38	441	! AI1824845 wb02f01.x1 NCI_CGAP
gb_est23:AI654506	- 426.00	855.18	1.6e-38	460	! AI654506 wb63d04.x1 NCI_CGAP
gb_est11:AA049522	- 426.00	854.80	1.7e-38	477	! AA049522 mj35f01.x1 Soares m
gb_est18:AI273619	- 422.00	846.19	5.2e-38	499	! AI273619 ql36c01.x1 Soares_N
gb_est18:AI272940	- 416.00	839.57	1.2e-37	292	! AI272940 ql36g01.x1 Soares_N
gb_est18:AI304490	- 416.00	835.08	2.1e-37	449	! AI304490 qo54e06.x1 NCI_CGAP
gb_est17:AI192407	- 414.00	833.67	2.6e-37	348	! AI192407 qc98c09.x1 Soares_P
gb_est20:AI421250	- 403.00	806.70	8.2e-36	540	! AI421250 tf14d02.x1 NCI_CGAP
gb_est49:AW600940	- 401.00	810.22	5.2e-36	261	! AW600940 RC1-BN0014-210100-0
gb_est29:AL530080	- 400.50	797.53	2.6e-35	798	! AL530080 RC1-BN0014-210100-0
gb_est49:AW600938	- 400.00	807.95	7.0e-35	267	! AW600938 RC1-BN0014-210100-0
gb_est11:AA021815	- 399.50	799.23	2.1e-35	558	! AA021815 mh85d06.r1 Soares m
gb_est11:W98872	- 395.00	792.77	4.9e-35	431	! W98872 mf89e01.r1 Soares mou
gb_est103:C87366	- 393.00	785.48	1.2e-34	587	! C87366 C87366 Mouse fertiliz
gb_est96:BG058796	- 387.00	779.23	2.8e-34	403	! BG058796 naf10f12.x1 Soares_
gb_est16:AI157673	- 387.00	779.00	2.8e-34	339	! AI157673 ue48g10.r2 Soares_m
gb_est22:AI604914	- 387.00	777.19	3.6e-34	403	! AI604914 me44c04.x1 Soares m
gb_est19:AI360877	- 379.00	763.06	2.2e-33	328	! AI360877 qy10c06.x1 NCI_CGAP
gb_est22:AI634937	- 377.00	756.71	5.0e-33	408	! AI634937 tz74f09.x1 NCI_CGAP
gb_est1:AA016742	- 375.00	749.47	1.3e-32	553	! AA016742 mh39e08.r1 Soares m
gb_est49:AW600947	- 374.00	755.93	5.5e-33	245	! AW600947 RC1-BN0014-210100-0
gb_est30:AU016439	- 364.50	729.91	1.5e-31	465	! AU016439 AU016439 Mouse two-
gb_est45:AW295761	- 351.00	703.78	4.4e-30	409	! AW295761 UI-H-B11-ath-a-02-0
gb_est110:W70801	- 349.00	702.91	4.9e-30	301	! W70801 me44c04.r1 Soares mou
gb_est30:AU050770	- 347.50	688.68	3.1e-29	878	! AU050770 AU050770 Paralichth
gb_est49:AW600942	- 343.50	693.29	1.7e-29	259	! AW600942 RC1-BN0014-210100-0
gb_est106:N36741	- 341.00	680.15	9.1e-29	560	! N36741 yy90e06.r1 Soares mel
gb_est28:AI918883	- 337.00	668.99	3.8e-28	748	! BF682938 602117568F1 Soares_
gb_est46:AW600960	- 337.50	640.10	1.6e-26	266	! AW600960 RC1-BN0014-210100-0
gb_est46:AW364559	- 313.00	626.92	8.4e-26	391	! AW364559 RC1-DT0028-131299-0
gb_est20:AI1414206	- 313.00	625.11	1.1e-25	465	! AI1414206 md58e04.x1 Soares m
gb_est70:BF074350	- 305.00	607.72	9.9e-25	517	! BF074350 QV3-BT0571-030200-0
gb_est51:AW798167	- 304.00	608.93	8.5e-25	379	! AW798167 RC3-UM0046-290200-0
gb_est28:AL362754	- 302.00	604.30	1.5e-24	400	! AL362754 AL362754 ICRFP 522
gb_est20:AI452742	- 301.00	602.37	2.0e-24	396	! AI452742 tj45a05.x1 Soares_N
gb_est13:AA927529	- 298.50	596.47	4.2e-24	428	! AA927529 om71a11.s1 NCI_CGAP
gb_est106:N55274	- 291.00	580.54	3.2e-23	456	! N55274 vv46g05.x1 Soares fet
gb_est22:AI610679	- 290.50	578.54	4.2e-23	501	! AI610679 tp17g12.x1 NCI_CGAP
gb_est91:BF723491	- 290.00	574.99	6.6e-23	639	! BF723491 ma632f06.y1 Soares_
gb_est98:BG247154	- 286.00	569.53	1.3e-22	494	! BG247154 602361136F1 NCI_CGA
gb_est107:R36467	- 284.00	567.72	1.7e-22	398	! R36467 yh88d11.s1 Soares pla
gb_est49:AW579188	- 281.00	566.55	1.9e-22	248	! AW579188 RC1-DT0028-130100-0
gb_est94:BF901708	- 279.00	562.19	3.4e-22	255	! BF901708 CM2-MT0190-091200-5

seq_name: gb_est46:AW412139

seq_documentation_block:

LOCUS AW412139 645 bp mRNA

DEFINITION uq46g03.y1 NCI_CGAP_Mam5 Mus musculus cDNA clone IMAGE:2812468 5' similar to gb:M32745 mouse transforming growth factor beta-3 mRNA, complete (MOUSE);, mRNA sequence.

ACCESSION AW412139

VERSION NCI_CGAP_Mam5

KEYWORDS EST, GI:6937994

SOURCE house mouse.

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 645) NCI-Cgap http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index Unpublished (1997) Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bdpr/image/image.html

MGI:1045080 Seq primer: -40RP from Gibco High quality sequence stop: 446. Location/Qualifiers 1. 645 /organism="Mus musculus" /strain="C57/B6" /db_xref="taxon:10090" /clone_lib="NCI-CGAP_Mam5" /tissue_type="tumor, gross tissue" /dev_stage="7 months" /lab_host="DH10B" /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sali; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dt. Library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Robin Humphreys, NIH" BASE COUNT 159 a 196 c 175 g 115 t ORIGIN

alignment_scores: Quality: 633.00 Length: 112 Ratio: 5.652 Gaps: 0 Percent Similarity: 100.000 Percent Identity: 100.000 alignment_block: TGF3P x AW412139 .. Align seg 1/1 to: AW412139 from: 1 to: 645

1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
109 GCCCTGGACACCAATTACTGCTCCGCAACCTGGAGGAACTGCTGTGT 158
17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
159 ACGCCCTTTATATTGACTTCGCGCAGGATCTAGGCTGGAATGGGTCC 208
34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
209 ACGAACCTAGGGTTACTATGCCAACTTCTGCTCAGGCCCTTGCCCATAC 258
51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
259 CTCGCGCAGCAGACACACCATAGACGGTGTGGACTATACAAAC 308
67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
309 CCTGAACCCAGAGCGCTGCTCGCATGCTGCTCCCGCAGGACCTGG 358
84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
359 AGCCCTTGACCATCTTGTACTATGTGGGCAGAACCCCGCAGGTGGAGC 408

101 LeuSerAsnMetValValLysSerCysLysCysSer 112
409 CTGTCCCAACATGGGTGAAGTCTGTGAAGTGCAGC 444
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LOCUS 602337778F1 NCI-CGAP_Mam1 Mus musculus cDNA clone IMAGE:4460706 5',
DEFINITION mRNA sequence.
ACCESSION BG175423 GI:12682126
VERSION BG175423
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 812)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAM10262 row: 1 column: 19
High quality sequence stop: 735.
Location/Qualifiers 1. 812 /organism="Mus musculus" /strain="FVB/N" /db_xref="taxon:10090" /clone="IMAGE:4460706" /clone_lib="NCI-CGAP_Mam1" /tissue_type="tumor, biopsy sample" /dev_stage="3 months, virgin" /lab_host="DH10B" /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sali; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dt. Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH" BASE COUNT 197 a 210 c 245 g 160 t ORIGIN

alignment_scores: Quality: 633.00 Length: 112 Ratio: 5.652 Gaps: 0 Percent Similarity: 100.000 Percent Identity: 100.000 alignment_block: TGF3P x BG175423 .. Align seg 1/1 to: BG175423 from: 1 to: 812

1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
59 GCCCTGGACACCAATTACTGCTCCGCAACCTGGAGGAACTGCTGTGT 108
17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
109 ACGCCCTTTATATTGACTTCGCGCAGGATCTAGGCTGGAATGGGTCC 158
34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
159 ACGAACCTAAGGGTTACTATGCCAACTTCTGCTCAGGCCCTTGCCCATAC 208
51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67

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|||||
209 CTCGCGAGCCGACACAAACCATAGACACGGTCTGGACTATACACAC 258
67 rLeuAsnProGluAlaSerProCysCysValProGlnAspLeuG 84
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259 CCTGAACCCAGAGCGCTCGCTGCCATCTGCTGGTCCCCAGACCTGG 308
84 luProLeuThrIleLeuTyrTyValGlyArgThrProLysValGluGln 100
309 AGCCCTGACCATCTTGTACTATGTGGGCAGAACCCCAAGGTGGAGCAG 358
101 LeuSerAsnMetValLysSerCysLysCysSer 112
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359 CTGTCCCAACATGGTGGTGAAGTCTGCTGAAGTGCAGC 394
seq_name: gb_est29:AL532438
seq_documentation_block:
LOCUS AL532438 964 bp mRNA EST 13-FEB-2001
DEFINITION AL532438 LTI_NFL001_NBC4 Homo sapiens cDNA clone CS0DM014YD15 5
prime, mRNA sequence.
ACCESSION AL532438
VERSION AL532438.1 GI:12795931
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 964)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
CONTACT: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segre@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES
Location/Qualifiers
1..964
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0DM014YD15"
/clone_lib="LTI_NFL001_NBC4"
/sex="male"
/tissue.type="neuroblastoma cells"
/lab_host="DH10B"
/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed
by Life Technologies. Contact : Feng Liang Life
Technologies, a division of Invitrogen 9800 Medical Center
Drive Rockville, Maryland 20850, USA Fax : (1) 301 610
8371 Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com"
BASE COUNT 245 a 248 c 269 g 200 t 2 others
ORIGIN
source
alignment_scores:
Quality: 633.00 Length: 112
Ratio: 5.652 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
alignment_block:
TGFB3P x AL532438
Align seg 1/1 to: AL532438 from: 1 to: 964
1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGlnAsnCysCysVa 17
|||||
311 GCCTTGACACCAATTAATCTGCTTCCGCAACTGTGGAGGAGAACTGCTGT 360
```

```
17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTyrLysTrpValH 34
|||||
361 GCGCCCCCTCTACATTGACTTCCGACAGGATCTGGGCTGGAAGTGGGTCC 410
34 isGluProLysGlyTyrTyrAlaAsnPheCysSerClyProCysProTyr 50
|||||
411 ATGAACCTTAAGGGCTACTATGCCAACTTCTGCTCAGGCCCTTGCCCATAC 450
51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
|||||
461 CTCGCCAGTGCAGACACAAACCCACAGCAGGCTGCTGGGACTGTACACAC 510
67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
|||||
511 TCTGAACCCCTGAAGCATCTGCCTCGCTTGTGCTGCGCCAGGACCTGG 560
84 luProLeuThrIleLeuTyrTyValGlyArgThrProLysValGluGln 100
|||||
561 AGCCCTGACCATCTGCTACTATGTGGGAGGACCCCAAGTGGAGCAG 610
101 LeuSerAsnMetValLysSerCysLysCysSer 112
|||||
611 CTCCTCAACATGGTGGTGAAGTCTTGTAAATGTAGC 646
seq_name: gb_est89:BF542567
seq_documentation_block:
LOCUS BF542567 503 bp mRNA EST 11-DEC-2000
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UI-R-C3-sm-a-12-0-UI 5', mRNA sequence.
ACCESSION BF542567
VERSION BF542567.1 GI:11633674
KEYWORDS EST.
SOURCE Norway rat.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE
1 (bases 1 to 503)
Bonaldi,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)
JOURNAL 97044477
MEDLINE
COMMENT Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: msoares@blue.weeg.uiowa.edu
cDNA Library Preparation: M.B. Soares Lab Clone Distribution:
clones will be available through Research Genetics (www.resgen.com)
This clone is also available through the I.M.A.G.E. Consortium at
LLNL (info@image.llnl.gov). IMAGE ID= 1768868
Seq primer: M13 Forward.
Location/Qualifiers
1..503
/organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-C3-sm-a-12-0-UI"
/clone_lib="UI-R-C3"
/dev_stage="adult"
/lab_host="DH10B (Life Technologies)"
/note="Vector: p7T3D-pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-C3
library is a subtracted library of a series, ultimately
derived from a mixture of individually tagged normalized
libraries from rat placenta, adult lung, brain, liver,
kidney, heart, spleen, ovary, muscle, and 8, 12 and 18-day
embryos, after a series of subtractions to reduce the
representation of cDNAs from which ESTs had already been
```

generated. The following serially subtracted libraries were generated in this process: UI-R-C3, UI-R-C2p, UI-R-C1, UI-R-C0, UI-R-A1, UI-R-E1. The tag is a string of 3-5 nucleotides present between the Not I site and the oligo-dr track which allows identification of the library of origin of a clone within themixture. The subtracted library (UI-R-C3) was constructed as follows: PCR amplified cDNA inserts from UI-R-C2p clones from which 3' ESTs had been derived was used as a driver in a hybridization with the UI-R-C2p library in the form of single-stranded circles. The remaining single-stranded circles (subtracted library) was purified by hydroxyapatite column chromatography, converted to double-stranded circles and electroporated into DH10B bacteria (Life Technologies) to generate the UI-R-C3 library. This procedure has been previously described (Bonaldio, Lennon and Soares, Genome Research 6:791-806, 1996)"

BASE COUNT 106 a 151 c 133 g 112 t 1 others
ORIGIN

alignment_scores:
Quality: 611.00 Length: 109
Ratio: 5.606 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 98.165

alignment_block:
TGFB3P x BF542567 ..

Align seg 1/1 to: BF542567 from: 1 to: 503

4 ThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysValArgProLe 20
|||||
62 ACCGACTACTGCTTCGCAACTTGGAGGAGAACTGCTGTGCGCCCT 111
20 uTyrIleAspPheArgGlnAspLeuGlyTrpIlystrpValHisGluProL 37
|||||
112 TCACATTGACTTCGCGCAGGACTCTAGGCTGGAAATGGGTCCACGAACTTA 161
37 ysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyrLeuArgSer 53
|||||
162 AGGGTTACTATGCCAACTCTGCTCAGGCCCTTGCCCTTACCTCCGACG 211
54 AlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnThrLeuAsnPr 70
|||||
212 TCAGACAAACCCACAGCAGCGTGTGGACTATACACACCTGAACCC 261
70 oGluAlaSerAlaSerProCysCysValProGlnAspLeuGluProLeuT 87
|||||
262 GGAGGCATCGGCTCGCATGCTGTGTCGCCCAAGACCTGGAGCCTCTGA 311
87 hrIleLeuTyrTyrValGlyArgThrProLysValGluGlnLeuSerAsn 103
|||||
312 CCATCTTGACTATGTGGCAACCCCAAGGTGGAGCAGCTGTCCACAC 361
104 MetValValLysSerCysLysCysSer 112
|||||
362 ATGGTGGTGAAGTCGTGTAAGTGACG 388

seq_name: gb_est83:BF101203

seq_documentation_block:
LOCUS BF101203 1820 bp mRNA EST 19-OCT-2000
DEFINITION 601754782F1 NCI_CGAP_Maml Mus musculus cDNA clone IMAGE:3983588 5',
mRNA sequence.

ACCESSION BF101203

VERSION BF101203.1 GI:10883729

KEYWORDS EST.

SOURCE house mouse.

ORGANISM Mus musculus

REFERENCE 1 (bases"1 to 1820)
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

AUTHORS
TITLE
JOURNAL
COMMENT

NIH-MGC <http://mgc.nci.nih.gov/>
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-re@mail.nih.gov
Tissue procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
DNA Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>

Plate: LLM9184 row: d column: 21
High quality sequence stop: 601.

FEATURES
source

Location/Qualifiers
1..1820
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:3983588"
/clone_lib="NCI_CGAP_Maml"
/tissue_type="tumor, biopsy sample"
/dev_stage="3 months, virgin"
/lab_host="DH10B"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dr.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"

BASE COUNT 513 a 533 c 590 g 184 t
ORIGIN

alignment_scores:
Quality: 605.00 Length: 112
Ratio: 5.402 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

TGFB3P x BF101203 ..

Align seg 1/1 to: BF101203 from: 1 to: 1820

1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
|||||
166 GCCTGGACACCAATTAAGTCTTCCGCAACTGGAGGAGAACTGCTGTGT 215
17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpIlystrpValH 34
|||||
216 ACGCCCTTTATATTGACTTCGCGCAGGATCTAGGCTGGAAATGGGTCC 265
34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
|||||
266 ACGAACCTAAGGGTTACTATGCCAACTTCTGTCAGGCCCTTGCCCATAC 315
51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
|||||
316 CTCGCGAGCGCAGACACCAACCCATAGCACGGTGTGGACTATACAACAC 365
67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
|||||
366 CCTGAACCCAGAGCGCTGCTCGCATGCTGCGTCCCGCAGGACCTGG 415
84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
|||||
416 AGCCCTTGACCACTTGTACTATGTGGGAGAAC.CCCAAAGTGGAGCAG 464
101 LeuSerAsnMetValValLysSerCysLysCysSer 112
|||||
465 CTGTCCAACATGTTGGTGAAGTCTGTAAAGTGACG 500

seq_name: gb_est50:AW670561

seq_documentation_block:

LOCUS AW670561 477 bp mRNA EST 09-JUL-2000
DEFINITION U14647 MARC 1P1G Sus scrofa cDNA 5', mRNA sequence.
ACCESSION AW670561
VERSION AW670561.1 GI:7527075
KEYWORDS EST.
SOURCE Pig.
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE 1 (bases 1 to 477)
AUTHORS Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Smith,T.P.L., Casas,E.,
Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Laegreid,W.W.
and Keele,J.W.
TITLE Design and use of two pooled tissue normalized cDNA libraries for
EST discovery in swine
JOURNAL Unpublished (2000)
COMMENT Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
PCR Primers
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTCACGTCAGCAGC
Plate: 43 row: B column: 5
Seq primer: APTTAGGTGACACTATAG.
FEATURES
Location/Qualifiers
1..477
/organism="Sus scrofa"
/db_xref="taxon:9823"
/clone_lib="MARC 1P1G"
/tissue_type="pooled"
/lab_host="DH10B"
/note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
Library made from pooled tissue from day 11, 13, 15, 20,
and 30 embryos."

BASE COUNT 114 a 138 c 135 g 90 t
ORIGIN
alignment_scores:
Quality: 535.00 Length: 94
Ratio: 5.691 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 98.936
alignment_block:
TGFB3P x AW670561 ..
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1 AlaleuAspThrAsnTyrCysPheArgAsnLeuGluAsnCysCysVa 17
195 GCCTGGACACCAACTACTCTCTCCGCAATTGGAGGAGAACTGCTGT 244
17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTyrLysTrpValH 34
245 GCGCCCTCTACATTGACHTCCGACAGGATCTGGGCTGGAAGTGGGTCC 294
34 iSGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
295 ATGAACCTAAGGCTACTATGCAACTTCTGCTCAGGCCCTTGCCCGTAC 344
51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
345 CTCGCAGTGCAGACACAAACCCACAGCTCGTGTGGGGCTGTACAAAC 394
67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
395 CCTGAACCCCGAGCCCTGGCCCTCTCGTGTCTGCGTCCCGCCACCTGG 444

84 luProLeuThrIleLeuTyrTyrValGlyArg 94
445 AGCCCTGACCATCTGTTACTAGTCGTCGGAGG 476
seq_name: gb_est82:BF042894
seq_documentation_block:
LOCUS BF042894 515 bp mRNA EST 10-OCT-2000
DEFINITION BP250019B10B3 Soares normalized bovine placenta Bos taurus CDNA
Clone BP250019B10B3 5', mRNA sequence.
ACCESSION BF042894
VERSION BF042894.1 GI:10759949
KEYWORDS EST.
SOURCE Cow.
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
REFERENCE 1 (bases 1 to 515)
AUTHORS Lewin,H.A., Soares,M.B., Rebeiz,M., Pardinas,J., Liu,L. and Larson
J.H.
TITLE Bovine ESTs
JOURNAL Unpublished (2000)
COMMENT Contact: Lewin, H. A.
W. M. Keck Center for Comparative and Functional Genomics
University of Illinois at Urbana-Champaign
340 Edward R. Madigan Laboratory, 1201 W. Gregory Dr., Urbana, IL
61801, USA
Tel: 217 333 5998
Fax: 217 244 5617
Email: h-lewin@uiuc.edu
Funding for cattle EST sequencing was provided by the USDA National
Research Initiative, Animal Genome Resource Grant AG 99-3205-8534
to H. A. Lewin and J. E. Womack. Base Calling/Quality Scores: PHRED
from Washington University Genome Center. Vector Trimm g:
Cross_match from Washington University Genome Center PHRAP suite.
This sequence is vector free and at least 200 bp in length.
PCR Primers
FORWARD: TAATACGACTCACTATAGGG
BACKWARD: ATTAACCCCTCACTAAAG
Insert Length: 515 Std Error: 0.00
Plate: BP250019B10 row: B column: 3
Seq primer: AGCGGATACAAATTCACACAGGA
High quality sequence stop: 515.
FEATURES
Location/Qualifiers
1..515
/organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="BP250019B10B3"
/sex="female"
/lab_host="DH10B"
/note="Organ: Placenta; Vector: pT7m3pac; Site_1: EcoRI;
Site_2: NotI; The cDNA library was contibuted by the
Soares laboratory and it was constructed and normalized
as described by Bonaldo, M.F., Lennon, G. and Soares,
M.B. (1996), Genome Research 6(9): 791-806."

BASE COUNT 126 a 113 c 111 g 165 t
ORIGIN
alignment_scores:
Quality: 535.00 Length: 112
Ratio: 5.095 Gaps: 0
Percent Similarity: 93.750 Percent Identity: 79.464
alignment_block:
TGFB3P x BF042894/rev ..
Align seg 1/1 to reverse of: BF042894 from: 1 to: 515
1 AlaleuAspThrAsnTyrCysPheArgAsnLeuGluAsnCysCysVa 17

5 AsnTyrCysPheArgAsnLeuGluGluAsnCysCysValArg.ProLeuT 21

```

:::||||||||||||||||||||||||||||||||||||||||||||||||||||||||
681 CATTACTGCTTCCGCAACCTGGAGGAGAACTGCTGTGTACGCCCCCTTGA 632
21 yrlleAspPheArgGlnAspLeuGlyTrpLysTrpValHisGluProLys 37
||||||||||||||||||||||||||||||||||||||||||||||||||||||||
631 TATGTGACTTCCGCGAGATCTAGC.TGGAAATGGGTCCACGAACTTAAG 583
38 GlyTyr.TyTAlaAsnPheCysSerGlyProCysProTyrLeuArgSerA 54
||||||||||||||||||||||||||||||||||||||||||||||||||||||||
582 GGTACTAATGCCAACTCTGCTCAGGCCCTTGCCCATACCTCCGACGG 533
54 laAspThr.ThrHisSerThrValLeuGlyLeuTyrAsnThrLeuAsnPr 70
||||||||||||||||||||||||||||||||||||||||||||||||||||||||
532 CAGACACAAACCCATAGACGGTCTTGGACTATACAAACACCCCTGAACCC 483
70 oGluAlaSerAlaSer.ProCysCysValProGlnAspLeuGluProLeu 86
482 AGAGGCTGTGCTCTGCCATGTGCTGCCCTCCCGACGACCTGGAGCCCTG 433
87 ThrIleLeuTyrTyTValGlyArgThrProLysValGluGlnLeuSerAs 103
432 ACCATCTGTACTATGTGGCAGAACCCCAAGGTGGAGCAGCTGTCCAA 383
103 nMetValValLysSerCysLysCysSer 112
||||||||||||||||||||||||||||||||||||||||||||||||||||||||
382 CATGGTGTGAAGTCGTGTAAGTGCAGC 355

```

seq_name: gb_est53:AW919738

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seq_documentation_block: 510 bp mRNA EST 25-MAY-2000
LOCUS AW919738
DEFINITION Rattus norvegicus cDNA clone RIGG52 5' end, mRNA sequence.
ACCESSION AW919738
VERSION AW919738.1 GI:8085539
KEYWORDS EST.
SOURCE Norway rat.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

```

```

REFERENCE 1 (bases 1 to 510)
AUTHORS Lee,N.H., Glodek,A., Chandra,I., Mason,T.M., Quackenbush,J.,
Kerlavage,A.R. and Adams,M.D.
TITLE Rat Genome Project: Generation of a Rat EST (REST) Catalog & Rat
Gene Index
JOURNAL Unpublished (1998)
COMMENT Contact: Lee, NH
The Institute for Genomic Research
9712, Medical Center Drive, Rockville, MD 20850, USA
Tel: (301)-838-3529
Fax: (301)-838-0208
Email: nhlee@tigr.org
This clone is available through the ATCC, contact the ATCC
tel#703-365-2700 for further information
Seq primer: M13 Reverse.

```

```

FEATURES             Location/Qualifiers
     source
     1..510
        /organism="Rattus norvegicus"
        /db_xref="taxon:10116"
        /clone="RGIGG52"
        /clone_lib="Rat gene index, normalized rat, norvegicus,
Bento Soares"
        /tissue_type="mix - brain, ovary, placenta, kidney, lung,
liver, embryo, heart, muscle, spleen"
        /lab_host="SOLR"
        /note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
XhoI; Estimated insert size approx.i kb"

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BASE COUNT 117 a 165 c 131 g 96 t 1 others

alignment_scores:

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Quality: 503.00 Length: 112
Ratio: 5.133 Gaps: 0
Percent Similarity: 87.500 Percent Identity: 77.679
alignment_block:
TGFB3P x AW919738
Align seg 1/1 to: AW919738 from: 1 to: 510
1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGlnAsnCysCysVa 17
||||||||||||||||||||||||||||||||||||||||||||||||||||||||
157 GCCCTGGATACCAACTACTGCTTCACTCCACAGAGAACTGCTGTGT 206
17 largProLeuTyrlleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
||||||||||||||||||||||||||||||||||||||||||||||||||||||||
207 ACGGACGCTGTACATGTGACCTTAGGAAGACCTGGTTGGAAGTGGATCC 256
34 lsGluProLysGlyTyrTyTAlaAsnPheCysSerGlyProCysProTyr 50
||||||||||||||||||||||||||||||||||||||||||||||||||||||||
257 ACGAGCCCAAGGGCTACCATGCCAATCTCTGTCTGGGGCCCTGCCCTAC 306
51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
::: ||| ||||| ::||| ||||| ::||| ::||| ::||| ::|||
307 ATTTGGAGCTGGACACACAGTACACGACGAGGTCTTGCCTCTACAACCA 356
67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeu 84
||||||||||||||||||||||||||||||||||||||||||||||||||||||||
357 ACACAAACCCGGGTGCTCCGCATCACCGTCTGCGTGGCCGACGCTTTGG 406
84 luProLeuThrIleLeuTyrTyTValGlyArgThrProLysValGluGln 100
||||||||||||||||||||||||||||||||||||||||||||||||||||||||
407 AGCCACTGCCCATCGTCTACTAGTGGTGGTCCGAAGCCCAAGGTGGAGCAG 456
101 LeuSerAsnMetValValLysSerCysLysCysSer 112
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457 TTGTCCAACATGATGCTGGCTCTCTGCAAGTGCAGC 492

```

seq_name: gb_est22:AI599959

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seq_documentation_block: 529 bp mRNA EST 21-APR-1999
LOCUS AI599959
DEFINITION EST251662 Normalized rat embryo, Bento Soares Rattus sp. cDNA clone
REMEK51 3' end, mRNA sequence.
ACCESSION AI599959
VERSION AI599959.1 GI:4609007
KEYWORDS EST.
SOURCE Rattus sp.
ORGANISM Rattus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

```

```

REFERENCE 1 (bases 1 to 529)
AUTHORS Lee,N.H., Glodek,A., Chandra,I., Mason,T.M., Quackenbush,J.,
Kerlavage,A.R. and Adams,M.D.
TITLE Rat Genome Project: Generation of a Rat EST (REST) Catalog & Rat
Gene Index
JOURNAL Unpublished (1998)
COMMENT Contact: Lee, NH
The Institute for Genomic Research
9712, Medical Center Drive, Rockville, MD 20850, USA
Tel: (301)-838-3529
Fax: (301)-838-0208
Email: nhlee@tigr.org
Seq primer: M13-21.

```

```

FEATURES             Location/Qualifiers
     source
     1..529
        /organism="Rattus sp."
        /db_xref="taxon:10118"
        /clone="REMEK51"
        /clone_lib="Normalized rat embryo, Bento Soares"
        /dev_stage="embryo 8, 12, 18 dpc"
        /note="Vector: p7T3Pac; Site_1: EcoRI; Site_2: NotI"

```

BASE COUNT 88 a 142 c 194 g 105 t

209 GCATAACCGGCGCTCGCGCGCGCGCTGCTGCTGCGCGCAGGCGCTGG 258

84 luProLeuThrIleLeuTyTyValglyArgThrProLysValGluGln 100

259 AGCCGCTGCCATCGTACTACGTGGCGCGCAAGCCCAAGTGGAGCAG 308

101 LeuSerAsnMetValLysSerCysLysCysSer 112

309 CTGTCCAACATGATCGTGGCTCTGCTGCAAGTGCAGC 344

seq_name: gb_est75:BE464068

seq_documentation_block: 568 bp mRNA EST 27-JUL-2000
 LOCUS BE464068
 DEFINITION hx84102.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3194547 3' similar to gb:X02812_cds1 TRANSFORMING GROWTH FACTOR BETA 1
 PRECURSOR (HUMAN); contains element TAR1 TAR1 repetitive element ; mRNA sequence.
 ACCESSION BE464068
 VERSION BE464068.1 GI:9509843
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 568)
 AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
 cDNA Library Preparation: M. Bento Soares, Ph.D.
 cDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL, send email to: info@image.llnl.gov
 Seq primer: -400P from Gibco
 High quality sequence stop: 395.
 Location/Qualifiers
 1..568
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="IMAGE:3194547"
 /clone_id="NCI_CGAP_Kid11"
 /lab_host="DH10B"
 /note="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Plasmid DNA from the normalized library NCI_CGAP_Kid3 was prepared, and ss circles were made in vitro. Following RAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1322376-1323911, 1456007-1456775, and 1500552-1502855). Subtraction by Bento Soares and M. Fatima Bonaldeo."

FEATURES

source
 96 a 159 c 203 g 110 t
 BASE COUNT
 ORIGIN
 alignment_scores:
 Quality: 500.00 Length: 112
 Ratio: 5.102 Gaps: 0
 Percent Similarity: 87.500 Percent Identity: 76.786
 alignment_block:
 TGFb3P x BE464068/rev ..
 Align seg 1/1 to reverse of: BE464068 from: 1 to: 568

1 AlaLeuAspThrAsnTyTyCysPheArgAsnLeuGluGluAsnCysCysVa 17

479 GCCTGTGACACCAACTATTCTTTCAGCTCCACGGAGAAGATTGCTGCGT 430

17 laqProLeuTyTrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34

429 GCGAAGCTGTACATTGACTTCCGAAGGACCTCGGTGGAAAGTGGATCC 380

34 isGluProLysGlyTyTyTrAlaAsnPheCysSerGlyProCysProTy 50

379 ACGAGCCCAAGGCTACCATGCCAACTTTTTCCTCGGCGCTGCCCTAC 330

51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyTrAsnTh 67

329 ATTTGGAGCTGTCGACACGACGATACGACCAAGTCTCTGCGCTGTACAACCA 280

67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84

279 GCATAACCGGCGCTCGCGCGCGCTGCTGCTGCGCAGGCGCTGG 230

84 luProLeuThrIleLeuTyTyValglyArgThrProLysValGluGln 100

229 AGCCGCTGCCATCGTACTACGTGGCGCGCAAGCCCAAGTGGAGCAG 180

101 LeuSerAsnMetValLysSerCysLysCysSer 112

179 CTGTCCAACATGATCGTGGCTCTGCTGCAAGTGCAGC 144

seq_name: gb_est27:AI951831

seq_documentation_block:
 LOCUS AI951831 598 bp mRNA EST 06-SEP-1999
 DEFINITION wx38b08.x1 NCI_CGAP_Pit1 Homo sapiens cDNA clone IMAGE:2545911 3' similar to gb:X02812_cds1 TRANSFORMING GROWTH FACTOR BETA 1
 PRECURSOR (HUMAN); contains PTR7.t3 MER22 repetitive element ; mRNA sequence.
 ACCESSION AI951831
 VERSION AI951831.1 GI:5744141
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 598)
 AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Chris Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: Christa Prange, The I.M.A.G.E. Consortium DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
 Seq primer: -400P from Gibco
 High quality sequence stop: 425.
 Location/Qualifiers
 1..598
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="IMAGE:2545911"
 /clone_id="NCI_CGAP_Pit1"
 /tissue_type="four pooled pituitary adenomas"
 /lab_host="DH10B"
 /note="Organ: brain; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dt. Library constructed by Life Technologies."

BASE COUNT 95 a 173 c 222 g 107 t

ORIGIN

```

/tissue_type="lens"
/dev_stage="Adult"
/lab_host="EMDH10B"
/note="Organ: Eye; Vector: pCMVSPORT6; Two human lenses
from different adults (both approximately 40 years old)
together yielded 20ug of total RNA and 150ng mRNA for cDNA
library synthesis. A directionally cloned cDNA library in
the pCMVSPORT6 vector was constructed at Life Technologies
, essentially following the protocols of the SuperScript
Plasmid System full details of which are contained in the
manufacturer's instruction manual
(http://www.lifetech.com/). First strand synthesis was
carried out using a Not I primer-adaptor
[5'-pCAGTAGTTCTAGATCGGAGCGGCCG(T)15-3']. Not I/blunt
end inserts were cloned into the Not I/EcoR V sites in the
vector. EST analysis was performed on the unamplified
library at the NIH Intramural Sequencing Center (NISC)."
```

BASE COUNT 91 a 170 c 216 g 122 t 1 others
ORIGIN

alignment_scores:
Quality: 500.00 Length: 112
Ratio: 5.102 Gaps: 0
Percent Similarity: 87.500 Percent Identity: 76.786

alignment_block:
TGFB3P x AF951831/rev ..

Align seg 1/1 to reverse of: BF726995 from: 1 to: 600

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1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluAsnCysCysVa 17
|||||
512 GCCCTGGACACCAACTATTGCTTCAGCTCCACGGAGAAGAACTGCTGCGT 463

17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTyrLysTyrValH 34
|||||
462 CGGCAGCTGTACATGACTTCCGCAAGGACCTCGGCTGGAAGTGGATCC 413

34 lGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
|||||
412 ACGAGCCCAAGGGCTACCATGCCAACTTCTGCTCGGCGCCCTGCCCTTAC 363

51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
::: ||| ||||| ::||| |||||:::|||||
362 ATTTGGAGCCTGGACGACGACGACGACGACGACGACGACGACGACGAC 313

67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
|||||
312 GCATAACCCGGCGCCTCGGCGCGCGCTGCTGCTGCGCGAGCGCTGG 263

84 lUpProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGln 100
|||||
262 AGCGCTGCCCATCGTGTACTGTCGCGCGCGCAAGCCCAAGGTGGAGCAG 213

101 LeuSerAsnMetValLysSerCysLysCysSer 112
|||||
212 CTGTCCCAACATGATCGTGCCTCTCTGCAAGTGACG 177

seq_name: gb_est16:AI131171

seq_documentation_block: 727 bp mRNA EST 27-OCT-1998
LOCUS AI131171
DEFINITION IMAGE:1709684 3' similar to gb:X02812.cds1 TRANSFORMING GROWTH
FACTOR BETA 1 PRECURSOR (HUMAN); contains element TARI TARI
repetitive element ;, mRNA sequence.
ACCESSION AI131171
VERSION AI131171.1 GI:3601187
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

alignment_scores:
Quality: 500.00 Length: 112
Ratio: 5.102 Gaps: 0
Percent Similarity: 87.500 Percent Identity: 76.786

alignment_block:
TGFB3P x AF951831/rev ..

Align seg 1/1 to reverse of: AF951831 from: 1 to: 598

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1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluAsnCysCysVa 17
|||||
476 GCCCTGGACACCAACTATTGCTTCAGCTCCACGGAGAAGAACTGCTGCGT 427

17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTyrLysTyrValH 34
|||||
426 GCGGACGCTGTACATTGACTTCGCAAGGACCTCGGCTGGAAGTGGATCC 377

34 lGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
|||||
376 ACAGCCCAAGGGCTACCATGCCAACTTCTGCTCGGCGCCCTGCCCTTAC 327

51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
::: ||| ||||| ::||| |||||:::|||||
326 ATTTGGAGCCTGGACGACGACGACGACGACGACGACGACGACGACGAC 277

67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
|||||
276 GCATAACCCGGCGCCTCGGCGCGCGCTGCTGCTGCGCGAGCGCTGG 227

84 lUpProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGln 100
|||||
226 AGCGCTGCCCATCGTGTACTAGTGGCGCGCAAGCCCAAGGTGGAGCAG 177

101 LeuSerAsnMetValLysSerCysLysCysSer 112
|||||
176 CTGTCCCAACATGATCGTGCCTCTCTGCAAGTGACG 141

seq_name: gb_est91:BF726995

seq_documentation_block: 600 bp mRNA EST 05-JAN-2001
LOCUS BF726995
DEFINITION by15c03.y1 Human Lens cDNA (Un-normalized, unamplified): BY Homo
sapiens cDNA clone by15c03 5', mRNA sequence.
ACCESSION BF726995
VERSION BF726995.1 GI:12042906
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 600)
AUTHORS Wistow,G.J., Bernstein,S., Behal,A. and Smith,D.
TITLE NEIBANK: EST analysis and bioinformatics for ocular genomics
JOURNAL Invest. Ophthalmol. Vis. Sci. 41 (2000) In press
COMMENT Contact: Wistow G
Section on Molecular Structure and Function
National Eye Institute
6/331, NIH, Bethesda, MD 20892-2740, USA
Tel: 301 402 3452
Fax: 301 496 0078
Email: graeme@helix.nih.gov
Plate: 15 row: c column: 03
Seq primer: M13rpl reverse primer (ABI).
FEATURES
source
1..600
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="by15c03"
/clone_lib="Human Lens cDNA (Un-normalized, unamplified):
BY"
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alignment_block:

TGFB3P x AI323037 ..

Align seg 1/1 to: AI323037 from: 1 to: 477

1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
|||||
141 GCCCTGGATACCAACTATTGCTTCCAGCTCCACAGAGAAGAACTGCTGTGT 190

17 largProLeuTyrIleAspPheArgGlnAspLeuGlyTyrIleAspValH 34
|||||
191 CGCGCAGCTGTACATTGACTTTAGGAAGAGCCTGGGTTGGAAGTGGATCC 240

34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
|||||
241 ACGAGCCCAAGGCTACCTGCCAACTTCTGTCTGGGACCTGCCCTAT 290

51 LeuArgSerAlaAspThrHisSerThrValLeuGlyLeuTyrAsnTh 67
::: ||| ||||| ::||| |||||
291 ATTTGGAGCCTGGACACACACATACAGCAAGTCTTGGCCCTCTACAACA 340

67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
|||||
341 ACACAACCGCGCGCTGCGGCTCACCGTGTGGTGGCGCAGCGCTTGG 390

84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
|||||
391 AGCCACTCCCATCGTCTACGTACGTGGGTGCGAAGCCCAATGTGGAGCAG 440

101 LeuSerAsnMetValValLysSerCysLysCysSer 112
|||||
441 TTGTCCACATGATGTGCGCTCTCTGCAAGTGCAGC 476

seq_name: gb_est49:AW600952

seq_documentation_block: 325 bp mRNA EST 23-MAR-2000

LOCUS AW600952

DEFINITION RCL-BN0014-210100-012-f11 BN0014 Homo sapiens cDNA, mRNA sequence.

ACCESSION AW600952

VERSION AW600952.1 GI:7305691

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE HCGP <http://www.ludwig.org.br/ORESTES>.

AUTHORS The FAPESP/LICR Human Cancer Genome Project

TITLE Unpublished (1999)

JOURNAL Contact: Simpson A.J.G.

COMMENT Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome project. This entry can be seen in the following URL
(<http://www.ludwig.org.br/scripts/gethtml2.pl?tl1=RCL1&tl2=RCL1&tl3=210100-012-f11&tl4=210100-012-f11&tl5=2000-01-21&tl6=1>)
Seq primer: puc 18 forward
High quality sequence start: 10
High quality sequence stop: 325.

FEATURES
source

1..325
Location/Qualifiers

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="BN0014"
/dev_stage="Adult"
/note="Organ: breast normal; Vector: puc18; Site_1: Sma1; Site_2: Sma1; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application

No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

BASE COUNT 98 a 76 c 63 g 88 t

ORIGIN

alignment_scores: Quality: 496.00 Length: 103
Ratio: 5.113 Gaps: 0
Percent Similarity: 94.175 Percent Identity: 79.612

alignment_block:

TGFB3P x AW600952 ..

Align seg 1/1 to: AW600952 from: 1 to: 325

10 AsnLeuGluGluAsnCysCysValArgProLeuTyrIleAspPheArgG1 26
|||||
10 AATGTGCAGGATAAATGCTGCCTACGTCACATTACATTGATTCAAGAG 59

26 nAspLeuGlyTyrIleAspValHisGluProLysGlyTyrTyrAlaAsnP 43
:|||||
60 GGACCTAGGTGGAATGATACACGAAACCCAAAGGTTACAATGCCAACT 109

43 heCysSerGlyProCysProTyrLeuArgSerAlaAspThrHisSer 59
|||||
110 TCTGTGCTGGAGCATGCCCGTATTTATGGAGTTCAGACACTCAGCAGC 159

60 ThrValLeuGlyLeuTyrAsnThrLeuAsnProGluAlaSerAlaSerPr 76
|||||
160 AGGGTCCCTGAGCTTATATATACATAAACCCAGAACATCTGCTCTTCC 209

76 oCysCysValProGlnAspLeuGluProLeuThrIleLeuTyrTyrValG 93
|||||
210 TTGCTGCGTGTCCCAAGATTAGAACTCTAACCATTTCTACTACATTG 259

93 lyArgThrProLysValGluGlnLeuSerAsnMetValValLysSerCys 109
|||
260 GCAAAACACCCCAAGATTGAACAGCTTTCTAATATGATGTAAAGTCTTGC 309

110 LysCysSer 112
|||||
310 AAATGCAGC 318

seq_name: gb_est42:AW073988

seq_documentation_block: 572 bp mRNA EST 13-OCT-1999

LOCUS AW073988

DEFINITION XB06A06.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2575474 3' similar to gb:X02812_cds1 TRANSFORMING GROWTH FACTOR BETA 1 PRECURSOR (HUMAN); contains element TAR1 repetitive element ;, mRNA sequence.

ACCESSION AW073988

VERSION AW073988.1 GI:6028986

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 572)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

JOURNAL Unpublished (1997)

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-r@mail.nih.gov
Tissue Procurement: Chris Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: Christa Prange, The I.W.A.G.E. Consortium DNA Sequencing by: Washington University Genome Sequencing Center


```

86 euThrIleLeuTyrTyrValGlyArgThrProLysValGluGlnLeuSer 102
221 TGGCCATCGTGTACTAGTGGGCGCAAGCCCAAGGTGGAGCAGCTGTCC 172
103 AsnMetValValLysSerCysLysCysSer 112
171 AACATGATCGTGGCTCCTCGAAGTGCAGC 142

seq_name: gb_est48:AW512491

seq_documentation_block:
LOCUS AW512491 646 bp mRNA EST 03-MAR-2000
DEFINITION xx75d02.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2849475 3'
similar to gb:X02812.cds1 TRANSFORMING GROWTH FACTOR BETA 1
PRECURSOR (HUMAN):contains element TAR1 repetitive element ;, mRNA
sequence.
ACCESSION AW512491
VERSION AW512491.1 GI:7150569
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 646)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Life Technologies catalog #: 11547-015
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
image.llnl.gov/image/html/lifresources.shtml
Seq primer: -400P from Gibco
High quality sequence stop: 396.
Location/Qualifiers
1. 646
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2849475"
/tissue_lib="NCI_CGAP_Lym12"
/tissue_type="lymphoma, follicular mixed small and large
cell"
/lab_host="DH10B"
/note="Organ: lymph node; Vector: pCMV-SPORT6; Site_1:
Salt; Site_2: NotI; Cloned unidirectionally. Primer:
Oligo dt. Average insert size 1.25 kb. Life Technologies
catalog #: 11547-015"

BASE COUNT 115 a 178 c 208 g 144 t 1 others
ORIGIN

alignment_scores:
Quality: 492.00 Length: 110
Ratio: 5.125 Gaps: 0
Percent Similarity: 87.273 Percent Identity: 76.364

alignment_block:
TGFB3P x AW512491/rev ..

Align seg 1/1 to reverse of: AW512491 from: 1 to: 646

2 LeuAspThrAsnTyrCysPheArgAsnLeuGluGlnLeuGluAsnCysValAr 18
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
493 TTGCACACAAATATTGCTTCACCTCCACGAGAGAACTGCTGGTGGC 444

18 gProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValHisG 35
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
443 GCAGCTGTACATTGACTTCGCAAGGACCTCGCGCTGGAAGTGGATCCACG 394

35 luProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyrLeu 51
```

```

|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
393 AGCCCAAGGGCTACCATCCCAACTTTTGCCTCGGGCCCTGCCCTACACT 344
52 ArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnThrLe 68
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
343 TGGAGCCTGGACACGACGACAGCAAGGTTCGTGGCCCTGTACACACAGA 294
68 uAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuGluP 85
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
293 TAACCCGGCGCCCTCGGCGCGCGCTGTTCGTCGCGCGAGGGCTGGAAC 244
85 roLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGlnLeu 101
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
243 CGCTGCCCATTTGTGTACTACGTGGCGCGCAAGCCCAAGGTGGAGCAGCTG 194
102 SerAsnMetValValLysSerCysLysCys 111
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
193 TCCAAACATGATTGTGCGCTCCTCGCAAGTGC 164

seq_name: gb_est16:A1148173

seq_documentation_block:
LOCUS A1148173 785 bp mRNA EST 26-OCT-1998
DEFINITION qb56d01.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:1704097 3'
similar to gb:X02812.cds1 TRANSFORMING GROWTH FACTOR BETA 1
PRECURSOR (HUMAN):contains PTR5.b3 TAR1 repetitive element ;, mRNA
sequence.
ACCESSION A1148173
VERSION A1148173.1 GI:3675855
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 785)
AUTHORS NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute / National Institute of Neurological
Disorders and Stroke, Brain Tumor Genome Anatomy Project
(CGAP/BRGAP), Tumor Gene Index
JOURNAL Unpublished (1998)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldino, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert length: 953 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 356.
Location/Qualifiers
1. 785
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1704097"
/tissue_lib="NCI_CGAP_Brn23"
/tissue_type="glioblastoma (pooled)"
/lab_host="DH10B"
/note="Organ: brain; Vector: pT73D-Pac (Pharmacia) with a
modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTACCAATCTCAACTGGGAGCGCGCATATCTTTTGTGTGTGTGTGTGTGT
T 3']; double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pT73 vector.
Library is normalized, and was constructed by Bento
Soares and M. Fatima Bonaldino."

BASE COUNT 137 a 217 c 267 g 164 t
ORIGIN
```

```

alignment_scores:
  Quality: 491.00      Length: 112
  Ratio: 5.010        Gaps: 0
  Percent Similarity: 87.500  Percent Identity: 75.000

alignment_block:
  TGF3P x A1148173/rev ..

Align seg 1/1 to reverse of: A1148173 from: 1 to: 785

1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
|||||.....:|||||...:|||||.....
497 GCCCTGGACACCAATATGCTTCAGCTCCACGGAGAACTGCTGGT 448

17 lArgProLeuTyrIleAspPheArgGlnAsnLeuGlyTyrLysTyrValH 34
|||||.....:|||||...:|||||.....
447 CGGCAGCTGTACATTGACTTCCCAAGGACCTCGGTGGAGGTGGATCC 398

34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
|||||.....:|||||...:|||||.....
397 ACAGCCCAAGGGCTACCATGCCCAACTTTTGGCTCGGGCCCTGCCCTTAC 348

51 LeuArgSerAlaAspThrHisSerThrValLeuGlyLeuTyrAsnTh 67
::: ||| ||||| :||| ||||| :||| ||||| :||| ||||| :||| |||||
347 ATTTGGAGCTGGACACGCGAGTACAGCAAGTCTCTGGCCCTGTACACCA 298

67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAsnLeuG 84
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
297 GCATACCCGGGCCCTCGGGCGGCGCTGCTGCTTCCGCGAGCGCTGG 248

84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
247 AGCCACTGCCATCGTCTACTACGTGGCGCCAGCCCAAGGTGGAGCAG 198

101 LeuSerAsnMetValValLysSerCysLysCysSer 112
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
197 CTGTCCCAACATGATCGTGGCGTCTCTGCAAGTGCAAC 162

seq_name: gb_est85:BF287476

seq_documentation_block:
LOCUS BF287476 529 bp mRNA EST 28-NOV-2000
DEFINITION EST452067 Rat Gene Index, normalized rat, Rattus norvegicus cDNA
Rattus norvegicus cDNA clone RGIG52 3' sequence, mRNA sequence.
ACCESSION BF287476
VERSION BF287476.1 GI:11218546
KEYWORDS EST.
SOURCE Norway rat.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 529)
AUTHORS Malek,R.L., Cho,J., Lee,Y., Karamycheva,S., Parvizi,B., Portea,G.,
Sultana,R., Tsai,J., White,J., Quackenbush,J. and Lee,N.H.
TITLE Generation of ESTs from Normalized Rat Embryo, Bento Soares
JOURNAL Unpublished (2000)
COMMENT Other_ESTs: EST351042
Contact: Lee, NH
The Institute for Genomic Research
9712, Medical Center Drive, Rockville, MD 20850, USA
Tel: (301)-838-3529
Fax: (301)-838-0208
Email: nhlee@tigr.org
This clone is available through the ATCC, contact the ATCC
tel#703-365-2700 for further information.
FEATURES
source
1...529
/organism="Rattus norvegicus"
/db_xref="taxon:10116"
/clone="RGIG52"

/clone_lib="Rat Gene Index, normalized rat, Rattus
norvegicus cDNA"
/tissue_type="mixed tissue"
/lab_host="DH5-alpha"
/note="Vector: p3T7Pac; Site_1: EcoRI; Site_2: NotI;
Combination of ROV, RBR, RLI, RPL, RLU, REM, RNU, RSP
, RHE, RPC, RPN"
BASE COUNT 91 a 141 c 190 g 107 t
ORIGIN

alignment_scores:
  Quality: 490.00      Length: 112
  Ratio: 5.052        Gaps: 0
  Percent Similarity: 86.607  Percent Identity: 76.786

alignment_block:
  TGF3P x BF287476/rev ..

Align seg 1/1 to reverse of: BF287476 from: 1 to: 529

1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
|||||.....:|||||...:|||||.....
477 GCCCTGGATACCAATGCTTCTCAGCTCCACAGAGAAGAACTGCTGTGT 428

17 lArgProLeuTyrIleAspPheArgGlnAsnLeuGlyTyrLysTyrValH 34
|||||.....:|||||...:|||||.....
427 ACGGCAGCTGTACATTGACTTTAGGAAGGACCTGGGTGGAGTGGATCC 378

34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
|||||.....:|||||...:|||||.....
377 ACAGCCCAAGGGCTACCATGCCCAACTTCTGTGGGCGCTGCCCTTAC 328

51 LeuArgSerAlaAspThrHisSerThrValLeuGlyLeuTyrAsnTh 67
::: ||| ||||| :||| ||||| :||| ||||| :||| ||||| :||| |||||
327 ATTTGGAGCTGGACACAGTACAGCAAGTCTTGGCCCTTTACACCA 278

67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAsnLeuG 84
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
277 ACACAAACCGGGTGTTCGCGCATCACCGTGATCGTGGCGCAGGCTTGG 228

84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
227 AGCCACTGCCATCGCTTACTACGTGGGTGCGCAAGCCCAAGGTGGAGCAG 178

101 LeuSerAsnMetValValLysSerCysLysCysSer 112
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
177 TGTCCCAACATGATCGTGGCGTCTCTGCAAGTGCGAGC 142

seq_name: gb_est1:AA000733

seq_documentation_block:
LOCUS AA000733 431 bp mRNA EST 18-JUL-1996
DEFINITION mg35006.r1 Soares mouse embryo NM0E13.5 14.5 Mus musculus cDNA
clone IMAGE:425747 5' similar to gb:X02812_cds1 TRANSFORMING GROWTH
FACTOR BETA 1 PRECURSOR (HUMAN); gb:M32745 mouse transforming
growth factor beta-3 mRNA, complete (MOUSE);, mRNA sequence.
ACCESSION AA000733
VERSION AA000733.1 GI:1436599
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 431)
AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.
TITLE The WashU-HMI Mouse EST Project
JOURNAL Unpublished (1996)
COMMENT Contact: Maria M/Mouse EST Project

```

WashU-HHMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu

This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.

MGI:260299

Putative full length read

vector to vector length is 661

Seq primer: ExPrimer

High quality sequence stop: 321.

FEATURES

source

```
1. .431
   Location/Qualifiers
     /organism="Mus musculus"
     /strain="C57BL/6J"
     /db_xref="taxon:10090"
     /clone_lib="Soares mouse embryo NbME13.5 14.5"
     /sex="unknown"
     /tissue_type="embryo"
     /dev_stage="13.5-14.5dpc total fetus"
     /lab_host="DH10B"
```

```
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5'
TGTTACCAATCTGAGTGGGACGGCGGGAATTTTTTTTTTTTTTTTTTTT
T 3'], on equal amounts of mRNA from 2 13.5dpc and 2
14.5dpc embryos [total RNA provided by Minoru KO, Wayne
State Univ., from 2 ]; double-stranded cDNA was ligated to
Eco RI adaptors (Pharmacia), digested with Not I and
cloned into the Not I and Eco RI sites of the modified
pT7T3 vector. Library went through one round of
normalization, and was constructed by Bento Soares and
M.Fatima Bonaldo."
```

BASE COUNT 94 a 140 c 113 g 84 t

ORIGIN

alignment_scores:

Quality: 488.00 Length: 112
Ratio: 5.031 Gaps: 0
Percent Similarity: 86.607 Percent Identity: 75.000

alignment_block:

TGFB3P x AA000733 ..

Align seg 1/1 to: AA000733 from: 1 to: 431

```
1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
|||||
93 GCCCTGGATACCAACTATGCTTCAGCTCCACAGAGAAGAACTGCTGTG 142

17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpIysTrpValH 34
|||||
143 GCGCAGTCATACATTGACTTGTAGGAGGACCTGGGTGGAGTGGATCC 192

34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
|||||
193 ACGAGCCACAGGGCTACATGCCAACTTCGTCTGGGACCTGCCCTAT 242

51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
::: |||
243 ATTTGGAGCTGGACACACAGTACAGCAAGTCTCTGCCCTCTACAACCA 292

67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
|||||
293 ACAACACCCGGCGCTTCGGCGTCACCGTCTGCGTGGCGCGCTTATGG 342

84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
|||||
343 AGCCATGCCCCATCGTCTACTACTGCTGGGTGCGAAGCCCAAGGTGGAGCA 392
```

```
101 LeuSerAsnMetValVallysSerCysLysCysSer 112
|||||
393 TTGTCCACATGATGTGGCTCCTGCAAGTGCAGC 428
```

seq_name: gb_est24:AI743724

seq_documentation_block:

```
LOCUS AI743724 778 bp mRNA EST 19-DEC-1999
DEFINITION wq53b06.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone
IMAGE:2368787 3' similar to gb:X02812.cdsl TRANSFORMING GROWTH
FACTOR BETA 1 PRECURSOR (HUMAN);contains element MSRI repetitive
element ;, mRNA sequence.
ACCESSION AI743724
VERSION AI743724.1 GI:5112012
KEYWORDS EST.
SOURCE human.

```

ORGANISM

```
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 778)
/NCBI-GAP http://www.ncbi.nlm.nih.gov/ncicgap.
```

REFERENCE

```
AUTHORS NCI-CGAP
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
```

Email: cgaps-r@mail.nih.gov

This clone is available royalty-free through LLNL ; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

Insert Length: 863 Std Error: 0.00

Seq primer: -40Up from Gibco

High quality sequence stop: 449.

FEATURES

source

```
1. .778
   Location/Qualifiers
     /organism="Homo sapiens"
     /db_xref="taxon:9606"
     /clone_lib="Soares_NSF_F8_9W_OT_PA_P_S1"
     /lab_host="DH10B"
```

```
/note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with
a modified polylinker; Site_1: Not I; Site_2: Eco RI;
Equal amounts of plasmid DNA from five normalized
libraries were mixed, and ss circles were made in vitro.
Following HAP purification, this DNA was used as tracer in
a subtractive hybridization reaction. The driver was
PCR-amplified cDNAs from pools of 5,000 clones made from
the same 5 libraries. The pools consisted of the following
libraries and cloneIDs: Soares NbHSF pool 1:
309384-310919, 323208-325895 Soares Nb2HP pool 1:
145032-147335, 147720-148103, 148872-149255, 15002 -
150407, 151176-152327 Soares Nb2HF8-9W pool 1:
758280-760583, 772104-774407 Soares NbHPA pool 1:
304776-306311, 320136-322823, 326280-326663 Soares NbHOT
pool 1: 723720-726407, 739080-740999 Subtraction by Bento
Soares and M. Fatima Bonaldo."
```

BASE COUNT

ORIGIN

131 a 223 c 269 g 151 t 4 others

alignment_scores:

Quality: 487.00 Length: 113
Ratio: 4.969 Gaps: 1
Percent Similarity: 86.726 Percent Identity: 76.106

alignment_block:

TGFB3P x AI743724/rev ..

Align seg 1/1 to reverse of: AI743724 from: 1 to: 778

```
1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
|||||
484 GCCCTGGACCACTATGCTTCAGCTCCACGGAGAGAAGTGTGCGT 435
```

17 largProLeuTyrrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
 434 GCGGAGCTGTACATTGATCTCCGAAAGGACCTCGGCTGGAAGTGGATCC 385

34 isGluproLysGlyTyrrValAlaAsnPheCysSerGlyProCysProTyr 50
 384 ACGAGCCCAAGGGCTACCATGCACTTCTGCTCGGGCCCTGCCCTAC 335

51 LeuArgSerAlaAspThrHisSerThrValLeuGlyLeuTyrrAsnTh 67
 334 ATTGGAGCGTGGACACGACGATACAGCAAGGTCTTGGCCCTGTACAACCA 285

67 rleuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
 284 GCATAAACCGGGCGCTCGGGCGCCCTGCTGCGTGGCGGAGCGCTGG 235

84 lu.ProLeuThrIleLeuTyrrValGlyArgThrProLysValGluGl 100
 234 AACCCCTGCCCATCGTGTACTACGTGGGCCCAAGCCCAAGTGGAGCA 185

100 nLeuSerAsnMetValLysSerCysLysCysSer 112
 184 GCTGTCCAAACATGATCGTGGCGCTCTCGCAAGTGCAGC 148

seq_name: gb_est77:BE645704

seq_documentation_block: 474 bp mRNA EST 05-SEP-2000
 LOCUS BE645704 7e74h10.x1 NCI-CGAP_Pr28 Homo sapiens cDNA clone IMAGE:3288259 3'
 DEFINITION similar to gb:X02812_cds1 TRANSFORMING GROWTH FACTOR BETA 1
 similar to gb:X02812_cds1 TRANSFORMING GROWTH FACTOR BETA 1
 PRECURSOR (HUMAN); contains element TAR1 repetitive element ;, mRNA

ACCESSION BE645704
 VERSION BE645704.1 GI:9970015
 KEYWORDS EST.
 SOURCE human.

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 474)
 AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index

JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.
 Emmert-Buck, M.D., Ph.D.
 cDNA Library Preparation: M. Bento Soares, Ph.D.
 DNA Sequencing by: Greg Lennon, Ph.D.
 CDNA Library Arrayed by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL, send email to:
 info@image.llnl.gov
 Seq primer: -400P from Gibco.

FEATURES
 source Location/Qualifiers
 1..474
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:3288259"
 /clone_lib="NCI-CGAP_Pr28"
 /sex="male"
 /dev_stage="adult"
 /lab_host="DH10B"
 /note="Organ: prostate; Vector: pT73D-Pac (Pharmacia)
 with a modified polylinker; plasmid DNA from the
 normalized library NCI-CGAP_Pr22 was prepared, and ss
 circles were made in vitro. Following HAP purification,
 this DNA was used as tracer in a subtractive hybridization
 reaction. The driver was PCR-amplified cDNAs from a pool
 of 5,000 clones made from the same library (clones
 985608-986759, 1101192-1101959, and 1217928-1220615).
 * Subtraction by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 75 a 138 c 176 g 85 t
 ORIGIN

alignment_scores:
 Quality: 486.00 Length: 109
 Ratio: 5.116 Gaps: 0
 Percent Similarity: 87.156 Percent Identity: 76.147

alignment_block:
 TGF3P x BE645704/rev ..

Align seg 1/1 to reverse of: BE645704 from: 1 to: 474

4 ThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysValArgProLe 20
 473 ACCAACTATTGCTTCAGCTCCACGGAGAAGAACTGCTGCGTGGCGAGCT 424

20 uTyrrIleAspPheArgGlnAspLeuGlyTrpLysTrpValHisGluProL 37
 423 GTACATTGACTTCGCAAGGACCTCGGCTGGAAGTGGATCCACGAGCCCA 374

37 ySGlyTyrTyrrAlaAsnPheCysSerGlyProCysProTyrLeuArgSer 53
 373 AGGGCTACCATGCCAACTTTTGCTCTGGGCCCTGCCCCCTACATTGGAGC 324

54 AlaAspThrHisSerThrValLeuGlyLeuTyrrAsnThrLeuAsnPr 70
 323 CTGACACGACGATACAGCAAGTCTTGGCCCTGTACAACCCAGCATACCC 274

70 oGluAlaSerAlaSerProCysCysValProGlnAspLeuGluProLeuT 87
 273 GGGCGCTCGGGCGCGCTGCTGCGTGGCGAGCGCTGGAGCGCGCTGC 224

87 hrIleLeuTyrrTyrrValGlyArgThrProLysValGluGlnLeuSerAsn 103
 223 CCATCTGTACTACGTGGGCCCAAGCCCAAGTGGAGCGAGCTGTCCAAC 174

104 MetValLysSerCysLysCysSer 112
 173 ATGATCGTGGCTCTCGCAAGTGCAGC 147

seq_name: gb_est27:AI991139

seq_documentation_block: 589 bp mRNA EST 27-OCT-1999
 LOCUS AI991139
 DEFINITION wu38g03.x1 Soares_Dieckgraebe_colon_NHCD Homo sapiens cDNA clone
 IMAGE:2522356 3' similar to gb:X02812_cds1 TRANSFORMING GROWTH
 FACTOR BETA 1 PRECURSOR (HUMAN); contains element TAR1 TAR1
 repetitive element ;, mRNA sequence.

ACCESSION AI991139
 VERSION AI991139.1 GI:5838043
 KEYWORDS EST.
 SOURCE human.

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 589)
 AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index

JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 This clone is available royalty-free through LLNL ; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Seq primer: -400P from Gibco
 High quality sequence stop: 459.

FEATURES
 source Location/Qualifiers
 1..589
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:2522356"

```

/clone_lib="Soares_Dieckgraeffe_colon_NHCD"
/tissue_type="colonic mucosa from 3 patients with Crohn's
disease"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: colon; Vector: pT73D-Pac (Pharmacia) with a
modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5',
TGTTCACCAATCGAAGTGGAGCGCGCGCTTTTTTTTTTTT 3'],
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT73 vector. Library
went through one round of normalization. Tissue samples
provided by Dr. Brian Dieckgraeffe (Washington University,
dieckim.wustl.edu); colonic mucosa represents a range of
disease involvement from moderate to severe Crohn's
disease; samples include both perforating (fistulas) and
non-perforating samples. Library constructed by Bento
Soares and M. Fatima Bonaldo."
BASE COUNT 93 a 171 c 215 g 105 t 5 others
ORIGIN

```

```

alignment_scores:
  Quality: 485.00      Length: 113
  Ratio: 4.899        Gaps: 1
  Percent Similarity: 87.611 Percent Identity: 75.221

alignment_block:
TGFB3P x A1991139/rev ..

Align seg 1/1 to reverse of: A1991139 from: 1 to: 589

1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluAsnCysCysVa 17
|||||.....::: |||.....
476 GCCCTGGACCACTATTGCTTCAGCTCCACGGAGAAGAACTGCTCGT 427

17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
|||||.....::: |||.....
426 CGGCAGCTGTACATTGACTTCGACAGGACCTCGGCTGGAAGTGGATCC 377

34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
|||||.....::: |||.....
376 ACAGCCCAAGGGCTACCATGCCAATCTCTGCCCTCGGGCTGCCCTAC 327

51 LeuArgSerAlaAspThrHisSerThrValLeuGlyLeuTyrAsn.T 67
::: ||| ||||| ::||| |||||.....
326 ATTTGGAGCCTGGAGCGAGTACAGCAAGGTCTCGGCCCTGTACAACCA 277

67 hrLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeu 83
::: ||| |||||.....::: |||.....
276 GCATAAACGGGGCGCTTCGGCGCGCGCTGCTGCGTCCGACGGCGCTG 227

84 GluProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGl 100
|||||.....::: |||.....
226 GAGCGCGTCCCATCGTGTACTAGTGGCGCGCAAGCCCAAGGTGGAGCA 177

100 nLeuSerAsnMetValValLysSerCysLysCysSer 112
|||||.....::: |||.....
176 GCTGTCCAACATGATCGTGGCGCTCTCTCAAGTGCAGC 140

```

```

seq_name: gb_est52:AW823286

```

```

seq_documentation_block:
LOCUS AW823286 509 bp mRNA EST 17-MAY-2000
DEFINITION ur7ic12.y1 NCI_CGAP_Mam3 Mus musculus cDNA clone IMAGE:3155734 5'
similar to gb:M32745 mouse transforming growth factor beta-3 mRNA,
complete (MOUSE);, mRNA sequence.
ACCESSION AW823286
VERSION AW823286.1 GI:7916363
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

```

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 509)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Other_ESTs: ur7ic12.xl
Contact: Robert Strausberg, Ph.D.
Email: cgaps-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
image.llnl.gov/image/html/iresources.shtml

```

```

MGI:1058490
Seq primer: -40RP from Gibco
High quality sequence stop: 418.

```

```

FEATURES
Source

```

```

1..509
/organism="Mus musculus"
/strain="129 - C57/B6 - FVB"
/db_xref="taxon:10090"
/clone="IMAGE:3155734"
/clone_lib="NCI_CGAP_Mam3"
/tissue_type="tumor, gross tissue"
/dev_stage="10 months"
/lab_host="DH10B"
/notes="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Chu-Xia Deng, NIH
Reference for transgenic model: Xu et al., Nature Genetics
22, 37-43 (1999)."
BASE COUNT 134 a 156 c 123 g 94 t 2 others
ORIGIN

```

```

alignment_scores:
  Quality: 481.00      Length: 94
  Ratio: 5.228        Gaps: 0
  Percent Similarity: 97.872 Percent Identity: 94.681

alignment_block:
TGFB3P x AW823286 ..

```

```

Align seg 1/1 to: AW823286 from: 1 to: 509

```

```

1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluAsnCysCysVa 17
|||||.....::: |||.....
228 GCCCTGGACCAATTAAGTCTCCGCAACCTGGAGAGAAGTGTGTGT 277

17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
|||||.....::: |||.....
278 ACGCCCTTTATATTGACTTCGGCAGGATCTAGCTGGAATGGGTCC 327

34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
|||||.....::: |||.....
328 ACGAACCTAAGGGTTACTATGCCAACTTCTGCTAGGCCCTTGCCCATAC 377

51 LeuArgSerAlaAspThrHisSerThrValLeuGlyLeuTyrAsnTh 67
|||||.....::: |||.....
378 CTCGCGAGCGAGACACCAACCATAGCAGCGGGCTTGGACTATACAACAC 427

67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeu 84
|||||.....::: |||.....
428 CCTGAACCCCGAGCGTCTGCTCGCC.TGCTGCCGCCCCNANGACCTGG 476

84 luProLeuThrIleLeuTyrTyrValGlyArg 94
|||||.....::: |||.....
477 AGCCCTCACCATCTTGTTACTATGTGGCCAGCA 508

```

```

seq_name: gb_est24:AI760533

seq_documentation_block:      546 bp   mRNA       EST      20-DEC-1999
LOCUS      AI760533.1          GI:5176200
DEFINITION wh8B09.x1 NCI_CGAP CLL1 Homo sapiens cDNA clone IMAGE:2387801 3'
            similar to gb:X02812.cds1 TRANSFORMING GROWTH FACTOR BETA 1
PRECURSORS (HUMAN):contains element TAR1 repetitive element ; , mRNA
sequence.
ACCESSION  AI760533
VERSION    AI760533.1
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 546)
AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL   Unpublished (1997)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-re@mail.nih.gov
            Tissue Procurement: Ash Alizadeh, John Byrd, M.D., Mike Grever,
            M.D., Louis M. Staudt, M.D., Ph.D.
            cDNA Library Preparation: M. Bento Soares, Ph.D.
            DNA Library Arrayed by: Greg Lennon, Ph.D.
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution Information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/dbrr/image/image.html
            Insert length: 714 Std Error: 0.00
            Seq primer: -40UP from Gibco
            High quality sequence stop: 465.
            Location/Qualifiers
              1..546
                /organism="Homo sapiens"
                /db_xref="taxon:9606"
                /clone="IMAGE:2387801"
                /clone_lib="NCI_CGAP_CLL1"
                /tissue_type="B-cell, chronic lymphocytic leukemia"
                /lab_host="DH10B"
                /note="Vector: pTT3D-Pac (Pharmacia) with a modified
                polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                was primed with a Not I - oligo(dT) primer [5']
                TGTTACCAATCTGAAGTCGGCGCCGATGTCTTTTTTTTTTTTTTTTTTTT
                T 3'; double-stranded cDNA was ligated to Eco RI
                adaptors (Pharmacia), digested with Not I and cloned into
                the Not I and Eco RI sites of the modified pT7T3 vector.
                Library is normalized, and was constructed by Bento
                Soares and M.Fatima Bonaldo."
BASE COUNT  86 a 157 c 204 g 98 t 1 others
ORIGIN

alignment_scores:
Quality: 481.00 Length: 108
Ratio: 5.117 Gaps: 0
Percent Similarity: 87.037 Percent Identity: 75.926

alignment_block:
TGFB3P x AI760533/rev ..
Align seg 1/1 to reverse of: AI760533 from: 1 to: 546

5 AsnTyrCysPheArgAsnLeuGluGlnAsnCysValArgProLeuTy 21
464 AACTATTTCCTGCAGTCACGAGAGAAGAACTGCTGCGCGGAGCTGA 415
21 rIleAspPheArgGlnAspLeuGlyTrpLysTrpValHisGluProLys 38
414 CATTGACTTCGGAAGAACCTCGCGTGGAAAGTGGATCCACGAGCCCAAAG 365

```

Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library went through one round of normalization, and was constructed by Bento Soares and M.Fatima Bonaldo.

BASE COUNT 106 a 155 c 126 g 90 t 1 others
ORIGIN

alignment_scores:
Quality: 480.00 Length: 112
Ratio: 4.898 Gaps: 0
Percent Similarity: 87.500 Percent Identity: 76.786

alignment_block:
TGFB3P x W45844 ..

Align seg 1/1 to: W45844 from: 1 to: 478

1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
|||||
141 GCCTGGATACCACTATTCCTCAGCTCCACAGAGAAGAACTGCTGTG 190

17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
|||||
191 GCGGCA.CTGTACATTGACTTTAGGAAGACCTGGCTTGAAGTGTATCC 239

34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
|||||
240 ACAGAGCCCAAGGCTACCACTTGTCTGGGACCTGCCCTAT 289

51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnH 67
:::
290 ATTGGAGCTGGACACAGTACACAGAGTCTTGCCTCTACAAACCA 339

67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
|||||
340 ACACAAACCCGGCGCTCGCGCTCACCGTCTCGCGCCGAGTTNATGG 389

84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
|||||
390 AGCCACTGCCATCGCTCTACTAGTGGTGGCAAGCCCAAGTGGAGCAG 439

101 LeuSerAsnMetValValLysSerCysLysCysSer 112
|||||
440 TTGTCCAACATGATTGCGCTCGCTCGCAAGTGCAGC 475

seq_name: gb_est49:AW627667

seq_documentation_block:
LOCUS AW627667 466 bp mRNA EST 31-MAR-2000
DEFINITION hb98h10.x1 NCI_CGAP_GUL Homo sapiens cDNA clone IMAGE:2970019 3'
similar to gb:X02812_cds1 TRANSFORMING GROWTH FACTOR BETA 1
PRECURSOR (HUMAN); contains element TAR1 repetitive element ;, mRNA
sequence.

ACCESSION AW627667
VERSION AW627667.1 GI:7374457
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 466)
AUTHORS Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

JOURNAL NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
COMMENT National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapb-r@mail.nih.gov

Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Life
Technologies, Inc. cDNA Library Arrayed by: Christa Prange, The
I.M.A.G.E. Consortium DNA Sequencing by: Washington University

Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
image.lnl.gov/image/html/iresources.shtml
Seq primer: -400P from Gibco
High quality sequence stop: 378.

FEATURES
Source

1..466
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2970019"
/clone_lib="NCI_CGAP_GUL"
/tissue_type="2 pooled high-grade transitional cell
tumors"
/lab_host="DH10B"
/note="Organ: genitourinary tract; Vector: PCMV-SPORT6;
Site_1: SalI; Site_2: NotI; Cloned unidirectionally.
Primer: Oligo dt. Library constructed by Life
Technologies."

BASE COUNT 77 a 136 c 167 g 86 t
ORIGIN

alignment_scores:

Quality: 471.00 Length: 107
Ratio: 5.065 Gaps: 0
Percent Similarity: 86.916 Percent Identity: 74.766

alignment_block:

TGFB3P x AW627667/rev ..

Align seg 1/1 to reverse of: AW627667 from: 1 to: 466

6 TyrCysPheArgAsnLeuGluGluAsnCysCysValArgProLeuTyrIl 22
|||||
466 TATTGCTTCAGCTCCACGGAGAAGAACTGTTGCGTGCAGCTGTACAT 417

22 eAspPheArgGlnAspLeuGlyTrpLysTrpValHisGluProLysGlyT 39
|||||
416 TGACTCCGCAAGGACTTCGGTTGGAGTGGATCCACGAGGCCAAGGGCT 367

39 yrTyraAlaAsnPheCysSerGlyProCysProTyrLeuArgSerAlaasp 55
|||||
366 ACCATGCCAATTTGGCTCGGGCCCTGCCCTACATTTGGAGCCTGGAC 317

56 ThrThrHisSerThrValLeuGlyLeuTyrAsnThrLeuAsnProGluAl 72
|||||
316 AGCAGTACAGCAAGGTCTTGGCCCTGTACAACACGACATACCCGGCGC 267

72 aSerAlaSerProCysCysValProGlnAspLeuGluProLeuThrIleL 89
|||||
266 CTCGGCGCGCGCTGCTCGCTGCAGCGCTGGAGCGCTGCCCATCG 217

89 euTyTyTyValGlyArgThrProLysValGluGlnLeuSerAsnMetVal 105
:::
216 TGTACTACGTGGCGCCGAAGCCCAAGGTGGAGCTGTCCAACATGATC 167

106 ValLysSerCysLysCysSer 112
|||||
166 GTGGCTCTCTCAAGTGCAGC 146

seq_name: gb_est97:BG180040

seq_documentation_block:

LOCUS BG180040 431 bp mRNA EST 06-FEB-2001
DEFINITION 602329596F1 NIH_MGC_91 Homo sapiens cDNA clone IMAGE:4431214 5',
mRNA sequence.

ACCESSION BG180040
VERSION BG180040.1 GI:12686743
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 431)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
JOURNAL
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTF
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10185 row: o column: 23
High quality sequence stop: 338.
Location/Qualifiers
1. 431
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4431214"
/clone_lib="NIH_MGC_91"
/tissue_type="adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: prostate; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally; oligo-dr primed.
Average insert size 1.4 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
95 a 126 c 148 g 62 t
BASE COUNT
ORIGIN
alignment_scores:
Quality: 468.00 Length: 106
Ratio: 5.087 Gaps: 0
Percent Similarity: 86.792 Percent Identity: 75.472
alignment_block:
TGFB3P x BG180040 ..
Align seg 1/1 to: BG180040 from: 1 to: 431
7 CysPheArgAsnLeuGluAsnCysCysValArgProLeuTyrIleAs 23
||||| : : : : :
17 TGCTTCAGCTCCAGGAGAGAACTGCTGCGGCGAGCTGTATGTA 66
||||| : : : : :
23 pPheArgGluAspLeuGlyTrpLysTrpValHisGluProLysGlyTyr 40
||||| : : : : :
67 CTTCCGCAAGGACCTCGGCTGGAAGTGGATCCAGGCCCAAGGGCTACC 116
40 YrAlaAsnPheCysSerGlyProCysProTyrLeuArgSerAlaAspThr 56
: : : : :
117 ATGCCAACTTCGCTCGGCGCCCTGCCCTACATTTGGAGCTGGACAG 166
57 ThrHisSerThrValLeuGlyLeuTyrAsnThrLeuAsnProGluAlaSe 73
: : : : :
167 CAGTACAGCAAGGTCCTGGCCCTGTACAAACCAGCATAAACCGGCGCTC 216
73 rAlaSerProCysCysValProGlnAspLeuGluProLeuThrIleLeuT 90
: : : : :
217 GGGCGCGCGCTGCTGCGCGAGCGCTGGAGCGCTGCCCATCGTGT 266
90 YrTyrValGlyArgThrProLysValGluGlnLeuSerAsnMetValVal 106
: : : : :
267 ACTACGTGGGCGGCAAGCCCAAGGTGGAGCAGCTGTCCAAACATGATCGT 316
107 LysSerCysLysCysSer 112
: : : : :
317 CGCTCCTGCAAGTGCAGC 334
seq_name: gb_est26-AI927187

seq_documentation_block:
LOCUS AI927187 578 bp mRNA EST 08-MAR-2000
DEFINITION WO86C02.x1 NCI_CGAP_Kid1 Homo sapiens cDNA clone IMAGE:2462402 3'
similar to gb:X02812 cds1 TRANSFORMING GROWTH FACTOR BETA 1
PRECURSOR (HUMAN); contains element MER22 repetitive element ;, mRNA
sequence.
ACCESSION AI927187
VERSION AI927187.1 GI:5663151
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 578)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1358 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 394.
Location/Qualifiers
1. 578
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2462402"
/clone_lib="NCI_CGAP_Kid1"
/lab_host="DH10B"
/note="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with
a modified polylinker; Site_1: Not I; Site_2: Eco RI;
Plasmid DNA from the normalized library NCI_CGAP_Kid3 was
prepared, and ss circles were made in vitro. Following HAP
purification, this DNA was used as tracer in a subtractive
hybridization reaction. The driver was PCR-amplified cDNAs
from a pool of 5,000 clones made from the same library
(cloneIDs 1322376-1323911, 1456007-1456775, and
1500552-1502855). Subtraction by Bento Soares and M.
Fatima Bonaldo."
127 a 166 c 175 g 105 t 5 others
BASE COUNT
ORIGIN
alignment_scores:
Quality: 463.00 Length: 112
Ratio: 4.874 Gaps: 0
Percent Similarity: 84.821 Percent Identity: 72.321
alignment_block:
TGFB3P x AI927187/rev ..
Align seg 1/1 to reverse of: AI927187 from: 1 to: 578
1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluAsnCysCysVa 17
||||| : : : : :
475 GCTTGGATACATACTATTGNTTACCTCTATGGAGAAGAANTGCTGT 426
17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
: : : : :
425 GTGGCAGCTGTACATGTACTTCGCAAGGACTTGGTGAAGTGGATCC 376
34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
||||| : : : : :
375 ACGAGCCCAAGGGCTACCATGCCAACTTTTGGCTCGGCGCTGCCCTAC 326

Insert Length: 2004 Std Error: 0.00

Seq primer: -400P from Gbco

High quality sequence stop: 376.

FEATURES

Location/Qualifiers
 1..505
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:2132156"
 /clone_lib="NCI_CGAP_Gas4"
 /tissue_type="poorly differentiated adenocarcinoma with
 signet ring cell features"
 /lab_host="DH10b"
 /note="Organ: stomach; Vector: pCMV-SPORT6; Site_1: SalI;
 Site_2: NotI; Cloned unidirectionally. Primer: Oligo dr.
 Average insert size 1.69 kb. Life Technologies catalog #:
 11549-011"

BASE COUNT 76 a 147 c 187 g 95 t

ORIGIN

alignment_scores:
 Quality: 448.00 Length: 101
 Ratio: 5.091 Gaps: 0
 Percent Similarity: 87.129 Percent Identity: 76.238

alignment_block:

TGFB3P x AI433146/rev ..

Align seg 1/1 to reverse of: AI433146 from: 1 to: 505

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12 GluGluAsnCysCysValArgProLeuTyrIleAspPheArgGlnAspLe 28
|||||
447 GAGAAGAACTGCTGCGCGCAGCTGTACATTGACTTCGCGAAGACCT 398
|||||
28 uGlyTrpLysTrpValHisGluProLysGlyTyrTyrAlaAsnPheCys 45
|||||
397 CGCTGGGAAGTGGATCCAGCGCCCAAGGCTACCATGCCAACTTCTGCC 348
|||||
45 erGlyProCysProTyrLeuArgSerAlaAspThrHisSerThrVal 61
|||||
347 TCGGGCCCTGCCCTACATTTGGAGCCTGGACAGCAGTACAGCAAGTC 298
|||||
62 LeuGlyLeuTyrAsnThrLeuAsnProGluAlaSerAlaSerProCysCy 78
|||||
297 CTGGCCCTGTACAACACAGCATAACCGCGCGCTCGCGGCGCGCTGCTG 248
|||||
78 svAlProGlnAspLeuGluProLeuThrIleLeuTyrTyrValGlyArgT 95
|||||
247 CGTGGCGGCGCGCTGGAGCGCGCTGCCCTCGTGTACTGCGGCGCGCA 198
|||||
95 hrProLysValGluGlnLeuSerAsnMetValValLysSerCysLysCys 111
|||||
197 AGCCCAAGTGGAGCAGCTGTCCACATGATGCTGCGCTCTGCAAGTGC 148
|||||
112 Ser 112
|||
147 AGC 145

```

seq_name: gb_est30:AU016729

seq_documentation_block:

LOCUS AU016729 576 bp mRNA EST 15-OCT-1998
 DEFINITION AU016729 Mouse two-cell stage embryo cDNA Mus musculus CDNA clone
 J0728H08 3', mRNA sequence.
 ACCESSION AU016729
 VERSION AU016729.1 GI:3371733
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Vertebrata; Eutelestomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 REFERENCE 1 (bases 1 to 576)
 AUTHORS Ko, M.S.H., Kitchen, J.R., Wang, X., Threat, T.A., Sun, T., DePalma, G.E.,

TITLE Liang, Y., Kargul, G.J., Sharara, R. and Doi, H.
 Systematic analyses of genes expressed in 2-cell stage mouse
 embryos (The ERATO/Doi Project at Wayne State University) (Ko
 M.S.H. et al.)
 JOURNAL Unpublished (1998)
 COMMENT Contact: Hirofumi Doi
 Doi Biosymmetry Project, ERATO
 Japan Science and Technology Corporation (JST)
 WBG Marine East 12F, 2-6 Nakase, Mihama-ku, Chiba 261-71, Japan
 Email: hdbioa.jst.go.jp.

FEATURES

Source

1..576
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="J0728H08"
 /clone_lib="Mouse two-cell stage embryo cDNA"
 /dev_stage="two-cell stage embryo"
 BASE COUNT 144 a 123 c 134 g 164 t 11 others
 ORIGIN

alignment_scores:
 Quality: 447.00 Length: 114
 Ratio: 4.298 Gaps: 2
 Percent Similarity: 91.228 Percent Identity: 76.316

alignment_block:

TGFB3P x AU016729/rev ..

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Align seg 1/1 to reverse of: AU016729 from: 1 to: 576
1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysV 17
|||||
452 GCTTGGATGCTCGCTACTGCTTTAGAAATGTCAGGAATAATGCTGCC 403
|||||
17 alArgProLeuTyrIleAsp.PheArgGlnAspLeuGlyTrpLysTrpVa 33
|||||
402 TTTCGCCCTCTTACATGAATTTTAAAGAGGGATCTTGGATGGAATGAT 353
|||||
33 HisGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProt 50
|||||
352 CCATGAACCCAA.GGGTACATGCTAACTTCTGTGCTGGGGNATGCCAT 304
|||||
50 YrLeuArgSerAlaAspThrHisSerThrValLeuGlyLeuTyrAsn 66
|||||
303 ATCTATGGAGTTCAGACACTCAACACACCAAGCTCTCAGCCTGTACAAC 254
|||||
67 ThrLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLe 83
|||||
253 ACCATAAATCCGAACT.TCCGCTTCCCTTGTGCTGTGTGCCAGGATCT 205
|||||
83 uGluProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluG 100
|||||
204 GGAACCACTGACCATCTCTATTACATTGGAATACGCCCAAGATCGAAC 155
|||||
100 InLeuSerAsnMetValValLysSerCysLysCysSer 112
|||||
154 ACCTTCCCAATATGATGTCAAGTCTTGTAAATGCAGC 117

```

seq_name: gb_est10:AA657145

seq_documentation_block:

LOCUS AA657145 530 bp mRNA EST 04-NOV-1997
 DEFINITION v126D03.r1 Barstead mouse myotubes MPLR5 Mus musculus cDNA clone
 IMAGE:1121765 5', similar to gb:J03241 TRANSFORMING GROWTH FACTOR
 BETA 3 PRECURSOR (HUMAN); gb:M32745 mouse transforming growth
 factor beta-3 mRNA, complete (MOUSE);, mRNA sequence.
 ACCESSION AA657145
 VERSION AA657145.1 GI:2593299
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus


```

101 euSerAsnMetValLysSerCysLysCysSer 112
|||||
151 TTTCCAATATGATTGCAAGTCTTGTAAATGCAGC 117

seq_name: gb_est91:BF682484

seq_documentation_block:
LOCUS BF682484 996 bp mRNA EST 21-DEC-2000
DEFINITION 602117568r1 Soares_mammary_gland_NMLMG Mus musculus cDNA clone
IMAGE:3468737 3', mRNA sequence.
ACCESSION BF682484
VERSION BF682484.1 GI:11956379
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus.
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 996)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: M. Bento Soares, Ph.D.
cDNA Library Preparation: Bento Soares and M. Fatima Bonaldo
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM8476 row: h column: 18
High quality sequence start: 37
High quality sequence stop: 636.
High quality sequence stop: 636.
Location/Qualifiers
1..996
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:3468737"
/clone_lib="Soares_mammary_gland_NMLMG"
/sex="female (lactating)"
/tissue_type="mammary gland"
/lab_host="DH10B"
/note="Vector: p7T3D-Pac (Pharmacia) with a modified
polylinker; 1st strand cDNA was prepared from mammary
gland tissue from a lactating female, and was then primed
with a Not I - oligo(dT) primer. Double-stranded cDNA was
ligated to Eco RI adaptors (Pharmacia), digested with Not
I and cloned into the Not I and Eco RI sites of the
modified p7T3 vector. Library is normalized. Library
was constructed by Bento Soares and M. Fatima Bonaldo."
BASE COUNT 239 a 243 c 317 g 197 t
ORIGIN

alignment_scores:
Quality: 428.50 Length: 114
Ratio: 4.359 Gaps: 4
Percent Similarity: 82.456 Percent Identity: 72.807

alignment_block:
TGFB3P x BF682484/rev ..

Align seg 1/1 to reverse of: BF682484 from: 1 to: 996

2 LeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCys.CysValA 18
|||||
434 CTGATACCTACTATTGCTTCAGCTCCACAGAGAAGAACTGCTGTGTC 385
|||||

18 rgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValHis 34
||
384 GGCAGCTGTACATTGACTTTAGGAAGACCTGGGTTGGAAGTGGATCCAC 335
|||||

35 GluProLysGlyTyrTyrAlaAsnPheCysSerGly.ProCysProTyrL 51

```

```

|||||
334 GAGCCCAAGGGCTACCATGCCAACTTCTGTCTGGGACCCCTGCCCTATA 285
|||||
51 euArgSerAlaAspThrHisSerThrValLeuGlyLeuTyrAsnThr 67
:: |||
284 TTTGGAGCCTGGACACACAGTACAGCAAGGCTCTTGCCTT...CCCCCA 238
|||||
68 Leu.AspProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
|||||
237 ACACAACCCGGCGCTTCGGCGTCACCGCTGCTGCGTGGCAGGCTTGG 188
|||||
84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
|||||
187 AGCCACTGCCCATCGTCTACTACGTGGGTGCGCAAGCCCAAGGTGGAGCAG 138
|||||
101 LeuSerAsnMetValLysSerCysLysCysSer 112
|||||
137 TTGTCCAACATGATGTGCGCTCCTGCAAGTGCAGC 102

seq_name: gb_est25:A1824845

seq_documentation_block:
LOCUS A1824845 441 bp mRNA EST 16-DEC-1999
DEFINITION wb02f01.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2304505 3'
similar to gb:X02812 cds1 TRANSFORMING GROWTH FACTOR BETA 1
PRECURSOR (HUMAN); contains element TAR1 MER22 repetitive element ;,
mRNA sequence.
ACCESSION A1824845
VERSION A1824845.1 GI:5445516
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 441)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bbrp/image/image.html
Insert Length: 497 Std Error: 0.00
Seq primer: -400P from Gibco
High quality sequence stop: 347.
Location/Qualifiers
1..441
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2304505"
/clone_lib="NCI_CGAP_GC6"
/tissue_type="pooled germ cell tumors"
/lab_host="DH10B"
/note="Vector: p7T3D-Pac (Pharmacia) with a modified
polylinker; plasmid DNA from the normalized library
NCI-CGAP_GC4 was prepared, and ss circles were made in
vitro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from a pool of 5,000 clones made
from the same library (cloneIDs 1257096-1258631,
1469064-1470983, and 1475592-1476743). Subtraction by
Bento Soares and M. Fatima Bonaldo."
BASE COUNT 66 a 129 c 165 g 81 t
ORIGIN

```

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alignment_scores:
  Quality: 426.00      Length: 97
  Ratio: 5.071         Gaps: 0
  Percent Similarity: 86.598  Percent Identity: 76.289

alignment_block:
  TGF3P x AI824845/rev ..

Align seg 1/1 to reverse of: AI824845 from: 1 to: 441

16 CysValArgProLeuTyrIleAspPheArgGlnAspLeuGlyTyrPlystr 32
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
439 TCGTGGCGGACGCTGATCTGACCTCCGAGGAGGACCTCGGCTGGAAGTG 390
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||

32 pValHisGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysP 49
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
389 GATCCAGGAGCCCAAGGCTACCATGCAACTCTGCTCGGGCCCTGCC 340
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||

49 roTyrLeuArgSerAlaAspThrHisSerThrValLeuGlyLeuTyr 65
|||||  |||  |||||  |||||  |||||  |||||  |||||  |||||
339 CCTACATTGGAGCGCTGGACAGCGAGTACAGCAAGGCTCTGGCCCTGTAC 290
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||

66 AsnThrLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAs 82
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
289 AACCAAGCATACCCGGCGCTCGGGCGCGCTGCTGCTGCCGAGGC 240
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||

82 pLeuGluProLeuThrIleLeuTyrTyrValGlyArgThrProLysValG 99
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
239 GCTGAGCGCGTCCCATCGTGTACTAGTGGCGCGCAAGCCAGGTGG 190
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||

99 LuGlnLeuSerAsnMetValValLysSerCysLysCysSer 112
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
189 AGCAGCTGTCAACATGATGTGTGCTCTCTGCAAGTGCAGC 149
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||

```

```
seq_name: gb_est23:AI654506
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```

seq_documentation_block:
LOCUS AI654506 460 bp mRNA EST 17-DEC-1999
DEFINITION wp63404.x1 NCI-CGAP_G06 Homo sapiens cDNA clone IMAGE:2310343 3'
similar to gb:X02812_cds1 TRANSFORMING GROWTH FACTOR BETA 1
PRECUSOR (HUMAN); contains PTRS.t3 PTR5 MSRI repetitive element ;
mRNA sequence.
ACCESSION AI654506
VERSION AI654506.1 GI:4738485
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 460)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps@mail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 519 Std Error: 0.00
Seq primer: -400P from Gibco
High quality sequence stop: 206.
FEATURES
source Location/Qualifiers
1..460
/organism="Homo sapiens"
/db_xref="taxon:9606"

```

```

/clone="IMAGE:2310343"
/clone_lib="NCI-CGAP_G06"
/tissue_type="pooled germ cell tumors"
/lab_host="DH10B"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Plasmid DNA from the normalized library
NCI-CGAP_G04 was prepared, and ss circles were made in
vitro. Following RAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from a pool of 5,000 clones made
from the same library (cloneIDs 1257096-1258631,
1469064-1470983, and 1475592-1476743). Subtraction by
Bento Soares and M. Fatima Bonaldo."
BASE COUNT 68 a 131 c 166 g 93 t 2 others
ORIGIN

alignment_scores:
  Quality: 426.00      Length: 101
  Ratio: 4.953         Gaps: 0
  Percent Similarity: 85.149  Percent Identity: 74.257

alignment_block:
  TGF3P x AI654506/rev ..

Align seg 1/1 to reverse of: AI654506 from: 1 to: 460

12 GluGluAsnCysCysValArgProLeuTyrIleAspPheArgGlnAspLe 28
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
458 GAAAGAAGTGTGCTGGTGGCGGAGCTGTACATTGCTCCGCAAGGACCT 409
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||

28 uGlyTyrLysTyrValHisGluProLysGlyTyrTyrAlaAsnPheCys 45
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
408 CGGCTGGAAGTGTATCCCGGAGCCCAAGGCTACCATGCCAACTTNTGCC 359
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||

45 erGlyProCysProTyrLeuArgSerAlaAspThrHisSerThrVal 61
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
358 TCGGGCGCTGCCCTACATTGGAGCCTGGACAGCAGTACAGCAAGGTC 309
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||

62 LeuGlyLeuTyrAsnThrLeuAsnProGluAlaSerAlaSerProCysC 78
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
308 CTGGCCCTGTACACAGCATATACCCGGCGCTCGGGCGCGCGTGTG 259
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||

78 sValProGlnAspLeuGluProLeuThrIleLeuTyrTyrValGlyArg 95
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
258 CGTGGCGGAGCGCTGGACCGCTGCCATTGTGTACTAGTGGCGCGCA 209
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||

95 hrProLysValGluGlnLeuSerAsnMetValValLysSerCysLysCys 111
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
208 AGCCCAAGTGGAGCAGCTGCCAACATGATCGTGGCTCTCTGCAAGTGC 159
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||

112 Ser 112
158 AGC 156

seq_name: gb_est1:AA049522

seq_documentation_block:
LOCUS AA049522 477 bp mRNA EST 09-SEP-1996
DEFINITION mj35f01.r1 Soares mouse embryo NDME13.5 14.5 Mus musculus cDNA
clone IMAGE:478105 5' similar to gb:X02812_cds1 TRANSFORMING GROWTH
FACTOR BETA 1 PRECURSOR (HUMAN); gb:M32745 mouse transforming
growth factor beta-3 mRNA, complete (MOUSE);, mRNA sequence.
ACCESSION AA049522
VERSION AA049522.1 GI:1529194
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 477)
AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,

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Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wyllie,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.

TITLE JOURNAL COMMENT

The WashU-HHMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project

WashU-HHMI Mouse EST Project
Washington University School
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810

Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.

MGI:288849
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 450.

FEATURES source

Location/Qualifiers
1. 477
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:478105"
/sex="unknown"
/tissue_type="embryo"
/dev_stage="13.5-14.5dpc total fetus"
/lab_host="DH10B"

/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site.1: Not I; Site.2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5',
TGTGACCAATCTGAAGTGGGAGCGCGCGGAATTTTGTGTTTTTTT
T 3'], on equal amounts of mRNA from 2 13.5dpc and 2
14.5dpc embryos [total RNA provided by Minoru Ko, Wayne
State Univ., from 2]; double-stranded cDNA was ligated to
Eco RI adaptors (Pharmacia), digested with Not I and
cloned into the Not I and Eco RI sites of the modified
pT7T3 vector. Library went through one round of
normalization, and was constructed by Bento Soares and
M.Fatima Bonaldo."

BASE COUNT 105 a 155 c 126 g 91 t
ORIGIN

alignment_scores:
Quality: 426.00 Length: 108
Ratio: 4.532 Gaps: 0
Percent Similarity: 87.037 Percent Identity: 75.926

alignment_block:
TGFB3P x AA049522 ..

Align seg 1/1 to: AA049522 from: 1 to: 477

1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluAlaAsnCysCysVa 17
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
142 GCCTGGATGACCAACATTTGCTGCTAC.TCCACAGAGAAGAAGCTGTGT 190
17 laArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
191 GCGGCA.CTGTACATTGACTTTAGGAGGACCTGGGTGGAGTGGATCC 239
34 isGluProLysGlyTyrTyraAlaAsnPheCysSerGlyProCysProTy 50
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
240 ACGAGCCCAAGGCGTACCATGCCAACTTCTGTCTGGGACCCCTGCCCTAT 289
51 LeuArgSerAlaAspThrThrTrhisSerThrValLeuGlyLeuTyrAsnTh 67
::: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
290 ATTTGGAGCGCTGGACACAGTACAGCAAGGTCCTTGCCTCTACAAACCA 339
67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
340 ACACACCCGGCGCTTCGGCGGTACCGGTCTGCTGCGCCGACAGTTTGG 389

84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
||||| |||:::||||| ||||||| ||||||| ||||||| ||||||| |||||||
390 AGCCACTGCCCATCGTCTACTAGTGGTGGCGCAAGCCCAAGGTGGAGCAG 439
101 LeuSerAsnMetValValLysSer 108
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
440 TTGTCCAACATGATTGTGCGCTCC 463
seq_name: gb_est18:AI273619

seq_documentation_block:
LOCUS AI273619 499 bp mRNA 29-JAN-1999
ql56c01.x1 Soares.NHMPU_S1 Homo sapiens cDNA clone IMAGE:1876320
3' similar to gb:X02812.cds1 TRANSFORMING GROWTH FACTOR BETA 1
PRECURSOR (HUMAN);contains PTR5.t3 PTR5 repetitive element ;, mRNA
sequence.

ACCESSION AI273619
VERSION AI273619.1 GI:3895887
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 499)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-r@mail.nih.gov
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.

Insert Length: 760 Std Error: 0.00
Seq primer: -400P from Gibco
High quality sequence stop: 366.
Location/Qualifiers
1. 499

FEATURES Source

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1876320"
/clone_lib="Soares.NHMPU_S1"
/tissue_type="Pooled human melanocyte, fetal heart, and
pregnant uterus"
/lab_host="DH10B"

/note="Organ: mixed (see below); Vector: pT7T3D-Pac
(Pharmacia) with a modified polylinker; Site.1: Not I;
Site.2: Eco RI; Equal amounts of plasmid DNA from three
normalized libraries (melanocyte 2NbHM, pregnant uterus
NBHPU, and fetal heart NBH19W) were mixed, and ss circles
were made in vitro. Following HAP purification, this DNA
was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from pools of
5,000 clones made from the same 3 libraries. The pools
consisted of I.M.A.G.E. clones 260232-265223,
340488-345479, and 484488-489479."

BASE COUNT 84 a 131 c 170 g 113 t 1 others
ORIGIN

alignment_scores:
Quality: 422.00 Length: 110
Ratio: 4.587 Gaps: 2
Percent Similarity: 83.636 Percent Identity: 70.000

alignment_block:
TGFB3P x AI273619/rev ..

Align seg 1/1 to reverse of: AI273619 from: 1 to: 499

5 AsnTyrCys.PheArgAsnLeuGluGlnAsnCysCysValArgPro.Leu 20
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
492 AATTTTGTGTTCTCCGCCGAAAAAAATTTGTTGGTGGGCCCAAGTTG 443

```

21 TyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValHisGluProLys 37
|||||  ::::::::::::::::::::::::::::::::::::::::::::
442 TACATTGCTCGCAGAGGAGCTGGTGGAGTGATCCACGAGCCCAA 393

37 sGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyrIleuArgSera 54
|||||  ::::::::::::::::::::::::::::::::::::::::::::
392 GGGCTACCATGCTCAACTTTTGGCGGGCCCTGCCCCCTACATTGGAGACC 343

54 laAspThrThrHisSerThrValLeuGlyLeuTyrAsnThrLeuAsnPro 70
|||||  ::::::::::::::::::::::::::::::::::::::::::::
342 TGGACACGACGTACAGCAAGTCTCTGGCCCTGTACAACACGACATAACCG 293

71 GluAlaSerAlaSerProCysCysValProGlnAspLeuGluProLeuTh 87
|||||  ::::::::::::::::::::::::::::::::::::::::::::
292 GCGCCTCGCGCGCGCGCTTNTGCGTGGCGCGCGCGCTGGAACCCCTGCC 243

87 rIleLeuTyrTyrValGlyArgThrProLysValGluGlnLeuSerAsnM 104
|||||  ::::::::::::::::::::::::::::::::::::::::::::
242 CATTTGTGTACTACGTGGCGCGCAAGCCCAAGTGGAGCAACTGTCCAACA 193

104 etValValLysSerCysLysCysSer 112
|||||  ::::::::::::::::::::::::::::::::::::::::::::
192 TGATCGTGGCTCTCGCAAGTGCAC 167

seq_name: gb_est18:AI272940

seq documentation_block: 292 bp mRNA EST 18-NOV-1998
LOCUS AI272940
DEFINITION gl56g01.x1 Soares_NhMHPu_S1 Homo sapiens cDNA clone IMAGE:1876368
3' similar to gb:X02812_cds1 TRANSFORMING GROWTH FACTOR BETA 1
PRECURSOR (HUMAN):contains element MER22 repetitive element ;, mRNA
sequence.
ACCESSION AI272940
VERSION AI272940.1 GI:3895208
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 292)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TUMOR National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
TITLE Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-r@mail.nih.gov
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Seq primer: -40UP from Gibco
High quality sequence stop: 1.
FEATURES
source
1. .292
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1876368"
/clone_lib="Soares_NhMHPu_S1"
/tissue_type="Pooled human melanocyte, fetal heart, and
pregnant uterus"
/lab_host="DH10B"
/note="Organ: mixed (see below); Vector: pT73D-Pac
(Pharmacia) with a modified polylinker; Site.1: Not I;
Site.2: Eco RI; Equal amounts of plasmid DNA from three
normalized libraries (melanocyte 2NDHM, pregnant uterus
NHDPu, and fetal heart NHH19W) were mixed, and ss circles
were made in vitro. Following HAP purification, this DNA
was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from pools of
5,000 clones made from the same 3 libraries. The pools
consisted of I.M.A.G.E. clones 260322-265223,
340488-345479, and 484488-489479."
BASE COUNT 55 a 87°C 95 g 55 t

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ORIGIN

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alignment_scores:
Quality: 416.00 Length: 97
Ratio: 5.012 Gaps: 0
Percent Similarity: 85.567 Percent Identity: 74.227

alignment_block:
TGFB3P x AI272940/rev ..
Align seg 1/1 to reverse of: AI272940 from: 1 to: 292

16 CysValArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTr 32
|||||  ::::::::::::::::::::::::::::::::::::::::::::
292 TCGCGCGCGCAGTTGTACATTGACTTCCGCAAGGACCTCGCTGGAAGTG 243

32 pValHisGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysP 49
|||||  ::::::::::::::::::::::::::::::::::::::::::::
242 GATCACAAAGCCCAAGGCTACCATGCCAACTTTGCCCTCGGGCCCTGCC 193

49 rOTyrLeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyr 65
|||||  ::::::::::::::::::::::::::::::::::::::::::::
192 CCTACATTGGAGCCTGGACACGACGACGACGAGTTCTGGCCCTGTAC 143

66 AsnThrLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAs 82
|||||  ::::::::::::::::::::::::::::::::::::::::::::
142 AACCAGCATAAACCGCGCGCTTGGCGCGCGCTGCTGCGTGGCCGAGGC 93

82 pLeuGluProLeuThrIleLeuTyrTyrValGlyArgThrProLysValG 99
|||||  ::::::::::::::::::::::::::::::::::::::::::::
92 GCTGGAGCCCTCGCCACTGTGTACTACGTGGCGCGCAAGCCCAAGGTGG 43

99 luGlnLeuSerAsnMetValValLysSerCysLysCysSer 112
|||||  ::::::::::::::::::::::::::::::::::::::::::::
42 ACCAACTGTCCAACATGATTGTGCGCTCTCTGCAAGTGCAGC 2

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seq_name: gb_est18:AI304490

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seq documentation_block: 449 bp mRNA EST 01-FEB-1999
LOCUS AI304490
DEFINITION q054e06.x1 NCI-CGAP_C08 Homo sapiens cDNA clone IMAGE:1912354 3'
similar to gb:X02812_cds1 TRANSFORMING GROWTH FACTOR BETA 1
PRECURSOR (HUMAN):contains PTR5.L3 TAR1 repetitive element ;, mRNA
sequence.
ACCESSION AI304490
VERSION AI304490.1 GI:3988179
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 449)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert length: 933 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 385.
Location/Qualifiers
1. .449
/organism="Homo sapiens"

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/db_xref="taxon:9606"
/clone="IMAGE:1912354"
/clone_lib="NCI_CGAP_C08"
/tissue_type="adenocarcinoma"
/lab_host="DH10B"
/note="Organ: colon; Vector: pT73B-Pac (Pharmacia) with a
modified polylinker; 1st strand cDNA was prepared from
colon adenocarcinoma, and was then primed with a Not I -
oligo(dT) primer. Double-stranded cDNA was ligated to Eco
RI adaptors (Pharmacia), digested with Not I and cloned
into the Not I and Eco RI sites of the modified pT73
vector. Library is normalized. Library was constructed by
Bento Soares and M. Fatima Bonaldo."
BASE COUNT      66 a 128 c 163 g  92 t
ORIGIN

```

```

alignment_scores:
  Quality: 416.00      Length: 93
  Ratio: 5.073         Gaps: 0
  Percent Similarity: 88.172 Percent Identity: 77.419

alignment_block:
TGFB3P x AI304490/rev ..

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Align seg 1/1 to reverse of: AI304490 from: 1 to: 449

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20 LeuTyriLeAspPheArgGlnAspLeuGlyTrpLysTrpValHisGluPr 36
|||||
444 CTGTACATTGACTTCGCAAGACCTCGGCTGGAAGTGGATCCACGAGCC 395
|||||
36 oLysGlyTyTrAlaAsnPhcCysSerGlyProCysProTyTrLeuArgS 53
|||||
394 CAAGGGCTACCATGCGCAACTTTTGCTCGGGCCCTGCCCTACATTGGA 345
|||||
53 erAlaAspThrHisSerThrValLeuGlyLeuTyTrAsnThrLeuAsn 69
|||||
344 GCCTGGACAGCGAGTACAGCAAGTCTGGCCCTGTACACACGACATAAC 295
|||||
70 ProGluAlaSerAlaSerProCysCysValProGlnAspLeuGluProLe 86
|||||
294 CCGGGCGCTCGCGCGCGCTGCTGCTGCCGCGCGCTGGAGCGGCT 245
|||||
86 uThrLeuTyTrTyValGlyArgThrProLysValGluGlnLeuSera 103
|||||
244 GCCCATCGTGTACTAGTGGCGGCAAGCCCAAGTGGAGCAGCTGTCCA 195
|||||
103 snMetValValLysSerCysLysCysSer 112
|||||
194 ACATGATCGTGGCTCCTCGCAAGTGCAGC 166
|||||

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seq_name: gb_est17:AI192407

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seq_documentation_block:
LOCUS      AI192407      348 bp      mRNA      EST      28-OCT-1998
DEFINITION qc98c09.x1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone
IMAGE:1722256 3' similar to gb:Y00083 TRANSFORMING GROWTH FACTOR
BETA 2 PRECURSOR (HUMAN); mRNA sequence.
ACCESSION  AI192407
VERSION     AI192407.1 GI:3743616
KEYWORDS   EST.
SOURCE      human.
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 348)
AUTHORS    NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE      National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL     Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            This clone is available royalty-free through LNL; contact the

```

```

IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 672 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 157.
FEATURES             Location/Qualifiers
     source            1..348
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1722256"
                     /clone_lib="Soares_pregnant_uterus_NbHPU"
                     /sex="female"
                     /dev_stage="adult"
                     /lab_host="DH10B"
     Site_2: Eco RI: 1st strand cDNA was primed with a Not I -
oligo(dT) primer [5',
AACTGGAAGAAATCCGGCGCCCTTTTTTTTTTTTTTTTTTTT 3'],
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT73 vector. Library
went through one round of normalization. Library
constructed by M. Fatima Bonaldo."
BASE COUNT      91 a 78 c 85 g  93 t  1 others
ORIGIN

```

```

alignment_scores:
  Quality: 414.00      Length: 88
  Ratio: 5.111         Gaps: 0
  Percent Similarity: 92.045 Percent Identity: 78.409

alignment_block:
TGFB3P x AI192407/rev ..

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Align seg 1/1 to reverse of: AI192407 from: 1 to: 348

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1 AlaLeuAspThrAsnTyrcysPheArgAsnLeuGluGluAsnCysCysVa 17
|||||
265 GCTTTGGATGGCGCTATTGCTTTAGAAATGTGAGGATAATTGCTGCTT 216
|||||
17 lArgProLeuTyriLeAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
|||||
215 ACGTCCACTTTACATTGATTTCAAGAGGATCTAGGTGGAAATGGATAC 166
|||||
34 isGluProLysGlyTyTrAlaAsnPhcCysSerGlyProCysProTyTr 50
|||||
165 ACGAACCCAAAGGGTACAATGCCAACTTCTGTGCTGGAGCATGCCGTAT 116
|||||
51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyTrAsnTh 67
|||||
115 TTATGGAGTTTCAGACACTCAGCACAGCAGGGTCTCTGAGCTTATATAATAC 66
|||||
67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
|||||
65 CATAAATCCAGAGCATCTGCTTCTCTCTGCTGCTGCCGCCAAGATTAG 16
|||||
84 luProLeuThrIle 88
|||||
15 AACCTCTAACCAT 2

```

seq_name: gb_est20:AI421250

```

seq_documentation_block:
LOCUS      AI421250      540 bp      mRNA      EST      28-MAR-1999
DEFINITION tf1402.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2096163 3'
similar to gb:X02812_cds1 TRANSFORMING GROWTH FACTOR BETA 1
PRECURSOR (HUMAN); contains element TAR1 repetitive element; mRNA
sequence.
ACCESSION  AI421250
VERSION     AI421250.1 GI:4267181
KEYWORDS   EST.
SOURCE      human.
ORGANISM    Homo sapiens

```



```

41 laasnPheCysSerGlyProCysProTyrLeuArgSerAlaAspThrThr 57
|||||
159 CCAACTTCTGTGTGGAGCATGCCGCTATTATGGAGTTCCAGACACTCAG 110
|||||
58 HisSerThrValLeuGlyLeuTyrAsnThrLeuAsnProGluAlaSerAl 74
|||||
109 CACAGCAGGCTCTGAGCTTATATATACATAAATCCAGAAGCATCTGC 60
|||||
74 aserProCysCysValProGlnAspLeuGluProLeuThrIleLeuTyr 91
|||||
59 TTTCTCTTCTGCTGTCCTCCAGATTAGAACCTCTAACCACTTCTCTATT 10
|||||
91 yrVal 92
|||||
9 ACATC 5

```

seq_name: gb_est29:AL530080

```

seq_documentation_block:
LOCUS AL530080 798 bp mRNA EST 13-FEB-2001
DEFINITION AL530080 LTI_NFL001_NBC4 Homo sapiens cDNA clone CS0DD009YM06 3
prime, mRNA sequence.

```

```

ACCESSION AL530080
VERSION AL530080.1 GI:12793573
KEYWORDS EST.
SOURCE human.

```

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 798)
Li.W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization

JOURNAL

Unpublished (2001)

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 Evry cedex - France

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES

source

```

1..798
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0DD009YM06"
/clone_lib="LTI_NFL001_NBC4"
/sex="male"
/tissue_type="neuroblastoma cells"
/lab_host="DH10B"
/notes="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed
by life technologies. Contact : Feng Liang Life
Technologies, a division of Invitrogen 9800 Medical Center
Drive Rockville, Maryland 20850, USA Fax : (1) 301 610
8371 Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com"

```

```

BASE COUNT 142 a 228 c 274 g 145 t 9 others
ORIGIN

```

alignment_scores:

```

Quality: 400.50 Length: 110
Ratio: 4.500 Gaps: 1
Percent Similarity: 80.909 Percent Identity: 66.364

```

alignment_block:

TGFB3P x AL530080/rev ..

Align seg 1/1 to reverse of: AL530080 from: 1 to: 798

```

1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
|||||

```

```

402 GCCCTGGACACCAACTATTGCTTCAGCTCCACGGAGAACTGCTGCGT 353
17 larProLeuTyrIleAspPheArgGlnAspLeuGlyTrpIlystrpValH 34
|||||
352 GCGCAGCTGTACATTAACCTCCGCAAGACCTCGCTGGGAGTGGATCC 303
|||||
34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
|||||
302 ACGAGCCCAAGGGCTWCCATGCCAACTTCTGCTCGGGCCCTGCCCTAC 253
|||||
51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
|||||
252 ATTTGGAGCCCTGGACACGAGCAGCAAGGTCCTGGCCCTGTACAACA 203
|||||
67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
|||||
202 GCATAACCCGGGCTCGCGGGGCC...GTGCGCGTGGCGAGCGGCTGG 156
|||||
84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
|||||
155 AGCGCTGCCCTTCGTGTACTACGTGGGCGCAAGCCCAAGGTGGGCGG 106
|||||
101 LeuSerAsnMetValValLysSerCysLys 110
|||||
105 CTGTCCAAACATGGTGTGCTCTCTGCAAG 76
|||||

```

seq_name: gb_est49:AW600938

seq_documentation_block:

```

LOCUS AW600938 267 bp mRNA EST 23-MAR-2000
DEFINITION RC1-BN0014-210100-012-c03_1 BN0014 Homo sapiens cDNA, mRNA
sequence.

```

ACCESSION AW600938

VERSION AW600938.1 GI:7305677

KEYWORDS EST.

SOURCE human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 267)

HCGP <http://www.ludwig.org.br/ORESTES>.

The FAPESP/LICR Human Cancer Genome Project

Unpublished (1999)

JOURNAL

Contact: Simpson A.J.G.

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar,

01509-010, Sao Paulo-SP,

Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC1&t2=RC1-BN0014-210100-012-c03_1&t3=2000-01-21&t4=1)

Seq primer: puc 18 forward

High quality sequence stop: 257.

FEATURES

Location/Qualifiers

```

1..267
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="BN0014"
/dev_stage="Adult"

```

```

/note="Organ: breast_normal; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the puc 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

```

BASE COUNT 69 a 52 c 62 g 84 t

ORIGIN

```

alignment_scores:
  Quality: 400.00      Length: 86
  Ratio: 5.063         Gaps: 0
  Percent Similarity: 91.860  Percent Identity: 80.233

alignment_block:
  TGF3P x AW600938/rev ..

Align seg 1/1 to reverse of: AW600938 from: 1 to: 267

27 AspLeuGlyTyrPLeuHisGluProLysGlyTyrAlaAsnPh 43
265 GATCTAGGTTGAAATGGATACCAACCAAGGATCAATGCCAATT 216
43 eCysSerGlyProCysProTyrLeuArgSerAlaAspThrThrHisserT 60
215 CTGCTCGGAGCATGCCGTATTTATGGATTCACACACTCAGCACAGCA 166
60 hrValLeuGlyLeuTyrAsnThrLeuAsnProGluAlaSerAlaSerPro 76
165 GGGCTCTGAGCTTATATATACCAATAATCCAGAAATCCAGAACATCTGCTACTCT 116
77 CysCysValProGlnAspLeuGluProLeuThrIleLeuTyrTyrValCl 93
115 TGCTCGGTGCCAGATTAGAACCTCTAACCATTTCTACTACATGG 66
93 YargThrProLysValGluGlnLeuSerAsnMetValValLysSerCysL 110
65 CAACACCCCAAGATTGACACGCTTCTAATATGATTGTAAAGTCTTGCA 16
110 yCysSer 112
15 AATGCAGC 8

```

```
seq_name: gb_est1:AA021815
```

```

seq_documentation_block:
  LOCUS      AA021815      558 bp      mRNA      EST      21-JAN-1997
  DEFINITION  mh85d06.r1 Soares mouse placenta 4NbMP13.5 14.5 Mus musculus CDNA
              clone IMAGE:457739 5' similar to gb:X02812.cds1 TRANSFORMING GROWTH
              FACTOR BETA 1 PRECURSOR (HUMAN); gb:M32745 mouse transforming
              growth factor beta-3 mRNA, complete (MOUSE);, mRNA sequence.
  ACCESSION  AA021815
  VERSION    AA021815.1 GI:1485570
  KEYWORDS   EST.
  SOURCE     house mouse.
             Mus musculus
             Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
  REFERENCE  1 (bases 1 to 558)
  AUTHORS    Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
             Geisler,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
             Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
             Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
             Waterston,R.
  TITLE      The WashU-HMI Mouse EST Project
  JOURNAL    Unpublished (1996)
  COMMENT    Contact: Marra M/Mouse EST Project
             WashU-HMI Mouse EST Project
             Washington University School
             4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
             Tel: 314 286 1800
             Fax: 314 286 1810
             Email: mouseest@watson.wustl.edu
             This clone is available royalty-free through LLNL; contact the
             IMAGE Consortium (info@image.llnl.gov) for further information.
             MGI:274627
  Seq primer: -28M13 rev2 from Amersham
  High quality sequence stop: 454.
             Location/Qualifiers
             1..558
             /organism="Mus musculus"

```

```

FEATURES
  source

```

```

/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:457739"
/clone_lib="Soares mouse placenta 4NbMP13.5 14.5"
/sex="unknown"
/tissue_type="placenta"
/dev_stage="adult"
/lab_host="DH10B"
/notes="Organ: placenta; Vector: pT7T3D-Pac (Pharmacia)
with a modified polylinker; Site_1: Not I; Site_2: Eco RI;
1st strand cDNA was primed with a Not I - oligo(dT) primer
[5',
TGTACCAATCTGAAGTCGGAGCGCGCGGAAATTTTTTTTTTTTTTTTTTTT
T 3']; double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT7T3 vector. Library
went through one round of normalization, and was
constructed by Bento Soares and M.Fatima Bonaldo."
BASE COUNT      130 a      172 c      150 g      105 t      1 others
ORIGIN

```

```

alignment_scores:
  Quality: 399.50      Length: 103
  Ratio: 4.540         Gaps: 2
  Percent Similarity: 85.437  Percent Identity: 74.757

alignment_block:
  TGF3P x AA021815 ..

```

```
Align seg 1/1 to: AA021815 from: 1 to: 558
```

```

1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
222 GCCTGGATACCAACTATTGCTTCAGCTCCACAGAGAAGAACTGCTGTG 271
17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTyrLysTrpValH 34
272 GCGGCAGTNGTACATTGACTTGTAGGAAGGACCTGGGTGGAGTGGATCC 321
34 isGluProLysGlyTyrTyrAlaAsnPhCysSerGlyProCysProTyr 50
322 ACAGAGCCCAAGGCTACCATGCCAATTCTGTCTGGGACCCCTGCCCTAT 371
51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
372 ATTTGGAGCTGGACACACAGTACAGCAAGGTCCTTCCCTCTACACCA 421
67 rLeuAsnProGluAlaSerAlaSerProCysCysValPro.GlnAspLeu 83
422 ACACAACCCGGCGCTTCGGCGTCCACCGTGGTGGCGGACGT...TTG 468
84 GluProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGl 100
469 GAGCCACTGCCCATCTCTACTACTAGTGGTGGTGGCAA.CCCAAGGTGGAGCA 517
100 nLeuSer 102
518 GTTGTC 524

```

```
seq_name: gb_est111:W98872
```

```

seq_documentation_block:
  LOCUS      W98872      431 bp      mRNA      EST      16-JUL-1996
  DEFINITION  mf89e01.r1 Soares mouse embryo NDME13.5 14.5 Mus musculus CDNA
              clone IMAGE:421464 5' similar to gb:X02812.cds1 TRANSFORMING GROWTH
              FACTOR BETA 1 PRECURSOR (HUMAN);, mRNA sequence.
  ACCESSION  W98872
  VERSION    W98872.1 GI:1428996
  KEYWORDS   EST.
  SOURCE     house mouse.
             Mus musculus
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

```

REFERENCE
AUTHORS
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 431)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,K.
The WashU-HHMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:256016
Seq primer: ETPprimer
High quality sequence stop: 1.
Location/Qualifiers
1..431
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:421464"
/clone_lib="Soares mouse embryo NDME13.5 14.5"
/sex="unknown"
/tissue_type="embryo"
/dev_stage="13.5-14.5dpc total fetus"
/lab_host="DH10B"
/notes="Vector: pPT73D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5',
TGTTCACCAATCTGAAGTCGGAGCGCGCGGAAATTTTTTTTTTTTTTTT
T 3'], on equal amounts of mRNA from 2 13.5dpc and 2
14.5dpc embryos [total RNA provided by Minoru Ko, Wayne
State Univ., from 2 ]; double-stranded cDNA was ligated to
Eco RI adaptors (Pharmacia), digested with Not I and
cloned into the Not I and Eco RI sites of the modified
pT73 vector. Library went through one round of
normalization, and was constructed by Bento Soares and
M.Fatima Bonaldo.
61 a 138 c 117 g 85 t

BASE COUNT
ORIGIN

alignment_scores
Quality: 395.00 Length: 107
Ratio: 4.438 Gaps: 0
Percent Similarity: 83.178 Percent Identity: 71.028

alignment_block
TGFB3P x W98872
..
Align seg 1/1 to: W98872 from: 1 to: 431
1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGlnAsnCysCysVa 17
|||||
98 GCCTGGATACCAACTATTGCTTCACGCTCCACAGAGAAGACGCTGTGT 147
|||||
17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTyrLysTrpValH 34
|||||
148 GCGGCAGTGCTACATTGACTTTAGGAAGGACCTGGCTTGGAGTGGATCC 197
|||||
34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
|||||
198 ACGAGCCCAAGGCGCTACCATGCCAAGCTTCTGTCTGGGACCGCTCCCTAT 247
|||||
51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
::: ||| ||||| ::::: |||||:::|||||

```

```

248 ATTGGAGCCCTGGACACACAGCTACAGCAAGGTCTTGGCCCTCTACAACA 297
67 rLeuAsnProGluAlaSerProCysCysValProGlnAspLeuG 84
||||| ||||||| ||||||| ||||||| ||||||| |||||||
298 ACACAACCCGGCGCTTCGGGTCTACCGTGTCTGCGTGGCGCAGTT.TGGG 346
84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
|||||:::|||||:::|||||:::|||||:::|||||:::|||||
347 AGCCACTGGTCTATGCTACTACGTGGGGGCAAGCCAGCGGTGTGTG.CAG 395
101 LeuSerAsnMetValValLys 107
||||| ||||||| |||:::
396 TTGTCCAACATGGATGCGC 416
seq_name: gb_est103:C87366

seq_documentation_block:
LOCUS C87366 587 bp mRNA EST 11-MAR-1998
DEFINITION C87366 Mouse fertilized one-cell-embryo cDNA Mus musculus cDNA
clone J0244G10 3', mRNA sequence.
ACCESSION C87366
VERSION C87366.1 GI:2919323
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 587)
AUTHORS Ko,M.S.H, Kitchen,J.R., Wang,X., Wang,X., Threat,T.A., Sun,T.,
DePalma,G.E., Liang,Y., Kargul,G.J., Sharara,R., Paonessa,P.D. and
Doi,H.
TITLE Systematic analyses of genes expressed in fertilized mouse eggs(The
ERATO/Doi project at Wayne State University)
JOURNAL Unpublished (1998)
COMMENT Contact: Hirofumi Doi
Doi Biosymmetry Project, ERATO
Japan Science and Technology Corporation (JST)
WBG Marive East 12F, 2-6 Nakase, Mihama-ku, Chiba 261-71, Japan
Email: hdo@bio.jst.go.jp.
FEATURES
source
1..587
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="J0244G10"
/dev_stage="fertilized one-cell-embryo"
/dev_stage="fertilized one-cell-embryo"
BASE COUNT 147 a 128 c 140 g 166 t 6 others
ORIGIN

alignment_scores
Quality: 393.00 Length: 110
Ratio: 4.052 Gaps: 3
Percent Similarity: 88.182 Percent Identity: 71.818

alignment_block
TGFB3P x C87366/rev ..
Align seg 1/1 to reverse of: C87366 from: 1 to: 587
6 TyrCysPheArgAsnLeuGlu.GluAsnCysCysVal.ArgProLeuTyr 21
|||||
438 TACTCGCTTTAGAAATGTGAGGATAATGCTGCTGCTTNGCCCTCTTTAC 389
22 lIleAsp.PheArgGlnAspLeuGlyTyrLysTrpValHisGluProLysG 38
:::|||||:::|||||:::|||||:::|||||:::|||||
388 ATGGATTTTTAAGAGGNATCTGGATGGATGGATGATCCATGAACCA.G 340
|||||
38 lYrTyrAlaAsnPheCysSerGlyProCysProTyrLeuArgSerAla 54
|||||
339 GGTACATGCTAACTTCGTCTGCTGGGGCATGCCATATCTATGGAGTTCA 290

```

Percent Similarity: 79.279 Percent Identity: 64.865

alignment_block:
TGFB3P x BG058796/rev ..

Align seg 1/1 to reverse of: BG058796 from: 1 to: 403

```

1 AlALeuAspThrAsnTyrCysPheArgAsnLeuGluAsnCysCysVa 17
||||| ||||| ||||| :||| :||| :||| :||| :|||
334 GCCCTGGACACCAACTAGTCCTTCAGCTCCAGCTAGAAGAAATGATGAGT 285

17 largProLeuTyrIleAspPheargGlnaspLeuGlyTrpLysTrpValH 34
||||| ||||| ||||| ||||| :||| :||| :||| :||| :|||
284 TCGACAGCTGTACATTGACTTCGCAGGACATAGCTCGGAAGTGGATGCC 235

34 iSgluPrOlysGlyTyrtYrAlaAsnPheCysSerGlyProCysProTyr 50
||||| ||||| ||||| ||||| :||| :||| :||| :||| :|||
234 ACAGAGCCCAAGGGCTACCATTGCCAACACTCTGCATCGGGCCCTGCCCTCAC 185

51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
::: ||| ||||| ||||| :||| :||| :||| :||| :|||
184 ATTTGGAGCCTGGACACGCAGTAGTACAGCAAGGTCCTGGCCCTGATCAACCA 135

67 rLeuasnProGluAlaSerAlasrProCysCysValProGlnaspLeuG 84
||||| ||||| ||||| ||||| :||| :||| :||| :||| :|||
134 GCATAACCCGGCGCCCTGGCGCGCGTGGTGGCTGCTTTCAGGTGCTGG 85

84 luProLeuthrIleLeuTyrTyrtValGlyArgThrProLysValGluGln 100
::: ||||| ||||| ||||| ||||| :||| :||| :||| :||| :|||
84 ACCCGCTGCCCATGTGTACTAGTGGCCGCAAGCCCAGGTGGAGCAG 35

101 LeuSerAsnMetValVallysSerCysLysCys 111
||||| ||||| ||||| ||||| :||| :||| :||| :||| :|||
34 CTGTCCAACATGATCGTGGCGCTCCTGCAAGTGC 2

seq_name: gb_estl6:AII57673

seq_documentation_block:
LOCUS AII57673 339 bp mRNA EST
DEFINITION uc48g10.r2 Soares,mammary_gland_NMLMG Mus musculus c
IMAGE:1494402 5' similar to gb.M32745 mouse transfo
factor beta-3 mRNA, complete (MOUSE); , mRNA sequenc
AII57673
ACCESSION AII57673.1 GI:3686142
VERSION AII57673
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae
REFERENCE
1 (bases 1 to 339)
AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Mo
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., W
Theising,B., Wyllie,T., Lennon,G., Soares,B., Wilson
Waterston,R.
TITLE The WashU-HMI Mouse EST Project
JOURNAL Unpublished (1996)
COMMENT Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 6
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ;
IMAGE Consortium (info@image.llnl.gov) for further i
MGI:932006
Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 267.
Location/Qualifiers
1..339
/organism="Mus musculus"
/db_xref="taxon:10090"
```



```

|||||
407 CTCGGCTGGAGTGGATCCAGAGCCCAAGGGCTACCATGCCACTTCTG 358
|||||
44 sSerGlyProCysProTyrLeuArgSerAlaAspThrHisSerThrV 61
|||||
357 CTCGGGCCCTGCCCTTACATTTGGAGCTGGACACGACGATACGCAAG 308
|||||
61 allLeuGlyLeuTyrAsnThrLeuAsnProGluAlaSerAlaSerProCys 77
|||||
307 TCCTGGCCCTGTACACACAGATACCCGGGGCGCTCGCGCGCGCTGC 258
|||||
78 CysValProGlnAspLeuGluProLeuThrIleLeuTyrTyrValGlyAr 94
|||||
257 TGCCTGCCGAGCGGCTGGAGCGCTGCCATCGTCTACTACGTGGGCG 208
|||||
94 gThrProLysValGluGlnLeuSerAsnMetValValLysSerCysLysC 111
|||||
207 CAAGCCCAAGGTGGAGCAGCTGTCCAACATGATCGCTCCTGCAAGT 158
|||||
111 ySer 112
|||||
157 GCAGC 153

```

seq_name: gb_est1:AA016742

seq_documentation_block: 553 bp mRNA EST 21-JAN-1997
 LOCUS AA016742 mn39e08.r1 Soares mouse placenta 4NbMpl3.5 14.5 Mus musculus cDNA
 DEFINITION clone IMAGE:444902 5' similar to gb:X02812_cds1 TRANSFORMING GROWTH
 FACTOR BETA 1 PRECURSOR (HUMAN); gb:M32745 mouse transforming
 growth factor beta-3 mRNA, complete (MOUSE);, mRNA sequence.

ACCESSION AA016742

VERSION AA016742.1 GI:1479043

KEYWORDS EST.

SOURCE house mouse.

ORGANISM Mus musculus

REFERENCE Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;

AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,

Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,

Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,

Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and

Waterston, R.

The WashU-HMI Mouse EST Project

Unpublished (1996)

Contact: Marra M/Mouse EST Project

WashU-HMI Mouse EST Project

Washington University School of MedicineP

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: mouseest@watson.wustl.edu

This clone is available royalty-free through LLNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

MGI:270238

Seq primer: -28M13 rev2 from Amersham

High quality sequence stop: 432.

Location/Qualifiers

FEATURES

source

1..553

/organism="Mus musculus"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="IMAGE:444902"

/clone_lib="Soares mouse placenta 4NbMpl3.5 14.5"

/sex="unknown"

/tissue_type="placenta"

/dev_stage="adult"

/lab_host="DH10B"

/note="Organ: placenta; Vector: pT7T3D-Pac (Pharmacia)

1st strand cDNA was primed with a Not I - oligo(gt) primer

15'

TGTTACAATCTGAAGTGGAGCGCGCGGAAATTTTTTTTTTTTTTTTTTTT
 T 3']; double-stranded cDNA was ligated to Eco RI adaptors
 (Pharmacia), digested with Not I and cloned into the Not I
 and Eco RI sites of the modified pT73 vector. Library
 went through one round of normalization, and was
 constructed by Bento Soares and M.Fatima Bonaldo."

BASE COUNT 129 a 168 c 150 g 106 t
 ORIGIN

alignment_scores:

Quality: 375.00 Length: 113

Ratio: 4.213 Gaps: 2

Percent Similarity: 78.761 Percent Identity: 65.487

alignment_block:

TGFB3P x AA016742 ..

Align seg 1/1 to: AA016742 from: 1 to: 553

1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17

|||||

222 GCCCTGGATACCACTATTGCTTCAGCTCCACAGAGAAGTCTGTGT 271

17 largProLeuTyrIleAspPheArgGlnAspLeuGlyTyrLysTyrValH 34

|||||

272 CGGCGACGTGTACATTGACTTTAGGAAGACCTGGTGTGAAGTGGATCC 321

34 lsGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50

|||||

322 ACGAGCCCAAGGGCTACCATGCAACTTCTGTCTGGGACCTGCCCTAT 371

51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnH 67

|||||

372 ATTTGGAGCTGGACACACAGTACAGCAAGTCTTGCCTCTACAACCA 421

67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84

|||||

422 ACACAACCGGGCGCTCGGCGTCCGCCGTGCTGCGTGGCCG.....ACGT 455

84 luProLeuThrIleLeuTyrTyr.ValGlyArgTyrProLysValGluG 100

|||||

466 TTGGAGCCACTGCCATCGTCTACTAGTGGTCCCAAGCCAGGTTGAGCA 515

100 nLeuSerAsnMetValValLysSerCysLysCysSer 112

|||||

516 GTTGTGTC.AACATGATTGTGCGTCTGCTGTCAGTGCAGCT 551

seq_name: gb_est49:AW600947

seq_documentation_block:

LOCUS AW600947 245 bp mRNA EST 23-MAR-2000

DEFINITION RC1-BN0014-210100-012-e04_1 BN0014 Homo sapiens cDNA, mRNA

sequence.

ACCESSION AW600947

VERSION AW600947.1 GI:7305686

KEYWORDS EST.

SOURCE human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 245)

AUTHORS HCGP <http://www.ludwig.org.br/ORESTES>.

TITLE The FAPESP/LICR Human Cancer Genome Project

JOURNAL Unpublished (1999)

COMMENT Contact: Simpson A.J.G.

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,

Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC1et2-RC1-BN0014-210100-012-e04-1st3-2000-01-21&t4=1>)
 Seq primer: puc 18 forward
 High quality sequence stop: 233.

FEATURES
 source
 1..245
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="BN0014"
 /dev_stage="Adult"
 /note="Organ: breast normal; Vector: puc18; Site:1: SmaI; Site:2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

BASE COUNT 67 a 43 c 62 g 73 t
 ORIGIN

alignment_scores:
 Quality: 374.00 Length: 79
 Ratio: 5.123 Gaps: 0
 Percent Similarity: 92.405 Percent Identity: 83.544

alignment_block:

TGFB3P x AW600947/rev ..

Align seg 1/1 to reverse of: AW600947 from: 1 to: 245

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34 HisGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProty 50
|||||
244 CACGAACCCARAGGTGACAAATGCCAACCTCTGTGCTGGAGCATGCCGTA 195
|||||
50 rleuArgSerAlaAspThrHisSerThrValLeuGlyLeuTyrAsnT 67
|||||
194 TTTATGGAGTTTCAGACACTCAGCACAGCAGGCTCTGAGCTTATATAATA 145
|||||
67 hrLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeu 83
|||||
144 CCTTAATCCAGAACATCTGCTCTCTGCTGGTGTCACAGATTGA 95
|||||
84 GluProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluG1 100
|||||
94 GAACCTCTAACCATTTCTACTACATTGGCAAAACACCCAGATTGAACA 45
|||||
100 nLeuSerAsnMetValValLysSerCysLysCysSer 112
|||||
44 GCTTTCTAATATGATTGTAAGTCTTGCAAAATGCAGC 8

```

seq_name: gb_est30:AU016439

seq_documentation_block:
 LOCUS AU016439 465 bp mRNA EST 15-OCT-1998
 DEFINITION AU016439 Mouse two-cell stage embryo cDNA Mus musculus cDNA clone J0725B08 3', mRNA sequence.
 ACCESSION AU016439
 VERSION AU016439.1 GI:3371443
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. Ko, M.S.H., Kitchen, J.R., Wang, X., Threat, T.A., Sun, T., DePalma, G.E., Liang, Y., Karqul, G.J., Sharara, R. and Doi, H.
 TITLE Systematic analyses of genes expressed in 2-cell stage mouse embryos (The ERATO/Doi Project at Wayne State University) (Ko, M.S.H. et al.)
 JOURNAL Unpublished (1998)

COMMENT

Contact: Hirofumi Doi
 Doi Biosymetry Project, ERATO
 Japan Science and Technology Corporation (JST)
 WBG Marine East 12F, 2-6 Nakase, Mihama-ku, Chiba 261-71, Japan
 Email: hd@bioa.jst.go.jp

FEATURES
 Location/Qualifiers
 source
 1..465
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone_lib="J0725B08"
 /clone_lib="Mouse two-cell stage embryo cDNA"
 /dev_stage="two-cell stage embryo"
 123 a 97 c 112 g 127 t 6 others

BASE COUNT 123 a 97 c 112 g 127 t 6 others
 ORIGIN

alignment_scores:
 Quality: 364.50 Length: 104
 Ratio: 4.238 Gaps: 3
 Percent Similarity: 82.692 Percent Identity: 70.192

alignment_block:

TGFB3P x AU016439/rev ..

Align seg 1/1 to reverse of: AU016439 from: 1 to: 465

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12 GluGluAsnCysCysValArgPro...LeuTyrIleAspPheArgGlnAs 27
|||
423 CAGNATAATGTCTGNCCTTCGCCCTCTCTTTTACATTGATTTTANGGGA 374
|||||
27 pLeuGlyTrpLysTrpValHisGluProLysGlyTyrTyrAlaAsn.Phe 43
|||||
373 TTGGNATGAAATGGATGCCATGACCAAGGTCACCAATGTAACATTC 324
|||||
44 CysSerGlyProCysProTyrLeuArgSerAlaAspThrThr.HisSerT 60
|||||
323 TGTGCTGGGGCATGCCCATATCTATGGAGTTCAGACACTTCAACACACCA 274
|||||
60 hrValLeuGlyLeuTyrAsnThrLeuAsnProGluAlaSerAlaSerPro 76
|||||
273 AGTCTCTACGCTGTACACACCAATAATCCGNACT.TCCGCTTCCCT 225
|||||
77 CysCysValProGlnAspLeuGluProLeuThrIleLeuTyrTyrValG1 93
|||||
224 TGTGTGTGTCTCCAGGATCTGGAACCACTGACCATCTCTATTACATTGG 175
|||||
93 yargThrProLysValGluGlnLeuSerAsnMetValValLysSerCysL 110
|||||
174 AAATAGCCCAAGATCGACAGCTTTCCAATATGATTGTCAAGTCTTGTA 125
|||||
110 yScysSer 112
|||||
124 AATGCAGC 117

```

seq_name: gb_est45:AW295761

seq_documentation_block:
 LOCUS AW295761 409 bp mRNA EST 16-JAN-2000
 DEFINITION UI-H-B11-afh-a-02-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2721675 3', mRNA sequence.
 ACCESSION AW295761
 VERSION AW295761.1 GI:6702397
 KEYWORDS EST.
 SOURCE human.

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 409)
 AUTHORS NCI-CCAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
 JOURNAL Unpublished (1997)

COMMENT

Contact: Robert Strausberg, Ph.D.
 Email: rcapbs-r@mail.nih.gov
 The sequence contained an oligo-dt track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. cDNA Library Preparation: M.B. Soares Lab Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
 www-bio.llnl.gov/bbrp/image/image.html The following repetitive elements were found in this cDNA sequence: 102-157,
 >GC-rich#Low.complexity
 Seq primer: M13 Forward
 POLYA=yes.

FEATURES

source

Location/Qualifiers

```

1. 409
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2721675"
/clone_lib="NCI_CGAP_Sub3"
/lab_host="DH10B (Life Technologies)"
/note="vector: pMT3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The
NCI_CGAP_Sub3 library is a subtracted library derived from
the NCI_CGAP_Sub1 library, which is a subtracted library
derived from B1. B1 constitutes a mixture of 21
normalized or subtracted NCI_CGAP libraries: NCI_CGAP_Co4
, NCI_CGAP_Pr22, NCI_CGAP_Pr28, NCI_CGAP_Co10,
NCI_CGAP_Co16, NCI_CGAP_Kid5, NCI_CGAP_Kid12,
NCI_CGAP_Kid3, NCI_CGAP_Kid11, NCI_CGAP_Lym2,
NCI_CGAP_Br2, NCI_CGAP_Co8, NCI_CGAP_CLI1, NCI_CGAP_Le12,
NCI_CGAP_Brn23, NCI_CGAP_Lu5, NCI_CGAP_Lu24,
NCI_CGAP_Lu19, NCI_CGAP_GC4, NCI_CGAP_GC6,
NCI_CGAP_Brn25. These 21 libraries were pooled and a
single-stranded DNA preparation of the resulting mixture
was used as a tracer in a subtractive hybridization with
a driver whose composition is detailed below:
NCI_CGAP_Kid3 pool 1 LLAM 3334-3337, 3682-3683,
3798-3803 (IMAGE CloneIDs 1322376-1323911, 1456008-1456775
, 1500552-1502855); NCI_CGAP_Kid5 pool 1 LLAM 3338-3342
, 3722-3725, 3776-3778 (IMAGE CloneIDs 1323912-1323831,
1471368-1472903, 1492104-1493255); NCI_CGAP_Lu5 pool 1
LLAM 3575-3582, 3851-3854 (IMAGE CloneIDs 1414920-1417991,
1520904-1522439); NCI_CGAP_GC4 pool 1 LLAM 3164-3167,
3716-3720, 3733-3735 (IMAGE CloneIDs 1257096-1258631,
1469064-1470983, 1475592-1476743); NCI_CGAP_Pr22 pool 1
LLAM 2457-2459, 2758-2759, 3062-3068 (IMAGE CloneIDs
985608-986759, 1101192-1101959, 1217928-1220615);
NCI_CGAP_Co10 pool 1 LLAM 2644-2653, 2871-2872 (IMAGE
CloneIDs 1057416-1061255, 1144584-1145351). Subtraction
was performed as previously described [Bonaldo, Lennon &
Soares (1996): Normalization and Subtraction: Two
Approaches To Facilitate Gene Discovery. Genome Research
6, 791-806.
TAG_LIB=NCI_CGAP_Pr22
TAG_TISSUE=prostate
TAG_SEQ=ACGTG"

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BASE COUNT 57 a 115 c 153 g 84 t

ORIGIN

alignment_scores:

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Quality: 351.00 Length: 82
Ratio: 5.014 Gaps: 0
Percent Similarity: 85.366 Percent Identity: 74.390

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alignment_block:

TGFB3P x AW295761/rev ..

Align seg 1/1 to reverse of: AW295761 from: 1 to: 409

31 LysTrpValHisGluProLysGlyTyrTyrAlaAsnPhcCysSerGlyPr 47

```

|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
409 AAGTGGATCCAGGCCAAGGGCTACCATCCCAACTTCTGCTCGGGCC 360

```

```

47 oCysProTyrLeuArgSerAlaAspThrThrHisSerThrValLeuGlyL 64
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
359 CTGCCCTACATTTGGAGCCTGGACACGACGACGACGAGTCTGTGGCC 310
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
64 eutyAsnThrLeuAsnProGluAlaSerAlaSerProCysCysValPro 80
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
309 TGTAAACACGACATAACCGCGCTCGCGCGCGCGCTGCTGCTGCGCG 260
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
81 GlnAspLeuGluProLeuThrThrLeuTyrTyrValGlyArgThrProLy 97
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
259 CAGCGCTGGAGCGCTGCCCATCGTGACTACGTGGCGCCCAAGCCAA 210
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
97 sValcGlnLeuSerAsnMetValVallySerCysLysCysSer 112
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
209 GGTGAGCAGCTGTCCACACATGATCGTGGCTCTGCAAGTGCAGC 164
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
seq_name: gb_est110.W70801

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seq_documentation_block:

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LOCUS W70801 301 bp mRNA EST 17-JUN-1996
DEFINITION me44c04.r1 Soares mouse embryo NbME13.5 14.5 Mus musculus cDNA
clone IMAGE:390342 5' similar to gb:X02812.cdsl TRANSFORMING GROWTH
FACTOR BETA 1 PRECURSOR (HUMAN); gb:M32745 mouse transforming
growth factor beta-3 mRNA, complete (MOUSE);, mRNA sequence.
W70801
ACCESSION W70801 GI:1380934
VERSION W70801.1
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 301)
AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisels,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.
The WashU-HMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:242174
Seq primer: mob.REGA+ET
High quality sequence stop: 289.
Location/Qualifiers
1. .301
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:390342"
/clone_lib="Soares mouse embryo NbME13.5 14.5"
/sex="unknown"
/tissue_type="embryo"
/dev_stage="13.5-14.5dpc total fetus"
/lab_host="DH10B"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5',
TGTTACCAATCTGAGTGGAGCGCGCGGAGATTTTCTTTTCTTTTCTTTT
T 3'], on equal amounts of mRNA from 2 13.5dpc and 2
14.5dpc embryos [total RNA provided by Minoru Ko, Wayne
Eco RI adaptors (Pharmacia), digested with Not I and
cloned into the Not I and Eco RI sites of the modified
pT7T3 vector. Library went through one round of

```

FEATURES

source

normalization, and was constructed by Bento Soares and

M.Fatima Bonaldo.
 BASE COUNT 65 a 88 c 84 g 64 t
 ORIGIN

alignment_scores:
 Quality: 349.00 Length: 100
 Ratio: 3.966 Gaps: 0
 Percent Similarity: 88.000 Percent Identity: 76.000

alignment_block:
 TGPB3P x W70801

Align seg 1/1 to: W70801 from: 1 to: 301

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13 GluAsnCysCysValArgProLeuTyrlleAspPheArgGlnAspLeuG1 29
:::|||||
3 AAGAACTGCTGTGTCGGCA.CTGTACATGTGACTTAGAAGGACCTGGG 51
29 yTrpLysTrpValHisGluProLysGlyTyrTyrAlaAsnPheCysSerg 46
|||||
52 TTGGAAGTGGATCCACGACGCCAA.GGGTACCATGCCAACTTCTCTGG 100
46 lyProCysProTyrLeuArgSerAlaAspThrHisSerThrValLeu 62
|||||
101 GACCTGCTTATATTTGGAGCTGGACACACAGTACAGCAAGTCTCT 150
63 GlyLeuTyraThrLeuAsnProGluAlaSerAlaSerProCysCysVa 79
:::|||||
151 GCCCTCTACACCAACACACACCCGGCGCTTCGGG.TCACCGTGTGGT 199
79 lProGlnAspLeuGluProLeuThrIleLeuTyrTyrValGlyArgThrP 96
|||||
200 GCCGACAGT.TTGGAGCCACTGCCATCTGTACTACGTGGTCCAGC 248
96 roLysValGluGlnLeuSerAsnMetValValLysSerCysLysCysSer 112
|||||
249 CCAAGTGGAGCAGTTGTCCACATGATTTGCGCTCTCTGCAAGTGCAGC 298

```

seq_name: gb_est30:AU050770

seq_documentation_block:
 LOCUS AU050770 878 bp mRNA EST 08-JUN-1999
 DEFINITION AU050770 Paralicthys olivaceus library (Aoki T) Paralicthys olivaceus cDNA clone WB11-23, mRNA sequence.
 ACCESSION AU050770
 VERSION AU050770.1 GI:5019223
 KEYWORDS EST.
 SOURCE bastard halibut.
 ORGANISM Paralicthys olivaceus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percormorpha; Pleuronectiformes; Pleuronectoidae; Bothidae; Paralicthys.

REFERENCE 1 (bases 1 to 878)
 AUTHORS Aoki,T.
 TITLE Japanese flounder leukocyte cDNA
 JOURNAL Unpublished (1999)
 COMMENT Contact: Takashi Aoki
 Genetics and Biochemistry
 Tokyo University of Fisheries
 Konan, 4-5-7, Minato 108, Japan
 Tel: 03-5463-0556
 Email: aoki@tokyo-u-fish.ac.jp
 clone WB11-23:similar to rainbow trout transforming growth factor beta(X99303).

FEATURES
 source 1..878
 /organism="Paralicthys olivaceus"
 /db_xref="taxon:8255"
 /clone="WB11-23"
 /clone_lib="Paralicthys olivaceus library (Aoki T)"

BASE COUNT 256 a 213 c 186 g 220 t 3 others
 ORIGIN

alignment_scores:
 Quality: 347.50 Length: 101
 Ratio: 4.088 Gaps: 2
 Percent Similarity: 84.158 Percent Identity: 66.337

alignment_block:
 TGPB3P x AU050770

Align seg 1/1 to: AU050770 from: 1 to: 878

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13 GluAsnCysCysValArgProLeuTyrlleAspPheArgGlnAspLeuG1 29
|||||
235 GAGACCTGCTGCTGCGGAN.CTGTACATCGACTTCAGGAAGATCTGGG 283
29 yTrpLysTrpValHisGluProLysGlyTyrTyrAlaAsnPheCysSer 45
|||||
284 CTGGAAGTGGATACATAAGCCGACAG...TACCACGCTAACTACTGCATG 330
46 GlyProCysProTyrLeuArgSerAlaAspThrHisSerThrValLe 62
|||||
331 GGATCTCGACCTACATCTGGAATGCTGAAACAAATATTTCTCAGATTTT 380
62 uGlyLeuTyraThrLeuAsnProGluAlaSerAlaSerProCysCysV 79
|||||
381 GGCCITGTACAAGCATCACAAACCAGGAGCTCTGCCAGCCCTGCTGTG 430
79 alProGlnAspLeuGluProLeuThrIleLeuTyrTyrValGlyArgThr 95
|||||
431 TTCCCCAGGCACCTGGACCCACTGCCAATCTCTACTACGTGGGCGAGCAA 480
96 ProLysValGluGlnLeuSerAsnMetValValLysSerCysLysCysSe 112
|||||
481 CACAAGTGGAGCAGCTGTCCAATATGATCGTGAAGTCTCTGCAAGTGTAG 530
112 r 112
531 C 531

```

seq_name: gb_est49:AW600942

seq_documentation_block:
 LOCUS AW600942 259 bp mRNA EST 23-MAR-2000
 DEFINITION RCI-BN0014-210100-012-d10_1 BN0014 Homo sapiens cDNA, mRNA sequence.
 ACCESSION AW600942
 VERSION AW600942.1 GI:7305681
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 259)
 AUTHORS HCGP http://www.ludwig.org.br/ORESTES.
 TITLE The FAPESP/LICR Human Cancer Genome Project
 JOURNAL Unpublished (1999)
 COMMENT Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?l=RC1&t2=RC1-BN0014-210100-012-d10_1&t3=2000-01-21&t4=1)
 Seq primer: puc 18 forward
 High quality sequence stop: 258.

FEATURES
source
Location/Qualifiers
1. .259
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="BN0014"
/dev_stage="Adult"
/note="Organ: breast_normal; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESPEC PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
BASE COUNT 69 a 48 c 62 g 80 t
ORIGIN
alignment_scores:
Quality: 343.50 Length: 79
Ratio: 4.838 Gaps: 1
Percent Similarity: 89.873 Percent Identity: 78.481
alignment_block:
TGFB3P x AW600942/rev ..
Align seg 1/1 to reverse of: AW600942 from: 1 to: 259
34 HisGluProLysGlyTyrTyrAlaAsnPhcCysSerGlyProCysProTy 50
||||:||||| :|||||:|||||
241 CACGCCCAAG...GTACATCCCACTCTGTGTCGAGCATGCCGTA 195
50 rLeuArgSerAlaAspThrHrHisSerThrValLeuGlyLeuTyrAsn 67
||||| :||||| :||||| :|||||:|||||
194 TTTATGAGTTCAGACACTCAGCACACGAGGCTCTGAGCTTATATA 145
67 hrLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeu 83
||||:||||| :||||| :||||| :|||||:|||||
144 CCATAATCCAGAAGCATCTGCTCTCTGCTGCTGCTGCCAGATT 95
84 GluProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGlu 100
||||:||||| :||||| :||||| :|||||:|||||
94 GAACCTCTAACCATCTCTACTACATTTGGCAAAACACCAAGATTGA 45
100 nLeuSerAsnMetValValLysSerCysLysCysSer 112
||||:||||| :||||| :||||| :|||||:|||||
44 GCCTTCTAATATGGTTGTAAGTCTTGCAATGCAGC 8
seq_name: gb_est106:N36741
seq_documentation_block:
LOCUS N36741 560 bp mRNA EST 16-JAN-1996
DEFINITION yx90e06.r1 Soares melanocyte 2NBHM Homo sapiens cDNA clone
IMAGE:269026 5' similar to gb:Y00083 TRANSFORMING GROWTH FACTOR
BETA 2 PRECURSOR (HUMAN); contains element OPR repetitive element ;,
mRNA sequence.
ACCESSION N36741
VERSION N36741.1 GI:1157883
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo..
REFERENCE 1 (bases 1 to 560)
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman
M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J.,
Rifkin,L., Rohlfing,T., Soares,M., Tap,F., Trevaskis,E., Waterston
R., Williamson,A., Wohlmann,P. and Wilson,R.
The WashU-Merck EST Project
Unpublished (1995)
CONTACT: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800

Fax: 314 286 1810
Email: estewatson.wustl.edu
High quality sequence stops: 470
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: T7
High quality sequence stop: 470.
Location/Qualifiers
1. .560
/organism="Homo sapiens"
/db_xref="GDB:3878668"
/db_xref="taxon:9606"
/clone="IMAGE:269026"
/clone_lib="Soares melanocyte 2NBHM"
/sex="Male"
/tissue_type="melanocyte"
/lab_host="DH10B (ampicillin resistant)"
/note="vector: p7T3D (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5',
TGTTACCAATCTGAAGTGGAGCGCGCGAGTCTTTTCTTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified p7T3 vector
(Pharmacia). Library constructed by Bento Soares and
M. Fatima Bonaldo. RNA from normal foreskin melanocytes
(FS374) was kindly provided by Dr. Anthony P. Albino."
BASE COUNT 195 a 102 c 107 g 154 t
ORIGIN
alignment_scores:
Quality: 341.00 Length: 74
Ratio: 5.015 Gaps: 0
Percent Similarity: 91.892 Percent Identity: 81.081
alignment_block:
TGFB3P x N36741 ..
Align seg 1/1 to: N36741 from: 1 to: 560
39 TyrTyrAlaAsnPhcCysSerGlyProCysProTyrLeuArgSerAlaAs 55
||||| :||||| :||||| :|||||:|||||
8 TACATGCCAACTCTGTGCTGGAGCATGCCGCTATTATGGAGTTCAGA 57
55 pThrThrHisSerThrValLeuGlyLeuTyrAsnThrLeuAsnProGlu 72
||||| :||||| :||||| :|||||:|||||
58 CACTCAGCACACGAGGCTCTGAGCTTATATATACCAATCCAGAAG 107
72 laSerAlaSerProCysCysValProGlnAspLeuGluProLeuThrIle 88
||||:||||| :||||| :||||| :|||||:|||||
108 CATCTGCTCTCCNTGCTCGTGTGCCAAGATTAGAACCTCTAACCAT 157
89 LeuTyrTyrValGlyArgThrProLysValGluGlnLeuSerAsnMetVa 105
||||:||||| :||||| :||||| :|||||:|||||
158 CTCTACTATTGGCAAAACACCAAGATTGAACAGCTTTCTAATATGAT 207
105 lValLysSerCysLysCysSer 112
:||||| :||||| :||||| :|||||:|||||
208 TGTAAGTCTTGCAATGCAGC 229
seq_name: gb_est91:BF682938
seq_documentation_block:
LOCUS BF682938 748 bp mRNA EST 21-DEC-2000
DEFINITION 602117568F1 Soares mammary_gland_NMLMG Mus musculus cDNA clone
IMAGE:3468737 5', mRNA sequence.
ACCESSION BF682938
VERSION BF682938.1 GI:11956937
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 748) NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: M. Bento Soares, Ph.D. cDNA Library Preparation: Bento Soares and M. Fatima Bonaldo cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAM8476 row: h column: 18 High quality sequence start: 26 High quality sequence stop: 746. High quality sequence stop: 746. Location/Qualifiers

FEATURES

source

1..748

/organism="Mus musculus"

/db_xref="taxon:10090"

/clone="IMAGE:3468737"

/clone_lib="Soares_mammary_gland_NMLMG"

/sex="female (lactating)"

/tissue_type="mammary gland"

/lab_host="DH10B"

/note="Vector: pT73D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from mammary gland tissue from a lactating female, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 189 a 220 c 189 g 150 t

ORIGIN

alignment_scores

Quality: 337.00 Length: 79

Ratio: 4.884 Gaps: 0

Percent Similarity: 87.342 Percent Identity: 75.949

alignment_block:

TGFB3P x BF682938 ..

Align seg 1/1 to: BF682938 from: 1 to: 748

1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluAsnCysCysVa 17

512 GCCCTGGATACCACTATTGCTTCCAGTCCACAGAGAAGAACTGCTGT 561

17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34

562 CGCGAGCTGTACATTGACTTGTAGAGGACCTGGTTGGAAGTGATCC 611

34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50

612 ACGAGCCCAAGGGCTACCATGCCAACTTCTGTCTGGGACCTGCCCTAT 661

51 LeuArgSerAlaAspThrHisSerThrValLeuGlyLeuTyrAsnTh 67

662 ATTTGGAGCCTGGACACACAGTACAGCAAGGTCTTGCCTCTCAACAA 711

67 rLeuAsnProGluAlaSerAlaSerProCysCysVal 79

712 CACAAACCGGGCGCTTCGGGTCACCGTCTGGGTG 747

seq_name: gb_est8:AA533093

seq_documentation_block:

LOCUS AA533093 542 bp mRNA EST 21-AUG-1997

DEFINITION

nj19q04.s1 NCI CGAP_AA1 Homo sapiens cDNA clone IMAGE:992982 3' similar to gb.X02812.cdsl TRANSFORMING GROWTH FACTOR BETA 1 PRECURSOR (HUMAN); contains element MER22 repetitive element ; mRNA sequence.

ACCESSION

AA533093

VERSION

AA533093.1 GI:2277189

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 542)

REFERENCE

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

AUTHORS

National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

TITLE

Unpublished (1997)

JOURNAL

Contact: Robert Strausberg, Ph.D.

COMMENT

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Stratagene, Inc., David B. Krizman, Ph.D. cDNA Library Arraying: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html Insert Length: 1687 Std Error: 0.00 Seq primer: -40ml3 fwd. ET from Amersham High quality sequence stop: 142. Location/Qualifiers

FEATURES

source

1..542

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:992982"

/clone_lib="NCI-CGAP_AA1"

/tissue_type="adrenal adenoma"

/lab_host="SOLR (kanamycin resistant)"

/note="Organ: adrenal gland; Vector: Bluescript SK-; Site 1: EcoRI; Site 2: XhoI; Cloned unidirectionally, Primer: Oligo dT. Two pooled bulk adrenal adenomas. 5' adaptor sequence: 5' GAATTCGGCAGAG 3' 3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3' Average insert size: 1.6 kb."

BASE COUNT 92 a 152 c 196 g 102 t

ORIGIN

alignment_scores

Quality: 395.00 Length: 115

Ratio: 3.564 Gaps: 5

Percent Similarity: 81.739 Percent Identity: 66.957

alignment_block:

TGFB3P x AA533093/rev ..

Align seg 1/1 to reverse of: AA533093 from: 1 to: 542

1 AlaLeuAspThrAsnTyrCysPheArgAsnLeu.GluGluAsnCysCysV 17

473 AGCCCTTGACCACTATTGCTTCCAGTCCAGGAGAAGAA...CTGCTGG 427

17 aLArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpVal 33

426 TCGGCAGCTGTACATTGA.TTCCGCAAGGACCTCGCTGGAATTGGATC 378

34 HisGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTy 50

377 CACGAGCCCAAGGGCTACCATGCCAACTTCTGCCCTCGGGCGCTGCCCTA 328

50 rLeuArgSerAlaAspThrHisSerThrValLeuGlyLeuTyrAsn. 66

327 CATTGGAGCCTGGACACGACAGTACAGCAAGGTCTCTGGCCTGTACAACC 278

```

67 ThrLeuAsn.ProGluAlaSerAlaSerProCysCysValProGlnAspL 83
   ::::::::::::::::::::
277 AGCATAAACGCCGGGTG...CGCGCGCGTGTCTGGGT.CCGAGGCGC 232
   ::::::::::::::::::::
83 euGluProLeuThrIleLeuTyrValGlyArgThrProLysValGlu 99
   ::::::::::::::::::::
231 TGGAGCGCGTGCCTACTGTCTACTACCTGGCGCGCAAGCGCAAGTGGAG 182
   ::::::::::::::::::::
100 GlnLeuSerAsnMetValValLysSerCysLysCysSer 112
   ::::::::::::::::::::
181 CAGTGTCACATGATGTCGCGCTCTGCAAGTGCAGC 143
seq_name: gb_est78:BE737006

seq_documentation_block:
LOCUS BE737006 915 bp mRNA EST 15-SEP-2000
DEFINITION 601306767F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3641081 5',
mRNA sequence.
ACCESSION BE737006
VERSION BE737006.1 GI:10150998
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 915)
NIH-MGC http://mgc.ncbi.nih.gov/.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-re@mail.nih.gov
Tissue procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LCM346 row: e column: 18
High quality sequence stop: 424.
FEATURES
Location/Qualifiers
1..915
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3641081"
/clone_lib="NIH_MGC_39"
/tissue_type="adenocarcinoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: pancreas; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCAGCAG(G). Library constructed
by Ling Hong in the laboratory of Gerald M. Rubin
(University of California, Berkeley) using ZAP-cDNA
synthesis kit (Stratagene) and Superscript II RT (Life
Technologies)."
```

```

189 GCCCTGGACACAACTATTGCTTACGCTCCACGGAGAGAACTGCTGCCT 238
17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTyrLysTyrValH 34
   ::::::::::::::::::::
239 CGGCGAGCTGTACATTGACTCCGCAAGGACCTCGGCTGGAAGTGGATCC 288
   ::::::::::::::::::::
34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
   ::::::::::::::::::::
289 ACGAGCCCAAGGGCTACCATGCAACTTCTGCTCGGGCCCTGCCCTAC 338
   ::::::::::::::::::::
51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
   ::::::::::::::::::::
339 ATTGGGAGCTGGACACGACGACGACAGGTCCTGGCCCTGTACAACCA 388
   ::::::::::::::::::::
67 rLeuAsnProGluAla.SerAlaSerProCysCysValProGln 81
   ::::::::::::::::::::
389 GCATAACCCGGCGCTCGGGCG...CCGTGCTGCTGCCGCCGAA 429
seq_name: gb_est17:A1179582

seq_documentation_block:
LOCUS A1179582 571 bp mRNA EST 20-JAN-1999
DEFINITION EST223304 Normalized rat spleen, Bento Soares Rattus sp. cDNA clone
RSPCJ23 3', end, mRNA sequence.
ACCESSION A1179582
VERSION A1179582.1 GI:3730220
KEYWORDS EST.
SOURCE Rattus sp.
ORGANISM Rattus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE
1 (bases 1 to 571)
Lee,N.H., Glodex,A., Chandra,I., Mason,T.M., Quackenbush,J.,
Kerlavage,A.R. and Adams,M.D.
Rat Genome Project: Generation of a Rat EST (REST) Catalog & Rat
Gene Index
JOURNAL Unpublished (1998)
COMMENT Contact: Lee, NH
The Institute for Genomic Research
9712, Medical Center Drive, Rockville, MD 20850, USA
Tel: (301)-838-3529
Fax: (301)-838-0208
Email: nhlee@tigr.org
Seq primer: M13-21.
FEATURES
Location/Qualifiers
1..571
/organism="Rattus sp."
/db_xref="ATCC (inhost):2033997"
/db_xref="taxon:10118"
/clone="RSPCJ23"
/clone_lib="Normalized rat spleen, Bento Soares"
/note="Organ: spleen; Vector: pT7T3Pac; Site_1: EcoRI;
Site_2: NotI"
BASE COUNT 144 a 111 c 121 g 195 t
ORIGIN

alignment_scores:
Quality: 331.00 Length: 72
Ratio: 4.940 Gaps: 0
Percent Similarity: 93.056 Percent Identity: 80.556

alignment_block:
TGFB3P x A1179582/rev ..
Align seg 1/1 to reverse of: A1179582 from: 1 to: 571

41 AlaAsnPheCysSerGlyProCysProTyrLeuArgSerAlaAspThrTh 57
   ::::::::::::::::::::
569 GCTAACTTCTGTGCTGGGCGCATGCCCTTATCTGTGGAGTTCAGACACA 520
   ::::::::::::::::::::
57 rHisSerThrValLeuGlyLeuTyrAsnThrLeuAsnProGluAlaSerA 74
   ::::::::::::::::::::
```


/clone_lib="NCI_CGAP_Pr28"
/sex="male"
/dev_stage="adult"
/lab_host="DH10B"
/note="Organ: prostate; Vector: pT7T3D-Pac (Pharmacia)
with a modified polylinker; Plasmid DNA from the
normalized library NCI_CGAP_Pr22 was prepared, and ss
circles were made in vitro. Following HAP purification,
this DNA was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from a pool
of 5,000 clones made from the same library (cloneIDs
985608-986759, 1101192-1101959, and 1217928-1220615).
Subtraction by Bento Soares and M. Fatima Bonaldo."
57 a 117 c 150 g 67 t 1 others

alignment_scores:
Quality: 321.00 Length: 82
Ratio: 4.586 Gaps: 0
Percent Similarity: 85.366 Percent Identity: 73.171

alignment_block:

TGFB3P x A1918883/rev ..

Align seg 1/1 to reverse of: A1918883 from: 1 to: 392

31 LysTrpValHisGluProLysGlyTyrTyrAlaAsnPheCysSerGlyPr 47
387 AAGTGGATCCACGAGCCCAAG.GGCTACCATGCCNACTTCTGCCTCGGGCC 339
47 oCysProTyrLeuArgSerAlaAspThrHisSerThrValLeuGlyL 64
338 CTGCCCCATATTGGAGCCTGGACACCGCAGTACAGCAAGTCTCGGCC 289
64 eutYrAsnThrLeuAsnProGluAlaSerAlaSerProCysCysValPro 80
288 TGTACAACAGCATAACCCGGCGCCTCGCGCGCGCTGCTGCGTCCG 239
81 GlnAspLeuGluProLeuThrIleLeuTyrTyrValGlyArgThrProLy 97
238 CAGCGCGTGGAGCGCTGCGCCTACTAGTGTGGCGCGCAAGCCAA 189
97 svalGluGlnLeuSerAsnMetValValLysSerCysLysCysSer 112
188 GGTGGAGCAGCTGTCCAAACATGATGCGTGGCGCTCTGCAAGTGCAGC 143

seq_name: gb_est49:AW600960

seq_documentation_block:
LOCUS AW600960 266 bp mRNA EST 23-MAR-2000
DEFINITION RC1-BN0014-210100-012-h01_1 BN0014 Homo sapiens cDNA, mRNA
sequence.
ACCESSION AW600960
VERSION AW600960.1 GI:7305699
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 266)
REFERENCE HCGP <http://www.ludwig.org.br/ORESTES>.
AUTHORS The FAPESP/LICR Human Cancer Genome Project
TITLE Unpublished (1999)
JOURNAL Contact: Simpson A.J.G.
COMMENT Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome

Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC1&t2=RC1-BN0014-210100-012-h01_1&t3=2000-01-21&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 218.

FEATURES
source

1. .266
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="BN0014"
/dev_stage="Adult"
/note="Organ: breast_normal; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

BASE COUNT 72 a 51 c 59 g 84 t
ORIGIN

alignment_scores:

Quality: 317.50 Length: 88
Ratio: 4.178 Gaps: 4
Percent Similarity: 86.364 Percent Identity: 71.591

alignment_block:

TGFB3P x AW600960/rev ..

Align seg 1/1 to reverse of: AW600960 from: 1 to: 266

26 GlnAspLeuGlyTyrLysTrpValHisGluPro.LysGlyTyrTyrAlaA 42
260 GAGGATTTAGT...GAAATGATACACGAGCCAAAG...TACAATGCAA 217
42 snPheCysSerGlyProCysProTyrLeuArgSerAlaAspThrThrHis 58
216 CTCGTGTC...TGGAGATGCCGCTATTATTGGAGTTCAGACACTCAGCAC 170
59 SerThrValLeuGlyLeuTyrAsnThrLeuAsnProGluAlaSerAlaSe 75
169 AGCAGGGTCTGAGCTTATATAATACCAATAATCAGAAAGCATCTGCTTC 120
75 rProCysCysValProGlnAspLeuGluProLeuThrIleLeuTyrTyrv 92
119 TCCTTGCTGCTGTCGCCAAGATTTAGAACCTCTAACCATTCCTACTACA 70
92 alGlyArgThrProLysValGluGlnLeuSerAsnMetValValLysSer 108
69 TTGCCAAACACCCCAAGATTGAACAGCTTCTTAATGATTGTTAAAGTCT 20
109 CysLysCysSer 112
19 TGCAAAATGCAGC 8

seq_name: gb_est46:AW364559

seq_documentation_block:
LOCUS AW364559 391 bp mRNA EST 04-FEB-2000
DEFINITION RC1-DT0028-131299-011-a06 DT0028 Homo sapiens cDNA, mRNA sequence.
ACCESSION AW364559
VERSION AW364559.1 GI:6869209
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 391)
REFERENCE HCGP <http://www.ludwig.org.br/ORESTES>.
AUTHORS The FAPESP/LICR Human Cancer Genome Project
TITLE Unpublished (1999)
JOURNAL Contact: Simpson A.J.G.
COMMENT


```
391 TGATTTAAGAGGATCTTGGAGGAATGATCCCAATAACCCAAAG...G 345
39 yrYrAlaAsnPheCysSerGlyProCysProTyrLeuArgSerAlaAsp 55
   ::::::::::::::::::::|
344 TACAATGCTAATCTGTGCTGGGCATGCCATATCTATGGAGTTCCAGAC 295
   ::::::::::::::::::::|
56 ThrThr.HisSer..ThrValLeuGlyLeuTyrAsnThr..LeuAsnProGl 71
   |||:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
294 ACTCTAACACACCAAAAGTCTCAGCTGTACAAACACCCATAAATCCGA 245
   |||:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
71 uAlaSerAlaSerProCysValProGlnAspLeuGluProLeuThrI 88
   |||:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
244 AGCTTCGCTCCCTTCCTGTGTGTCGCCAGGATCTGGAAACCACTGACCA 195
   |||:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
88 leLeuTyrTyrValGlyArgThrProLysValGluGlnLeuSerAsnMet 104
   |||:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
194 TTCTCTATTACATTTGGAATACGCCCAAGATCGAACACGCTTCCAATATG 145
   |||:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
105 ValValLysSerCysLysCysSer 112
   ::::::::::::::::::::|
144 ATTGTCAAGTCTTGTAAATGCAGC 121
```

seq_name: gb_est70:BE074350

```
seq_documentation_block:
LOCUS      BE074350      517 bp      mRNA      EST      09-JUN-2000
DEFINITION QV3-BT0571-030200-078-d08 BT0571 Homo sapiens cDNA, mRNA sequence.
ACCESSION  BE074350
VERSION    BE074350.1  GI:8422187
KEYWORDS  EST.
SOURCE    human.
ORGANISM  Homo sapiens
```

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 517)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.

Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001

Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=st2-QV3-BT0571-030200-078-d08&t3=2000-02-03&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 9
High quality sequence stop: 516.
Location/Qualifiers

1. .517
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="BT0571"
/dev_stage="Adult"
/note="Organ: breast; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196 ,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

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BASE COUNT      130 a      131 c      150 g      106 t
ORIGIN
alignment_scores:
  Quality: 305.00      Length: 58
  Ratio: 5.259      Gaps: 0
  Percent Similarity: 100.000      Percent Identity: 98.276
alignment_block:
  TGFb3p x BE074350      ..
Align seg 1/1 to: BE074350 from: 1 to: 517
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55 AspThrThrHisSerThrValLeuGlyLeuTyrAsnThrLeuAsnProGl 71
   ::::::::::::::::::::|
8  AACACACCCACAGACGCTGCTGGACTGTACAACACTCTGAACCCCGA 57
   |||:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
71 uAlaSerAlaSerProCysValProGlnAspLeuGluProLeuThrI 88
   |||:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
58 AGCATCTGCCTCGCTTCTGCTGGTCCCCAGGACCTGGAGCCCTGACCA 107
   |||:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
88 leLeuTyrTyrValGlyArgThrProLysValGluGlnLeuSerAsnMet 104
   |||:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
108 TCCTGTACTATGTTGGGAGGACCCCCAAAGTGGAGCAGCTCTCCAACATG 157
   |||:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
105 ValValLysSerCysLysCysSer 112
   |||:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
158 GTGCTGAAGTCTTGTAAATGTAGC 181
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seq_name: gb_est51:AW798167

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seq_documentation_block:
LOCUS      AW798167      379 bp      mRNA      EST      16-MAY-2000
DEFINITION RC3-UM0046-290200-011-a06 UM0046 Homo sapiens cDNA, mRNA sequence.
ACCESSION  AW798167
VERSION    AW798167.1  GI:7850141
KEYWORDS  EST.
SOURCE    human.
ORGANISM  Homo sapiens
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 379)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.

Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
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Tel: +55-11-2704922
Fax: +55-11-2707001

Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=st2-RC3-UM0046-290200-011-a06&t3=2000-02-29&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 17
High quality sequence stop: 379.
Location/Qualifiers

1. .379
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="UM0046"

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/dev_stage="Adult"
/notes="Organ: uterus; Vector: puc18; Site_1: SmaI; Site_2:
SmaI; A mini-library was made by cloning products derived
from ORESTES PCR (U.S. Letters Patent application No. 196
,716 - Ludwig Institute for Cancer Research) profiles
into the pUC 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."
BASE COUNT      84 a 128 c 98 g 69 t
ORIGIN

alignment_scores:
  Quality: 304.00      Length: 66
  Ratio: 5.241        Gaps: 0
  Percent Similarity: 87.879  Percent Identity: 75.758

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  163 GCCCTGGACCACTATGCTTCAGCTCCACGAGAGAACTGCGCT 212

  17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
  ||| |||||||:|||||:|||||:|||||:|||||:|||||:|||||:
  213 GCGGAGCTGTACATTGATCTCCGCAAGGACCTCGCTGGAAGTGATCC 262

  34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
  263 ACGAGCCCAAGGCTACCATGCCAATCTCTGCTGGGCCCTGCGCCCTAC 312

  51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsn 66
  :||: ||| |||||:|||||:|||||:|||||:|||||:|||||:|||||:
  313 AFTTGAGCTGGACCGACGATACAGCAAGGTCCTGGCCCTGTACAAC 360

seq_name: gb_est28:AL362754

seq_documentation_block:
LOCUS      AL362754      400 bp      mRNA      EST      04-AUG-2000
DEFINITION AL362754 ICRFP 522 and 523 Mus musculus cDNA clone K9222B41 5',
mRNA sequence.
ACCESSION  AL362754
VERSION    AL362754.1 GI:9692237
KEYWORDS   EST.
SOURCE     house mouse.
ORGANISM   Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE  1 (bases 1 to 400)
AUTHORS   Elckhoff,H., Schuchardt,J., Ivanov,I., Meier-Ewert,S., O'Brien,J.,
            Malik,A., Tandon,N., Wolski,E., Rohlf,E., Nyarsik,L., Reinhardt,R.,
            Nietfeld,W. and Lehrach,H.
TITLE     Tissue gene expression analysis using arrayed normalized cDNA
            libraries
JOURNAL   Genome Res. (2000) In press
COMMENT   Contact: MPIMG
            Abt.Lehrach
            Max Planck Institut Fuer Molekulare Genetik
            Innestrasse 73, Berlin, 14195 Germany
            The cDNA libraries ICRFP 522 and 523 were normalized with
            oligonucleotide fingerprinting, resulting in a unique subset of
            5376 cDNA clones.
            Location/Qualifiers
            source
              1..400
              /organism="Mus musculus"
              /strain="Black 6"
              /db_xref="taxon:10090"
              /clone="K9222B41"
              /clone_lib="ICRFP 522 and 523"
              /tissue_type="embryo"

/dev_stage="Adult"
/notes="Organ: uterus; Vector: puc18; Site_1: SmaI; Site_2:
SmaI; A mini-library was made by cloning products derived
from ORESTES PCR (U.S. Letters Patent application No. 196
,716 - Ludwig Institute for Cancer Research) profiles
into the pUC 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."
BASE COUNT      108 a 105 c 91 g 96 t
ORIGIN

alignment_scores:
  Quality: 302.00      Length: 66
  Ratio: 5.033        Gaps: 0
  Percent Similarity: 90.909  Percent Identity: 72.727

alignment_block:
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  Align seg 1/1 to: AL362754 from: 1 to: 400
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  202 GCTTGGATGCTGCTACTACTGCTTTAGAAATGTCAGGATAATTGCTGCCT 251

  17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
  :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
  252 TCGCCCTCTTTACATTGATTTTAAGAGGGATCTTGGATGGAATGGATCC 301

  34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
  302 ATGAACCCAAAGGTCACATGCTAACTTCTGCTGGGGCATGCCCATAT 351

  51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsn 66
  ||| |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
  352 CTTAGGAGTTCACTCACTCAACACACAAAGTCTCAGCTGTACAAC 399

seq_name: gb_est20:AI452742

seq_documentation_block:
LOCUS      AI452742      396 bp      mRNA      EST      13-APR-1999
DEFINITION tJ45a05.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone
IMAGE:2144432 3' similar to gb:X02812 cds1 TRANSFORMING GROWTH
FACTOR BETA 1 PRECURSOR (HUMAN); contains PTR5.t3 MSRI repetitive
element ;, mRNA sequence.
ACCESSION  AI452742
VERSION    AI452742.1 GI:4287481
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 396)
AUTHORS   NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
            National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
            Unpublished (1997)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: ccapbs-r@mail.nih.gov
            This clone is available royalty-free through LNL; contact the
            IMAGE Consortium (info@image.lnl.gov) for further information.
            Insert Length: 529 Std Error: 0.00
            Seq primer: -40UP from Gibco.
            Location/Qualifiers
            source
              1..396
              /organism="Homo sapiens"
              /db_xref="taxon:9606"
              /clone="IMAGE:2144432"
              /clone_lib="Soares_NSF_F8_9W_OT_PA_P_S1"
              /lab_host="DHI08"
              /note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with
              a modified polylinker; Site_1: Not I; Site_2: Eco RI;
              Equal amounts of plasmid DNA from five normalized
              libraries were mixed, and ss circles were made in vitro. In
              Following HAP purification, this DNA was used as tracer in
              a subtractive hybridization reaction. The driver was
              PCR-amplified cDNAs from pools of 5,000 clones made from
              the same 5 libraries. The pools consisted of the following
              libraries and cloneIDs: Soares NbHSF pool 1;

```

BASE COUNT 57 a 106 c 144 q 88 t 1 others

alignment_scores:		
Quality:	301.00	Length: 75
Ratio:	4.778	Gaps: 0
Percent Similarity:	84.000	Percent Identity: 73.333

alignment_block:
TGFB3P x AI452742/rev

Align seg 1/1 to reverse of: AI452742 from: 1 to: 396

38 GlyTyrTrpAlaAsnPheCysSerGlyProCysProTyrIleuArgSerAl 54
|||||:::|||||::| |||||::|||::|
396 GGCTACCATGCCAACATTGCCTGGGGCCCTGCCCTACATTTGGAGCCT 347

54 aAspThrThrHisSerThrValLeuGlyLeuTyrAsnThrLeuAsnProG 71
||||| ::||| |||||:::||||| |||||
346 GGACACGCATACAGCAAGTCTCGGCCCTGTACACACCAGCATACCGG 297

71 luAlaSerAlaSerProCysCysValProGlnAspLeuGluProLeuThr 87
 |||||:::| ||||| ||||| |||||
 296 GCGGCTCGGCGCGCGGTTNTGGTTCGACAGGCGGTGGACCGCTGCC 247

88 IleLeuTyrTyrValclyArgThrProLysValGluGlnLeuSerAsnMe 104
|||:::||||||||||| |||||||||||||||||
246 ATCGTGTACTAGTGGCCGCAAGCCCAAGGTGGACAGTGTCCAACAT 197

104 tValValLysSerCysLysCysSer 112
|:::|:::|:::|:::|:::|:::|
196 GATGTTGGCTCTCTGAAGTGCAGC 172

seq_name: gb_est13:AA927529

seq_documentation_block:	
LOCUS	AA927529 428 bp mRNA EST 17-JUN-1998
DEFINITION	om71a11.s1 NCI_CGAP_G04 Homo sapiens cDNA clone IMAGE:1552604 3' similar to gb:X02812_cds1 TRANSFORMING GROWTH FACTOR BETA 1 PRECURSOR (HUMAN); mRNA sequence.

ACCESSION AA927529
VERSION AA927529.1 GI:3076426

KEYWORDS EST.
SOURCE human.
ORGANISM Homo s

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
1 (bases 1 to 428)
AUTHORS
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL
Unpublished (1997)

COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cqapbs-r@mail.nih.gov

Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael Emmert-Buck, M.D., Ph.D.

cdNA Library Preparation: M. Bento Soares, Ph.D.
cdNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio1.llnl.gov/bbrp/image/image.html
Insert length: 501 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 141.


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/clone_lib="DT0028"
/dev_stage="Adult"
/Note="Organ: denis_drash; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
BASE COUNT      65 a      49 c      58 g      76 t
ORIGIN

alignment_scores:
  Quality: 281.00      Length: 71
  Ratio: 4.607        Gaps: 0
  Percent Similarity: 85.915      Percent Identity: 73.239

alignment_block:
TGFB3P x AW579188/rev ..
Align seg 1/1 to reverse of: AW579188 from: 1 to: 248

42 AsnPheCysSerGlyProCysProTyrLeuArgSerAlaAspThrHrH1 58
||||: ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
220 AACATCAGAGCTGGAGCATGCCCGTATTTATGGAGTTCAGACACTCAGCA 171

58 sSerThrValLeuGlyLeuTyrAsnThrLeuAsnProGluAlaSerAla 75
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
170 CACAGGGTCTCGAGCTTATATATACCAATGAAGTCTGAAGCATCTGCTT 121

75 erProCysCysValProGlnAspLeuGluProLeuThrIleLeuTyrTyr 91
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
120 CTCCTGCTCGGGTCCCAAGATTGAACCTCTAACCATTCTCTACTAC 71

92 ValClyArgThrProLysValGluGlnLeuSerAsnMetValValLysSe 108
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
70 ATTGGCATTTACACCCCAAGATTGAACGCTTCTTATATGATTGTAAAGTC 21

108 rCysLysCysSer 112
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20 TTGCAAAATGCAGC 8

seq_name: gb_est94-BF901708

seq_documentation_block:
LOCUS      BF901708      255 bp      mRNA      EST      18-JAN-2001
DEFINITION CM2-MT0190-091200-595-a10 MT0190 Homo sapiens cDNA, mRNA sequence.
ACCESSION  BF901708
VERSION     BF901708.1 GI:12293167
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 255)
AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
            ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
            Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
            Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001

```

```

Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM2&t2=CM2-MT0190-
091200-595-a10&t3=2000-12-09&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 7
High quality sequence stop: 234.
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                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone_lib="MT0190"
                     /dev_stage="Adult"
                     /note="Organ: marrow; Vector: puc18; Site_1: SmaI; Site_2:
                     SmaI; A mini-library was made by cloning products derived
                     from ORESTES PCR (U.S. Letters Patent application No. 196
                     ,716 - Ludwig Institute for Cancer Research) profiles
                     into the pUC 18 vector. Reverse transcription of tissue
                     mRNA and cDNA amplification were performed under low
                     stringency conditions."
BASE COUNT      47 a      72 c      85 g      51 t
ORIGIN

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  Percent Similarity: 77.215      Percent Identity: 62.025

alignment_block:
TGFB3P x BF901708/rev ..
Align seg 1/1 to reverse of: BF901708 from: 1 to: 255

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239 GCATTGGACACCACTATTGCTTCAGTTCACGCGAGAGAACTGCTGCGT 190

17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTyrLysTyrValH 34
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
189 GCGGCAGCTGTACATTGACTTCCGCAAGGACCCCGCTGGAAGTGGATCC 140

34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
139 ACGAGCCCAAGGGCTACCATGCCAACTTCTGCTCGGGCCCTGCCCCATA 90

51 LeuArgSerAlaAspThrThrHisSerThr.....ValLeuGlyLeuTy 65
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
89 .....CATTTGGAGCCCTGTACAGCAGTACAGAGGTCTCTGGGCTGTGA 46

65 rAsnThrLeuAsnProGluAlaSerAlaSerProCys 77
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
45 CAACCAAGCAAAACCCGGCGCCTACGCGGCGCGCGCTGC 9

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Query Match 99.8%; Score 633; DB 3; Length 112;
Best Local Similarity 100.0%; Pred. No. 2.3e-61;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALDNTYCFRNLENCVRLYIDFRDLGKWKVHEPKGYANFCGPGPYLRSADTTHT 60
|||||
Db 1 ALDNTYCFRNLENCVRLYIDFRDLGKWKVHEPKGYANFCGPGPYLRSADTTHT 60

QY 61 VLGLYNTLNPEASPCCVQDLEPLTILYVGRTPKVEQLSNMVKCKS 112
|||||
Db 61 VLGLYNTLNPEASPCCVQDLEPLTILYVGRTPKVEQLSNMVKCKS 112

RESULT 6
US-08-481-377-25
; Sequence 25, Application US/08481377
; Patent No. 5808007
; GENERAL INFORMATION:
; APPLICANT: JOHNS HOPKINS UNIVERSITY
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-3
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SPENSLEY HORN JUBAS & LUBITZ
; STREET: 1880 CENTURY PARK EAST, FIFTH FLOOR
; CITY: LOS ANGELES
; STATE: CALIFORNIA
; COUNTRY: US
; ZIP: 90067

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/481.377
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/00666
; FILING DATE: 12-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: WETHERELL, JR. Ph.D., JOHN R.
; REGISTRATION NUMBER: 31,678
; REFERENCE/DOCKET NUMBER: FD2279 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 455-5100
; TELEFAX: (619) 455-5110

; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 114 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; IMMEDIATE SOURCE:
; CLONE: TGF-beta 3
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..114

US-08-481-377-25

Query Match 99.8%; Score 633; DB 1; Length 114;
Best Local Similarity 100.0%; Pred. No. 2.3e-61;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALDNTYCFRNLENCVRLYIDFRDLGKWKVHEPKGYANFCGPGPYLRSADTTHT 60
|||||
Db 3 ALDNTYCFRNLENCVRLYIDFRDLGKWKVHEPKGYANFCGPGPYLRSADTTHT 62

QY 61 VLGLYNTLNPEASPCCVQDLEPLTILYVGRTPKVEQLSNMVKCKS 112
|||||

Db 63 VLGLYNTLNPEASPCCVQDLEPLTILYVGRTPKVEQLSNMVKCKS 114

RESULT 7
US-08-491-835-23
; Sequence 23, Application US/08491835
; Patent No. 5821056
; GENERAL INFORMATION:
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-9
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Spensley Horn Jubas & Lubitz
; STREET: 1880 Century Park East, Suite 500
; CITY: Los Angeles
; STATE: California
; COUNTRY: US
; ZIP: 90067

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/491,835
; FILING DATE: 23-OCT-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/00685
; FILING DATE: 12-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Wetherell, Jr. Ph.D., John R.
; REGISTRATION NUMBER: 31,678
; REFERENCE/DOCKET NUMBER: FD3288
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 455-5100
; TELEFAX: (619) 455-5110

; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 114 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; IMMEDIATE SOURCE:
; CLONE: TGF-beta3
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..114

US-08-491-835-23

Query Match 99.8%; Score 633; DB 2; Length 114;
Best Local Similarity 100.0%; Pred. No. 2.3e-61;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALDNTYCFRNLENCVRLYIDFRDLGKWKVHEPKGYANFCGPGPYLRSADTTHT 60
|||||
Db 3 ALDNTYCFRNLENCVRLYIDFRDLGKWKVHEPKGYANFCGPGPYLRSADTTHT 62

QY 61 VLGLYNTLNPEASPCCVQDLEPLTILYVGRTPKVEQLSNMVKCKS 112
|||||
Db 63 VLGLYNTLNPEASPCCVQDLEPLTILYVGRTPKVEQLSNMVKCKS 114

RESULT 8
US-09-153-733A-25
; Sequence 25, Application US/09153733A
; Patent No. 6025475
; GENERAL INFORMATION:
; APPLICANT: JOHNS HOPKINS UNIVERSITY
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-3
; NUMBER OF SEQUENCES: 29

NAME: Wetherell, Jr., Ph.D., John R.
REGISTRATION NUMBER: 31,678
REFERENCE/DOCKET NUMBER: FD3288
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
TELEFAX: (619) 455-5110
INFORMATION FOR SEQ ID NO: 23
SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
IMMEDIATE SOURCE:
CLONE: TGF-beta3
FEATURE:
NAME/KEY: Protein
LOCATION: 1..114
US-09-172-062-23

Query Match 99.8%; Score 633; DB 4; Length 114;
Best Local Similarity 100.0%; Pred. No. 2.3e-61;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALDNTYCFRNLEENCVRPLYIDFRQDLGKWKVHPEKGYANFCGPGPYLRSADTTHT 60
|||||
Db 3 ALDNTYCFRNLEENCVRPLYIDFRQDLGKWKVHPEKGYANFCGPGPYLRSADTTHT 62
|||||
QY 61 VLGLYNTLNPEASAPCCVPQDLEPLTILYYVGRTPKVEQLSNMVKSKCS 112
|||||
Db 63 VLGLYNTLNPEASAPCCVPQDLEPLTILYYVGRTPKVEQLSNMVKSKCS 114
|||||

RESULT 11
PCT-US94-00624-635-24
Sequence 24, Application US/08624635
Patent No. 6204047
GENERAL INFORMATION:
APPLICANT: Lee, Se-Jin
APPLICANT: Cunningham No. 6204047een
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-10
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Spensley Horn Jubas & Lubitz
STREET: 1880 Century Park East, Suite 500
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90067
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/624,635
FILING DATE: 16-AUG-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/134,078
FILING DATE: 08-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Wetherell, Jr., Ph.D., John R.,
REGISTRATION NUMBER: 31,678
REFERENCE/DOCKET NUMBER: PD-3054
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
TELEFAX: (619) 455-5110
INFORMATION FOR SEQ ID NO: 24
SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acids
TYPE: amino acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
IMMEDIATE SOURCE:
CLONE: TGF-beta-3
FEATURE:
NAME/KEY: Protein
LOCATION: 1..114
US-08-624-635-24

Query Match 99.8%; Score 633; DB 4; Length 114;
Best Local Similarity 100.0%; Pred. No. 2.3e-61;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALDNTYCFRNLEENCVRPLYIDFRQDLGKWKVHPEKGYANFCGPGPYLRSADTTHT 60
|||||
Db 3 ALDNTYCFRNLEENCVRPLYIDFRQDLGKWKVHPEKGYANFCGPGPYLRSADTTHT 62
|||||
QY 61 VLGLYNTLNPEASAPCCVPQDLEPLTILYYVGRTPKVEQLSNMVKSKCS 112
|||||
Db 63 VLGLYNTLNPEASAPCCVPQDLEPLTILYYVGRTPKVEQLSNMVKSKCS 114
|||||

RESULT 12
PCT-US94-00666-25
Sequence 25, Application PC/TUS9400666
GENERAL INFORMATION:
APPLICANT: JOHNS HOPKINS UNIVERSITY
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-3
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: SPENSLEY HORN JUBAS & LUBITZ
STREET: 1880 CENTURY PARK EAST, FIFTH FLOOR
CITY: LOS ANGELES
STATE: CALIFORNIA
COUNTRY: US
ZIP: 90067
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/00666
FILING DATE: 12-JAN-1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: WETHERELL, JR. Ph.D., JOHN R.
REGISTRATION NUMBER: 31,678
REFERENCE/DOCKET NUMBER: FD2279 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
TELEFAX: (619) 455-5110
INFORMATION FOR SEQ ID NO: 25
SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
IMMEDIATE SOURCE:
CLONE: TGF-beta 3
FEATURE:
NAME/KEY: Protein
LOCATION: 1..114
PCT-US94-00666-25

Query Match 99.8%; Score 633; DB 5; Length 114;
Best Local Similarity 100.0%; Pred. No. 2.3e-61;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALDNTYCFRNLENCVRLYIDFRDLGKWKVHEPKGYANFCSGPCPYLRSADTTHST 60
|||||
Db 3 ALDNTYCFRNLENCVRLYIDFRDLGKWKVHEPKGYANFCSGPCPYLRSADTTHST 62
QY 61 VLGLYNTLNPEASASCCVPPQDLEPLTILYYVGRTPKVEQLSNMVKSKCS 112
|||||
Db 63 VLGLYNTLNPEASASCCVPPQDLEPLTILYYVGRTPKVEQLSNMVKSKCS 114

RESULT 13

PCT-US94-00685-23

; Sequence 23, Application PC/TUS9400685

; GENERAL INFORMATION:

; APPLICANT: THE JOHNS HOPKINS UNIVERSITY

; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-9

; NUMBER OF SEQUENCES: 26

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Spensley Horn Jubas & Lubitz

; STREET: 1880 Century Park East, Suite 500

; CITY: Los Angeles

; STATE: California

; COUNTRY: US

; ZIP: 90067

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US94/00685

; FILING DATE: 12-JAN-1994

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: Wetherell, Jr. Ph.D., John R.

; REGISTRATION NUMBER: 31,678

; REFERENCE/DOCKET NUMBER: FD3288

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (619) 455-5100

; TELEFAX: (619) 455-5110

; INFORMATION FOR SEQ ID NO: 23:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 114 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; IMMEDIATE SOURCE:

; CLONE: TGF-beta3

; FEATURE:

; NAME/KEY: Protein

; LOCATION: 1..114

PCT-US94-00685-23

Query Match

Best Local Similarity 99.8%; Score 633; DB 5; Length 114;

Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALDNTYCFRNLENCVRLYIDFRDLGKWKVHEPKGYANFCSGPCPYLRSADTTHST 60
|||||
Db 3 ALDNTYCFRNLENCVRLYIDFRDLGKWKVHEPKGYANFCSGPCPYLRSADTTHST 62

QY 61 VLGLYNTLNPEASASCCVPPQDLEPLTILYYVGRTPKVEQLSNMVKSKCS 112

|||||

Db 63 VLGLYNTLNPEASASCCVPPQDLEPLTILYYVGRTPKVEQLSNMVKSKCS 114

RESULT 14

US-08-581-529B-21

; Sequence 21, Application US/08581529B

; Patent No. 5770444

; GENERAL INFORMATION:

; APPLICANT: Lee, Se-Jin

; APPLICANT: Huynh, Thanh
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-6
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: California
; COUNTRY: USA
; ZIP: 92037

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/581,529B

; FILING DATE: 15-APR-1996

; CLASSIFICATION: 536

; ATTORNEY/AGENT INFORMATION:

; NAME: Lisa A. Haile, Ph.D.

; REGISTRATION NUMBER: 38,347

; REFERENCE/DOCKET NUMBER: 07265/082001

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (619) 678-5070

; TELEFAX: (619) 678-5099

; INFORMATION FOR SEQ ID NO: 21:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 115 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; IMMEDIATE SOURCE:

; CLONE: TGF-beta-3

; FEATURE:

; NAME/KEY: Protein

; LOCATION: 1..115

; US-08-581-529B-21

Query Match

Best Local Similarity 99.8%; Score 633; DB 1; Length 115;

Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALDNTYCFRNLENCVRLYIDFRDLGKWKVHEPKGYANFCSGPCPYLRSADTTHST 60
|||||
Db 4 ALDNTYCFRNLENCVRLYIDFRDLGKWKVHEPKGYANFCSGPCPYLRSADTTHST 63

QY 61 VLGLYNTLNPEASASCCVPPQDLEPLTILYYVGRTPKVEQLSNMVKSKCS 112

|||||

Db 64 VLGLYNTLNPEASASCCVPPQDLEPLTILYYVGRTPKVEQLSNMVKSKCS 115

RESULT 15

US-08-455-559-27

; Sequence 27, Application US/08455559

; Patent No. 5801014

; GENERAL INFORMATION:

; APPLICANT: LEE, SE-JIN

; APPLICANT: HUYNH, THANH

; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-5

; NUMBER OF SEQUENCES: 27

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SPENSLEY HORN JUBAS & LUBITZ

; STREET: 1880 CENTURY PARK EAST, FIFTH FLOOR

; CITY: LOS ANGELES

; STATE: CALIFORNIA

; COUNTRY: US

; ZIP: 90067

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/455,559
FILING DATE: 31-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/003,144
FILING DATE: 12-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: WETHERELL, JR. PH.D., JOHN R.
REGISTRATION NUMBER: 31,678
REFERENCE/DOCKET NUMBER: PD280
TELEPHONE: 619/455-5100
TELEFAX: 619/455-5110
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 115 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
IMMEDIATE SOURCE:
CLONE: TGF-beta-3
FEATURE:
NAME/KEY: Protein
LOCATION: 1..115
US-08-455-559-27

Query Match 99.8%; Score 633; DB 1; Length 115;
Best Local Similarity 100.0%; Pred. No. 2.4e-61;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALDNTNYCFRNLEENCCVRPLYIDFRQDLGKWKVHPEKGYANFCGPGPYLRSADTTHTST 60
Db 4 ALDNTNYCFRNLEENCCVRPLYIDFRQDLGKWKVHPEKGYANFCGPGPYLRSADTTHTST 63

Qy 61 VLGLYNTLNPEASAPCCVPQDLEPLTILYVGRTPKVEQLSNMVKSCKS 112
Db 64 VLGLYNTLNPEASAPCCVPQDLEPLTILYVGRTPKVEQLSNMVKSCKS 115

RESULT 16
US-08-581-528A-21
Sequence 21, Application US/08581528A
Patent No. 5986058
GENERAL INFORMATION:
APPLICANT: Lee, Se-Jin
APPLICANT: Huynh, Thanh
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-7
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/581,528A
FILING DATE: 03-Sept-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/089,670
FILING DATE: 09-JUL-1993
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Lisa A. Haile, Ph.D.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/081001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 115 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
IMMEDIATE SOURCE:
CLONE: TGF-beta-3
FEATURE:
NAME/KEY: Protein
LOCATION: 1..115
US-08-581-528A-21

Query Match 99.8%; Score 633; DB 2; Length 115;
Best Local Similarity 100.0%; Pred. No. 2.4e-61;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALDNTNYCFRNLEENCCVRPLYIDFRQDLGKWKVHPEKGYANFCGPGPYLRSADTTHTST 60
Db 4 ALDNTNYCFRNLEENCCVRPLYIDFRQDLGKWKVHPEKGYANFCGPGPYLRSADTTHTST 63

Qy 61 VLGLYNTLNPEASAPCCVPQDLEPLTILYVGRTPKVEQLSNMVKSCKS 112
Db 64 VLGLYNTLNPEASAPCCVPQDLEPLTILYVGRTPKVEQLSNMVKSCKS 115

RESULT 17
US-09-097-616-21
Sequence 21, Application US/09097616
Patent No. 6090563
GENERAL INFORMATION:
APPLICANT: Lee, Se-Jin
APPLICANT: Huynh, Thanh
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-6
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: California
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/097,616
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/581,529
FILING DATE: 15-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Lisa A. Haile, Ph.D.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/082001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 678-5070
TELEFAX: (619) 678-5099
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 115 amino acids


```

: Sequence 21, Application PC/TUS9407762
:
: GENERAL INFORMATION:
:
: APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
: TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-6
: NUMBER OF SEQUENCES: 21
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Spensley Horn Jubas & Lubitz
: STREET: 1880 Century Park East, Suite 500
: CITY: Los Angeles
: STATE: California
: COUNTRY: USA
: ZIP: 90067
:
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: PCT/US94/07762
: FILING DATE: 08-JUL-1994
: CLASSIFICATION:
:
: ATTORNEY/AGENT INFORMATION:
: NAME: TUMARKIN, LISA A., PH.D.
: REGISTRATION NUMBER: P-38,347
: REFERENCE/DOCKET NUMBER: PD2349
:
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (619) 455-5100
: TELEFAX: (619) 455-5110
: INFORMATION FOR SEQ ID NO: 21:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 115 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: IMMEDIATE SOURCE:
: CLONE: TGF-beta-3
: FEATURE:
:
: NAME/KEY: Protein
: LOCATION: 1..115
:
: PCT-US94-07762-21

```

```

Query Match          99.8%; Score 633; DB 5; Length 115;
Best Local Similarity 100.0%; Pred. NO. 2.4e-61;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALDNTYCFRNLNLENCPCVRPLYIDFRQDLGKWKWHEPKGYANFCSGPCPYLRSADTTTST 60
    |||||
Db 4 ALDNTYCFRNLNLENCPCVRPLYIDFRQDLGKWKWHEPKGYANFCSGPCPYLRSADTTTST 63
    |||||
QY 61 VLGLYNTLNPEASAPCCVPQDLEPLTILYYVGRTPKVEQLSNMVKSKCS 112
    |||||
Db 64 VLGLYNTLNPEASAPCCVPQDLEPLTILYYVGRTPKVEQLSNMVKSKCS 115
    |||||

RESULT 21
PCT-US94-07799-21
; Sequence 21, Application PC/TUS9407799
; GENERAL INFORMATION:
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-7
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Spensley Horn Jubas & Lubitz
; STREET: 1880 Century Park East, Suite 500
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

```

```

> OPERATING SYSTEM: PC-DOS/MS-DOS
> SOFTWARE: Patentin Release #1.0, Version #1.25
> CURRENT APPLICATION DATA:
> APPLICATION NUMBER: PCT/US94/07799
> FILING DATE: 08-JUL-1994
> CLASSIFICATION:
> ATTORNEY/AGENT INFORMATION:
> NAME: TUMARKIN, LISA A., PH.D.
> REGISTRATION NUMBER: P-38,347
> REFERENCE/DOCKET NUMBER: FD-2348
> TELECOMMUNICATION INFORMATION:
> TELEPHONE: (619) 455-5100
> TELEFAX: (619) 455-5110
> INFORMATION FOR SEQ ID NO: 21:
> SEQUENCE CHARACTERISTICS:
> LENGTH: 115 amino acids
> TYPE: amino acid
> STRANDEDNESS: single
> TOPOLOGY: linear
> MOLECULE TYPE: protein
> IMMEDIATE SOURCE:
> CLONE: TGF-beta-3
> FEATURE:
> NAME/KEY: Protein
> LOCATION: 1..115
> PCT-US94-07799-21

Query Match 99.8%; Score 633; DB 5; Length 115;
Best Local Similarity 100.0%; Pred. No. 2.4e-61;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALDTNYCFRNLEENCVRPLYIDFRQDLGKWKWHEPKGYANFCGPGCYLRSADTTHST 60
Db 4 ALDTNYCFRNLEENCVRPLYIDFRQDLGKWKWHEPKGYANFCGPGCYLRSADTTHST 63

Qy 61 VLGLYNTLNPRASAPCCVPQDLPLTLTYVVGRTPKVEQLSNMVKSCKGS 112
Db 64 VLGLYNTLNPRASAPCCVPQDLPLTLTYVVGRTPKVEQLSNMVKSCKGS 115

RESULT 22
PCT-US91-01861-3
> Sequence 3, Application PC/TUS9101861
> GENERAL INFORMATION:
> APPLICANT: Genentech, Inc.
> TITLE OF INVENTION: Method of Predisposing Mammals to
> TITLE OF INVENTION: Accelerated Tissue Repair
> NUMBER OF SEQUENCES: 5
> CORRESPONDENCE ADDRESS:
> ADDRESSEE: Genentech, Inc.
> STREET: 460 Point San Bruno Blvd
> CITY: South San Francisco
> STATE: California
> COUNTRY: USA
> ZIP: 94080
> COMPUTER READABLE FORM:
> MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
> COMPUTER: IBM PC compatible
> OPERATING SYSTEM: PC-DOS/MS-DOS
> SOFTWARE: patin (Genentech)
> CURRENT APPLICATION DATA:
> APPLICATION NUMBER: PCT/US91/01861
> FILING DATE: 19910320
> CLASSIFICATION: 514
> PRIOR APPLICATION DATA:
> APPLICATION NUMBER: U.S. Ser. No. 07/504,495
> FILING DATE: 4 April 1990
> ATTORNEY/AGENT INFORMATION:
> NAME: Hasak, Janet E.
> REGISTRATION NUMBER: 28,616
> REFERENCE/DOCKET NUMBER: 637
> TELECOMMUNICATION INFORMATION:

```

TELEPHONE: 415/266-1896
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO.: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 410 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
PCT-US91-01861-3

```
Query Match          99.8%; Score 633; DB 5; Length 410;
Best Local Similarity 100.0%; Pred. No. 1.1e-60;
Matches 112; Conservative 0; Mismatches 0; Indels
```

[illegible]

RESULT 23
US-08-132-405-3
: Sequence 3, Application US/08132405
: Patent No. 5409896 ✓
: GENERAL INFORMATION:
: APPLICANT: Ammann, Arthur J.
: APPLICANT: Rudman, Christopher G.
: TITLE OF INVENTION: Method of Inducing Bone Growth Using
: TITLE OF INVENTION: TGF-Beta
: NUMBER OF SEQUENCES: 5
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Genentech, Inc.
: STREET: 460 Point San Bruno Blvd
: CITY: South San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94080

```

COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/132,405
FILING DATE: 06-OCT-1993
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/063841
FILING DATE: 18-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/790856
FILING DATE: 12-NOV-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/401906
FILING DATE: 01-SEP-1989
ATTORNEY/AGENT INFORMATION:
NAME: Hasak, Janet E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: 597D1C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1896
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 412 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-132-405-3

```

```

Query Match          99.8%; Score 633; DB 1; Length 412;
Best Local Similarity 100.0%; Pred. No. 1.1e-60;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

[illegible]

RESULT 24
US-08-395-939A-3
Sequence 3, Application US/08395939A
Patent No. 5604204
GENERAL INFORMATION:
APPLICANT: Ammann, Arthur J.
APPLICANT: Rudman, Christopher G.
TITLE OF INVENTION: TGF-BETA COMPOSITION FOR INDUCING BONE
TITLE OF INVENTION: TGF-BETA COMPOSITION FOR INDUCING BONE
TITLE OF INVENTION: TGF-BETA COMPOSITION FOR INDUCING BONE
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/395,939A
FILING DATE: 27-FEB-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/132405
FILING DATE: 12-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/063841
FILING DATE: 18-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/790856
FILING DATE: 12-NOV-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/401906
FILING DATE: 1-SEP-1989
ATTORNEY/AGENT INFORMATION:
NAME: Hasak, Janet E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: P0597D1C2D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1896
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO. 3
SEQUENCE CHARACTERISTICS:
LENGTH: 412 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-395-939A-3

Query Match 99.8%; Score 633; DB 1; Length 412;
Best Local Similarity 100.0%; Pred. No. 1.1e-60;
Matches 112; Conservative 0; Mismatches 0; Indels

QY 1 ALDNYCFRNLENCVRPLYIDFRQDLGKWKVHPEKGYANFCSGCPYLRSDTTHST 60
Db 301 ALDNYCFRNLENCVRPLYIDFRQDLGKWKVHPEKGYANFCSGCPYLRSDTTHST 360
QY 61 VLGLYNTLNPEASPCCVQDLEPLTILYVGRTPKVEQLSNMVKSKCS 112
Db 361 VLGLYNTLNPEASPCCVQDLEPLTILYVGRTPKVEQLSNMVKSKCS 412

RESULT 25
PCT-US91-04541-2
; Sequence 2, Application PC/TUS9104541
; GENERAL INFORMATION:
; APPLICANT: Oncogene Science Inc.
; TITLE OF INVENTION: TISSUE DERIVED TUMOR GROWTH INHIBITORS
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PC-DOS/MS-DOS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/04541
; FILING DATE: 19910625
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 1919/22669-F-PCT
; TELEPHONE: (212)977-9550
; TELEX: 422523 COOP UI
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 412 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US91-04541-2

Query Match 99.8%; Score 633; DB 5; Length 412;
Best Local Similarity 100.0%; Pred. No. 1.le-60;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ALDNYCFRNLENCVRPLYIDFRQDLGKWKVHPEKGYANFCSGCPYLRSDTTHST 60
Db 301 ALDNYCFRNLENCVRPLYIDFRQDLGKWKVHPEKGYANFCSGCPYLRSDTTHST 360
QY 61 VLGLYNTLNPEASPCCVQDLEPLTILYVGRTPKVEQLSNMVKSKCS 112
Db 361 VLGLYNTLNPEASPCCVQDLEPLTILYVGRTPKVEQLSNMVKSKCS 412

RESULT 26
5262319-2
; Patent No. 5262319
; APPLICANT: IWATA, KENNETH K.; FOULKES, J. GORDON; DIJKE,
; PETER T.; HALEY, JOHN D.
; TITLE OF INVENTION: METHOD FOR OBTAINING BONE MARROW FREE
; OF TUMOR CELLS USING TRANSFORMING GROWTH FACTOR B3
; NUMBER OF SEQUENCES: 9
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/543,341
; FILING DATE: 25-JUN-1990

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 353,410
; FILING DATE: 17-MAY-1989
; APPLICATION NUMBER: 183,410
; FILING DATE: 20-APR-1988
; APPLICATION NUMBER: 111,022
; FILING DATE: 20-OCT-1987
; APPLICATION NUMBER: 922,121
; FILING DATE: 20-OCT-1986
; APPLICATION NUMBER: 847,931
; FILING DATE: 07-APR-1986
; APPLICATION NUMBER: 725,003
; FILING DATE: 19-APR-1985
; SEQ ID NO: 2:
; LENGTH: 412
5262319-2

Query Match 99.8%; Score 633; DB 6; Length 412;
Best Local Similarity 100.0%; Pred. No. 1.le-60;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALDNYCFRNLENCVRPLYIDFRQDLGKWKVHPEKGYANFCSGCPYLRSDTTHST 60
Db 301 ALDNYCFRNLENCVRPLYIDFRQDLGKWKVHPEKGYANFCSGCPYLRSDTTHST 360
QY 61 VLGLYNTLNPEASPCCVQDLEPLTILYVGRTPKVEQLSNMVKSKCS 112
Db 361 VLGLYNTLNPEASPCCVQDLEPLTILYVGRTPKVEQLSNMVKSKCS 412

RESULT 27
US-08-927-433-4
; Sequence 4, Application US/08927433
; Patent No. 6107476
; GENERAL INFORMATION:
; APPLICANT: Erlander, Mark G.
; APPLICANT: Huang, Shaoming
; APPLICANT: Jackson, Michael A.
; APPLICANT: Peterson, Per A.
; TITLE OF INVENTION: PROTEIN GROWTH FACTOR FOR TREATING PROSTATE CANCER, AND REL
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Johnson & Johnson
; STREET: One J & J Plaza
; CITY: New Brunswick
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 08933
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/927,433
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Morrison, Alan J.
; REGISTRATION NUMBER: 37,399
; REFERENCE/DOCKET NUMBER: ORT-849
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 732-524-3592
; TELEFAX: 732-524-2808
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 112 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-927-433-4


```

Query Match          93.8%; Score 595; DB 3; Length 112;
Best Local Similarity 92.9%; Pred. No. 2.9e-57;
Matches 104; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 ALDNTYCFRNLENCVVRPLYIDFRQDLGKWKWHEHPKGYGANFCSGCPYLRSADTTHT 60
DB 1 ALDNTYCFSSFNCCVQRQLYIDFRKDLGKWKWHEHPKGYHANFCSGCPYLRSADTTHT 60

QY 61 VLGLYNTLNPEASASPCCVQDLEPLTILYYVGRTPKVEQLSNMVKSKCKS 112
DB 61 VLGLYNTLNPEASASPCCVQDLEPLTILYYVGRTPKVEQLSNMVKSKCKS 112

RESULT 33
US-09-123-233-10
; Sequence 10, Application US/09123233
; Patent No. 6057430
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: No. 6057430el process for the production of
; TITLE OF INVENTION: biologically active dimeric protein
; NUMBER OF SEQUENCES: 14
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/123,233
; FILING DATE:
; CLASSIFICATION: 530
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 112 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-123-233-10

Query Match          93.2%; Score 591; DB 3; Length 112;
Best Local Similarity 91.1%; Pred. No. 7.8e-57;
Matches 102; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY 1 ALDNTYCFRNLENCVVRPLYIDFRQDLGKWKWHEHPKGYGANFCSGCPYLRSADTTHT 60
DB 1 ALDAAACYFNRVQDNCCLRLPYIDFRKDLGKWKWHEHPKGYNANFCSGCPYLRSADTTHT 60

QY 61 VLGLYNTLNPEASASPCCVQDLEPLTILYYVGRTPKVEQLSNMVKSKCKS 112
DB 61 VLGLYNTLNPEASASPCCVQDLEPLTILYYVGRTPKVEQLSNMVKSKCKS 112

RESULT 34
US-09-123-233-12
; Sequence 12, Application US/09123233
; Patent No. 6057430
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: No. 6057430el process for the production of
; TITLE OF INVENTION: biologically active dimeric protein
; NUMBER OF SEQUENCES: 14
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/123,233
; FILING DATE:
; CLASSIFICATION: 530
; INFORMATION FOR SEQ ID NO: 12:

```


APPLICANT: KECK, PETER
APPLICANT: SMART, JOHN
TITLE OF INVENTION: SINGLE-CHAIN ANALOGS OF TGF-B
TITLE OF INVENTION: SUPERFAMILY (MORPHONS)
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: PATENT ADMINISTRATOR; TESTA, HURWITZ &
ADDRESSEE: THIBEAULT, LLP
STREET: 125 HIGH STREET
CITY: BOSTON
STATE: MA
COUNTRY: USA
ZIP: 02110
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/478,097A
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: PITCHER ESO, EDMUND R
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: CRP-080
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-248-7000
TELEFAX: 617-248-7100
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 98 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: protein
LOCATION: 1..98
OTHER INFORMATION: /note= "TGF-B3 SEQUENCE"
US-08-478-097A-3

Query Match 85.38; Score 541; DB 3; Length 98;
Best Local Similarity 99.08; Pred. No. 1.7e-51;
Matches 97; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 15 CCVRPLYIDFQDLGKWKVHPKGYANFCGPGCPYLRSADTTHSTVLGLYNTLNPEASA 74
Db 1 CCVRPLYIDFQDLGKWKVHPKGYANFCGPGCPYLRSADTTHSTVLGLYNTLNPEASA 60
Qy 75 SPCCVPQDLEPLTILYVVGRTPKVEQLSNMVKSKCS 112
Db 61 SPCCVPQDLEPLTILYVVGRTPKVEQLSNMVKSKCS 98
RESULT 38
US-07-979-441-2
Sequence 2, Application US/07979441
Patent No. 5462925
GENERAL INFORMATION:
APPLICANT: OGAWA, YASUSHI
APPLICANT: SCHMIDT, DAVID
APPLICANT: DASCH, JAMES
TITLE OF INVENTION: NOVEL BETA-TYPE TRANSFORMING GROWTH
TITLE OF INVENTION: FACTOR
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: California
COUNTRY: USA

ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/979,441
FILING DATE: 19921120
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/614,306
FILING DATE: 16-NOV-1990
ATTORNEY/AGENT INFORMATION:
NAME: CIOTLI, THOMAS E.
REGISTRATION NUMBER: 21,013
REFERENCE/DOCKET NUMBER: 220952024800
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-813-5600
TELEFAX: 415-494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 112 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-979-441-2
Query Match 84.48; Score 535; DB 1; Length 112;
Best Local Similarity 79.5%; Pred. No. 8.6e-51;
Matches 89; Conservative 14; Mismatches 9; Indels 0; Gaps 0;
Qy 1 ALDTNYCFRNLENCVRLPYIDFQDLGKWKVHPKGYANFCGPGCPYLRSADTTHST 60
Db 1 ALDAAVCFRNVDNCCRLPYIDFKRDLGKWKVHPKGYANFCGPGCPYLRSADTTHST 60
Qy 61 VLGLYNTLNPEASAPCCVPQDLEPLTILYVVGRTPKVEQLSNMVKSKCS 112
Db 61 VLGLYNTLNPEASAPCCVPQDLEPLTILYVVGRTPKVEQLSNMVKSKCS 112
RESULT 39
US-08-486-057B-42
Sequence 42, Application US/08486057B
Patent No. 5650494
GENERAL INFORMATION:
APPLICANT: Cerletti, Nico
APPLICANT: McMaster, Gary K.
APPLICANT: Cox, David
APPLICANT: Schmitz, Albert
APPLICANT: Meyhack, Bernd
TITLE OF INVENTION: Process for Refolding Recombinantly
TITLE OF INVENTION: Produced TGF-beta-like Proteins
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Henry P. No. 5650494ak
STREET: 520 White Plains Road, P.O. Box 2005
CITY: Tarrytown
STATE: New York
COUNTRY: U.S.A.
ZIP: 10591-9005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,057B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:

TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 277-5110
TELEFAX: (908) 277-4306
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 112 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-789-588-42

Query Match 84.4%; Score 535; DB 2; Length 112;
Best Local Similarity 79.5%; Pred. No. 8.6e-51;
Matches 89; Conservative 14; Mismatches 9; Indels 0; Gaps 0;
QY 1 ALDNTYCFRNLENCVVRPLYIDFRDLGKWKVHEPKGYANFCGPPYLRSDTTHST 60
||| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 ALDAAFCFRNVQDNCCLRPYIDFKRDLGKWKVHEPKGYANFCAGACPYLWSSDTHSR 60
||| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 61 VLGlyNTLNPEASAPCCVPQDLEPLTILYVGRTPKVEQLSNMIVKSKCS 112
||| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 VLSLYNTINPEASAPCCVSQDLEPLTILYIGKTPKIEQLSNMIVKSKCS 112
||| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 42
US-08-691-794-5
Sequence 5, Application US/08691794
Patent No. 6057428
GENERAL INFORMATION:
APPLICANT: Keyt, Bruce A.
APPLICANT: Nguyen, Francis H.
APPLICANT: Ferrara, Napoleone
APPLICANT: Cunningham, Brian C.
APPLICANT: Wells, James A.
APPLICANT: Li, Bing
TITLE OF INVENTION: Variants of Vascular Endothelial Cell
TITLE OF INVENTION: Growth factor, Their Uses, and Processes for their
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: United States
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/691,794
FILING DATE: 02-AUG-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/002,827
FILING DATE: 25-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/567,200
FILING DATE: 05-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Walter H.
REGISTRATION NUMBER: 24,190
REFERENCE/DOCKET NUMBER: A-63758/WHO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 112 amino acids

TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-691-794-5
Query Match 84.4%; Score 535; DB 3; Length 112;
Best Local Similarity 79.5%; Pred. No. 8.6e-51;
Matches 89; Conservative 14; Mismatches 9; Indels 0; Gaps 0;
QY 1 ALDNTYCFRNLENCVVRPLYIDFRDLGKWKVHEPKGYANFCGPPYLRSDTTHST 60
||| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 ALDAAFCFRNVQDNCCLRPYIDFKRDLGKWKVHEPKGYANFCAGACPYLWSSDTHSR 60
||| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 61 VLGlyNTLNPEASAPCCVPQDLEPLTILYVGRTPKVEQLSNMIVKSKCS 112
||| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 VLSLYNTINPEASAPCCVSQDLEPLTILYIGKTPKIEQLSNMIVKSKCS 112
||| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
RESULT 43
US-09-123-233-4
Sequence 4, Application US/09123233
Patent No. 6057430
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: No. 6057430el process for the production of
TITLE OF INVENTION: biologically active dimeric protein
NUMBER OF SEQUENCES: 14
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/123,233
FILING DATE:
CLASSIFICATION: 530
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 112 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-123-233-4

Query Match 84.4%; Score 535; DB 3; Length 112;
Best Local Similarity 79.5%; Pred. No. 8.6e-51;
Matches 89; Conservative 14; Mismatches 9; Indels 0; Gaps 0;
QY 1 ALDNTYCFRNLENCVVRPLYIDFRDLGKWKVHEPKGYANFCGPPYLRSDTTHST 60
||| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 ALDAAFCFRNVQDNCCLRPYIDFKRDLGKWKVHEPKGYANFCAGACPYLWSSDTHSR 60
||| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 61 VLGlyNTLNPEASAPCCVPQDLEPLTILYVGRTPKVEQLSNMIVKSKCS 112
||| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 VLSLYNTINPEASAPCCVSQDLEPLTILYIGKTPKIEQLSNMIVKSKCS 112
||| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
RESULT 44
US-08-927-433-3
Sequence 3, Application US/08927433
Patent No. 6107476
GENERAL INFORMATION:
APPLICANT: Erlanger, Mark G.
APPLICANT: Huang, Shaoming
APPLICANT: Jackson, Michael A.
APPLICANT: Peterson, Per A.
TITLE OF INVENTION: PROTEIN GROWTH FACTOR FOR TREATING PROSTATE CANCER, AND REL
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Johnson & Johnson

```
; STREET: One J & J Plaza
; CITY: New Brunswick
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 08933
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/927,433
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Morrison, Alan J.
; REGISTRATION NUMBER: 37,399
; REFERENCE/DOCKET NUMBER: ORT-849
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 732-524-3592
; TELEFAX: 732-524-2808
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 112 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-927-433-3

Query Match      84.4%; Score 535; DB 3; Length 112;
Best Local Similarity 79.5%; Pred. No. 8.6e-51;
Matches 89; Conservative 14; Mismatches 9; Indels 0; Gaps 0;

QY 1 ALDNTNYCFRNLEENCCVRPLYIDFRDLGKWKVHEPKGYANFCGPGCPYLRSADTTHST 60
   ||| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 ALDAAAYCFRNVDNCCLRPLYIDFKRDLGKWKVHEPKGYANFCAGACPYLWSSDTQHSR 60

QY 61 VLGLYNTLNPEASAPCCVPQDLEPLTILYVGRTPKVEQLSNMVKSKCS 112
   || |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 VLSLYNTINPEASAPCCVSDLEPLTILYVGRTPKVEQLSNMVKSKCS 112

RESULT 45
US-08-481-377-24
; Sequence 24, Application US/08481377
; Patent No. 5808007
; GENERAL INFORMATION:
; APPLICANT: JOHNS HOPKINS UNIVERSITY
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-3
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SPENSLEY HORN JUBAS & LUBITZ
; STREET: 1880 CENTURY PARK EAST, FIFTH FLOOR
; CITY: LOS ANGELES
; STATE: CALIFORNIA
; COUNTRY: US
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/481,377
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/00666
; FILING DATE: 12-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: WETHERELL, JR. Ph.D., JOHN R.
```

```
; REGISTRATION NUMBER: 31,678
; REFERENCE/DOCKET NUMBER: FD2279 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 455-5100
; TELEFAX: (619) 455-5110
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 114 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; IMMEDIATE SOURCE:
; CLONE: TGF-beta 2
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..114
; US-08-481-377-24

Query Match      84.4%; Score 535; DB 1; Length 114;
Best Local Similarity 79.5%; Pred. No. 8.8e-51;
Matches 89; Conservative 14; Mismatches 9; Indels 0; Gaps 0;

QY 1 ALDNTNYCFRNLEENCCVRPLYIDFRDLGKWKVHEPKGYANFCGPGCPYLRSADTTHST 60
   ||| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 3 ALDAAAYCFRNVDNCCLRPLYIDFKRDLGKWKVHEPKGYANFCAGACPYLWSSDTQHSR 62

QY 61 VLGLYNTLNPEASAPCCVPQDLEPLTILYVGRTPKVEQLSNMVKSKCS 112
   || |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 63 VLSLYNTINPEASAPCCVSDLEPLTILYVGRTPKVEQLSNMVKSKCS 114

RESULT 46
US-08-491-835-22
; Sequence 22, Application US/08491835
; Patent No. 5821056
; GENERAL INFORMATION:
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-9
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Spensley Horn Jubas & Lubitz
; STREET: 1880 Century Park East, Suite 500
; CITY: Los Angeles
; STATE: California
; COUNTRY: US
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/491,835
; FILING DATE: 23-OCT-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/00685
; FILING DATE: 12-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Wetherell, Jr. Ph.D., John R.
; REGISTRATION NUMBER: 31,678
; REFERENCE/DOCKET NUMBER: FD3288
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 455-5100
; TELEFAX: (619) 455-5110
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 114 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
```

MOLECULE TYPE: protein
IMMEDIATE SOURCE:
CLONE: TGF-beta2
FEATURE:
NAME/KEY: Protein
LOCATION: 1..114
US-08-491-835-22

Query Match 84.4%; Score 535; DB 2; Length 114;
Best Local Similarity 79.5%; Pred. No. 8.8e-51;
Matches 89; Conservative 14; Mismatches 9; Indels 0; Gaps 0;

QY 1 ALDTNYCFRNLENCVRRPLYIDFRDLGKWKVHEPKGYANFCGPGPYLRSADTTHST 60
||| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 3 ALDAAVCFRNVQDNCCLRPYIDFKRDLGKWKIHEPKGYANFCAGACPYLWSSDTQHSR 62

QY 61 VLGLYNTLNPEASAPCCVPQDLEPLTILYVGRTPKVEQLSNMIVKSCKS 112
|| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 63 VLSLYNTINPEASAPCCVSQDLEPLTILYIGTKPKIEQLSNMIVKSCKS 114

RESULT 47
US-09-153-733A-24
; Sequence 24, Application US/09153733A
; Patent No. 6025475
; GENERAL INFORMATION:
; APPLICANT: JOHNS HOPKINS UNIVERSITY
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-3
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SPENSLEY HORN JUBAS & LUBITZ
; STREET: 1880 CENTURY PARK EAST, FIFTH FLOOR
; CITY: LOS ANGELES
; STATE: CALIFORNIA
; COUNTRY: US
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/153.733A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/481,377
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: WETHERELL, JR. Ph.D., JOHN R.
; REGISTRATION NUMBER: 31,678
; REFERENCE/DOCKET NUMBER: FD2279 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 455-5100
; TELEFAX: (619) 455-5110
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 114 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; IMMEDIATE SOURCE:
; CLONE: TGF-beta 2
; NAME/KEY: Protein
; LOCATION: 1..114
US-09-153-733A-24

Query Match 84.4%; Score 535; DB 3; Length 114;
Best Local Similarity 79.5%; Pred. No. 8.8e-51;

Matches 89; Conservative 14; Mismatches 9; Indels 0; Gaps 0;

QY 1 ALDTNYCFRNLENCVRRPLYIDFRDLGKWKVHEPKGYANFCGPGPYLRSADTTHST 60
||| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 3 ALDAAVCFRNVQDNCCLRPYIDFKRDLGKWKIHEPKGYANFCAGACPYLWSSDTQHSR 62

QY 61 VLGLYNTLNPEASAPCCVPQDLEPLTILYVGRTPKVEQLSNMIVKSCKS 112
|| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 63 VLSLYNTINPEASAPCCVSQDLEPLTILYIGTKPKIEQLSNMIVKSCKS 114

RESULT 48
US-08-946-092A-22
; Sequence 22, Application US/08946092A
; Patent No. 6030617
; GENERAL INFORMATION:
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-9
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Spensley Horn Jubas & Lubitz
; STREET: 1880 Century Park East, Suite 500
; CITY: Los Angeles
; STATE: California
; COUNTRY: US
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/946,092A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/491,835
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Wetherell, Jr. Ph.D., John R.
; REGISTRATION NUMBER: 31,678
; REFERENCE/DOCKET NUMBER: FD3288
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 455-5100
; TELEFAX: (619) 455-5110
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 114 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; IMMEDIATE SOURCE:
; CLONE: TGF-beta2
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..114
US-08-946-092A-22

Query Match 84.4%; Score 535; DB 3; Length 114;
Best Local Similarity 79.5%; Pred. No. 8.8e-51;

Matches 89; Conservative 14; Mismatches 9; Indels 0; Gaps 0;

QY 1 ALDTNYCFRNLENCVRRPLYIDFRDLGKWKVHEPKGYANFCGPGPYLRSADTTHST 60
||| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 3 ALDAAVCFRNVQDNCCLRPYIDFKRDLGKWKIHEPKGYANFCAGACPYLWSSDTQHSR 62

QY 61 VLGLYNTLNPEASAPCCVPQDLEPLTILYVGRTPKVEQLSNMIVKSCKS 112
|| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 63 VLSLYNTINPEASAPCCVSQDLEPLTILYIGTKPKIEQLSNMIVKSCKS 114

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RESULT 49
US-09-172-062-22
; Sequence 22, Application US/09172062
; Patent No. 6191261
; GENERAL INFORMATION:
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-9
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Spensley Horn Jubas & Lubitz
; STREET: 1880 Century Park East, Suite 500
; CITY: Los Angeles
; STATE: California
; COUNTRY: US
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/172,062
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/491,835
; FILING DATE: 23-OCT-1995
; APPLICATION NUMBER: PCT/US94/00685
; FILING DATE: 12-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Wetherell, Jr., Ph.D., John R.
; REGISTRATION NUMBER: 31,678
; REFERENCE/DOCKET NUMBER: FD3288
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 455-5100
; TELEFAX: (619) 455-5110
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 114 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; IMMEDIATE SOURCE:
; CLONE: TGF-beta2
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..114
US-09-172-062-22

Query Match 84.4%; Score 535; DB 4; Length 114;
Best Local Similarity 79.5%; Pred. No. 8.8e-51;
Matches 89; Conservative 14; Mismatches 9; Indels 0; Gaps 0;

QY 1 ALDNTNYCFRNLENCVRRPLYIDFRODLGKWKVHEPKGYANFCSGPCPYLRSADTTHTST 60
Db 3 ALDAAYCFRNVQDNCCLRPYIDFKRDLGKWKVHEPKGYANFCAGACPYLWSSDTQHSR 62
QY 61 VLGLYNTLNPEASAPCCVPQDLEPLTILYVYGRTPKVEQLSNMVKSKCS 112
Db 63 VLSLYNTLNPEASAPCCVSQDLEPLTILYIGKTPKIEQLSNMIVKSKCS 114

RESULT 50
US-08-624-635-23
; Sequence 23, Application US/08624635
; Patent No. 6204047
; GENERAL INFORMATION:
; APPLICANT: Lee, Se-Jin
; APPLICANT: Cunningham, No. 6204047een
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-10
; NUMBER OF SEQUENCES: 26
```

```
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Spensley Horn Jubas & Lubitz
; STREET: 1880 Century Park East, Suite 500
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/624,635
; FILING DATE: 16-AUG-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/134,078
; FILING DATE: 08-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Wetherell, Jr., Ph.D., John R.,
; REGISTRATION NUMBER: 31,678
; REFERENCE/DOCKET NUMBER: PD-3054
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 455-5100
; TELEFAX: (619) 455-5110
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 114 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; IMMEDIATE SOURCE:
; CLONE: TGF-beta-2
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..114
US-08-624-635-23

Query Match 84.4%; Score 535; DB 4; Length 114;
Best Local Similarity 79.5%; Pred. No. 8.8e-51;
Matches 89; Conservative 14; Mismatches 9; Indels 0; Gaps 0;

QY 1 ALDNTNYCFRNLENCVRRPLYIDFRODLGKWKVHEPKGYANFCSGPCPYLRSADTTHTST 60
Db 3 ALDAAYCFRNVQDNCCLRPYIDFKRDLGKWKVHEPKGYANFCAGACPYLWSSDTQHSR 62
QY 61 VLGLYNTLNPEASAPCCVPQDLEPLTILYVYGRTPKVEQLSNMVKSKCS 112
Db 63 VLSLYNTLNPEASAPCCVSQDLEPLTILYIGKTPKIEQLSNMIVKSKCS 114

RESULT 51
PCT-US94-00666-24
; Sequence 24, Application PC/TUS9400666
; GENERAL INFORMATION:
; APPLICANT: JOHNS HOPKINS UNIVERSITY
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-3
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SPENSLEY HORN JUBAS & LUBITZ
; STREET: 1880 CENTURY PARK EAST, FIFTH FLOOR
; CITY: LOS ANGELES
; STATE: CALIFORNIA
; COUNTRY: US
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
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;;
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US94/006666
;; FILING DATE: 12-JAN-1994
;; CLASSIFICATION:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: WETHERELL, JR. Ph.D., JOHN R.
;; REGISTRATION NUMBER: 31,678
;; REFERENCE/DOCKET NUMBER: FD2279 PCT
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (619) 455-5100
;; TELEFAX: (619) 455-5110
;; INFORMATION FOR SEQ ID NO: 24:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 114 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; IMMEDIATE SOURCE:
;; CLONE: TGF-beta 2
;; FEATURE:
;; NAME/KEY: Protein
;; LOCATION: 1..114
PCT-US94-00666-24

Query Match 84.4%; Score 535; DB 5; Length 114;
Best Local Similarity 79.5%; Pred. No. 8.8e-51;
Matches 89; Conservative 14; Mismatches 9; Indels 0; Gaps 0;
Qy 1 ALDNYCFRNLENCVRPLYIDFRQDLGWKWHPEKGYIANFCGCPYLRSDTTHST 60
Db 3 ALDAAFCFRNVQNCCLRPYIDFKRDLGWKWHPEKGYIANFCAGACPYLWSSDTQHSR 62
Qy 61 VLGLYNTLNPEASAPCCVPQDLEPLTILYYVGRTPKVEQLSNMVKSKCS 112
Db 63 VLSLYNTLNPEASAPCCVSQDLEPLTILYYIGTKPKIEQLSNMIVKSKCS 114

RESULT 52
PCT-US94-00685-22
;; Sequence 22, Application PC/TUS9400685
;; GENERAL INFORMATION:
;; APPLICANT: THE JOHNS HOPKINS UNIVERSITY
;; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-9
;; NUMBER OF SEQUENCES: 26
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Spensley Horn Jubas & Lubitz
;; STREET: 1880 Century Park East, Suite 500
;; CITY: Los Angeles
;; STATE: California
;; COUNTRY: US
;; ZIP: 90067
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US94/00685
;; FILING DATE: 12-JAN-1994
;; CLASSIFICATION:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Wetherell, Jr. Ph.D., John R.
;; REGISTRATION NUMBER: 31,678
;; REFERENCE/DOCKET NUMBER: FD3288
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (619) 455-5100
;; TELEFAX: (619) 455-5110
;; INFORMATION FOR SEQ ID NO: 22:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 114 amino acids
;; TYPE: amino acid

;;
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; IMMEDIATE SOURCE:
;; CLONE: TGF-beta2
;; FEATURE:
;; NAME/KEY: Protein
;; LOCATION: 1..114
PCT-US94-00685-22

Query Match 84.4%; Score 535; DB 5; Length 114;
Best Local Similarity 79.5%; Pred. No. 8.8e-51;
Matches 89; Conservative 14; Mismatches 9; Indels 0; Gaps 0;
Qy 1 ALDNYCFRNLENCVRPLYIDFRQDLGWKWHPEKGYIANFCGCPYLRSDTTHST 60
Db 3 ALDAAFCFRNVQNCCLRPYIDFKRDLGWKWHPEKGYIANFCAGACPYLWSSDTQHSR 62
Qy 61 VLGLYNTLNPEASAPCCVPQDLEPLTILYYVGRTPKVEQLSNMVKSKCS 112
Db 63 VLSLYNTLNPEASAPCCVSQDLEPLTILYYIGTKPKIEQLSNMIVKSKCS 114

RESULT 53
US-08-581-529B-20
;; Sequence 20, Application US/08581529B
;; Patent No. 5770444
;; GENERAL INFORMATION:
;; APPLICANT: Lee, Se-Jin
;; APPLICANT: Huynh, Thanh
;; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-6
;; NUMBER OF SEQUENCES: 21
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Fish & Richardson
;; STREET: 4225 Executive Square, Suite 1400
;; CITY: La Jolla
;; STATE: California
;; COUNTRY: USA
;; ZIP: 92037
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/581,529B
;; FILING DATE: 15-APR-1996
;; CLASSIFICATION: 536
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Lisa A. Haile, Ph.D.
;; REGISTRATION NUMBER: 38,347
;; REFERENCE/DOCKET NUMBER: 07265/082001
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (619) 678-5070
;; TELEFAX: (619) 678-5099
;; INFORMATION FOR SEQ ID NO: 20:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 115 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; IMMEDIATE SOURCE:
;; CLONE: TGF-beta-2
;; FEATURE:
;; NAME/KEY: Protein
;; LOCATION: 1..115
US-08-581-529B-20

Query Match 84.4%; Score 535; DB 1; Length 115;
Best Local Similarity 79.5%; Pred. No. 8.9e-51;

[illegible]

```

US-08-581-528A-20
; Sequence 20, Application US/08581528A
; Patent No. 5986058
; GENERAL INFORMATION:
; APPLICANT: Lee, Se-Jin
; APPLICANT: Huynh, Thanh
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-7
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:

```

ADDRESS: Fish & Richardson, P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/581,528A
FILING DATE: 03-Sept-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/089,670
FILING DATE: 09-JUL-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Lisa A. Haile, Ph.D.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/081001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 115 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
IMMEDIATE SOURCE:
CLONE: TGF-beta-2
FEATURE:
NAME/KEY: Protein
LOCATION: 1..115
US-08-581-528A-20
Query Match 84.4%; Score 535; DB 2; Length 115;
Best Local Similarity 79.5%; Pred. No. 8.9e-51;
Matches 89; Conservative 14; Mismatches 9; Indels 0; Gaps 0;
QY 1 ALDNYCFRNLENCVRLPYIDFRQDLGWKWHPEKGYANFCGCPYLRSDTTHST 60
Db 4 ALDAAFCFRNVQDNCCLRPYIDFKRDLGWKWHPEKGYANFCAGACPYLWSSDTQHSR 63
QY 61 VLGLYNTLNPEASPCCVQDLEPLTILYVVGRTPKVEQLSNMVKSKCS 112
Db 64 VLSLYNTINPEASPCCVQDLEPLTILYVVGRTPKIEQLSNMVKSKCS 115
RESULT 57
US-09-097-616-20
Sequence 20, Application US/09097616
Patent No. 6090563
GENERAL INFORMATION:
APPLICANT: Lee, Se-Jin
APPLICANT: Huynh, Thanh
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-6
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESS: Fish & Richardson
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: California
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/097,616
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/581,529
FILING DATE: 15-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Lisa A. Haile, Ph.D.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/082001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 678-5070
TELEFAX: (619) 678-5099
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 115 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
IMMEDIATE SOURCE:
CLONE: TGF-beta-2
FEATURE:
NAME/KEY: Protein
LOCATION: 1..115
US-09-097-616-20
Query Match 84.4%; Score 535; DB 3; Length 115;
Best Local Similarity 79.5%; Pred. No. 8.9e-51;
Matches 89; Conservative 14; Mismatches 9; Indels 0; Gaps 0;
QY 1 ALDNYCFRNLENCVRLPYIDFRQDLGWKWHPEKGYANFCGCPYLRSDTTHST 60
Db 4 ALDAAFCFRNVQDNCCLRPYIDFKRDLGWKWHPEKGYANFCAGACPYLWSSDTQHSR 63
QY 61 VLGLYNTLNPEASPCCVQDLEPLTILYVVGRTPKVEQLSNMVKSKCS 112
Db 64 VLSLYNTINPEASPCCVQDLEPLTILYVVGRTPKIEQLSNMVKSKCS 115
RESULT 58
US-09-177-860A-30
Sequence 30, Application US/09177860A
Patent No. 6096506
GENERAL INFORMATION:
APPLICANT: Huynh, Thanh
APPLICANT: Lee, Se-Jin
TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR GROWTH DIFFERENTIATION FACTOR-8 AN
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Gray Cary Ware & Freidenrich LLP
STREET: 4365 Executive Drive, Suite 1600
CITY: San Diego
STATE: CA
COUNTRY: US
ZIP: 92121
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSEO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/177,860A
FILING DATE: 23-OCT-1998
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/525,596
FILING DATE: 19-SEP-1995
ATTORNEY/AGENT INFORMATION:

```

;
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; IMMEDIATE SOURCE:
; CLONE: TGF-beta-2
; US-09-145-060-26

Query Match 84.4%; Score 535; DB 4; Length 115;
Best Local Similarity 79.5%; Pred. No. 8.9e-51;
Matches 89; Conservative 14; Mismatches 9; Indels 0; Gaps 0;

QY 1 ALDNTNYCFRNLNECCVRPLYIDFRODLGKWKWHEPKGYANFCGCPYLRSDTTHST 60
   ||| |||||:::||:|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db 4 ALDAAAYCFRNVQNCCLRPYIDFKRDLGKWKWIHEPKGYANFCAGACPYLWSSDTHSR 63

QY 61 VLIGLYNTLNPEASAPCCVPQDLEPLTILYXVGTPEQLSNMVKSKCS 112
   || |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 64 VLSLYNTLNPEASAPCCVSODLEPLTILYIGTKIEQLSNMIVKSKCS 115

RESULT 60
PCT-US94-00657-26
; Sequence 26, Application PC/TUS9400657
; GENERAL INFORMATION:
; APPLICANT: SE-JIN LEE
; APPLICANT: HUYNH, THANH
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-5
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SPENSLEY HORN JUBAS & LUBITZ
; STREET: 1880 CENTURY PARK EAST, FIFTH FLOOR
; CITY: LOS ANGELES
; STATE: CALIFORNIA
; COUNTRY: US
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/00657
; FILING DATE: 1/12/94
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: WETHERELL, JR. PH.D., JOHN R.
; REGISTRATION NUMBER: 31,678
; REFERENCE/DOCKET NUMBER: FD3256 CIP OF PD2280
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/455-5100
; TELEFAX: 619-455-5110
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 115 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; IMMEDIATE SOURCE:
; CLONE: TGF-beta-2
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..115
; PCT-US94-00657-26

Query Match 84.4%; Score 535; DB 5; Length 115;
Best Local Similarity 79.5%; Pred. No. 8.9e-51;
Matches 89; Conservative 14; Mismatches 9; Indels 0; Gaps 0;

QY 1 ALDNTNYCFRNLNECCVRPLYIDFRODLGKWKWHEPKGYANFCGCPYLRSDTTHST 60
   ||| |||||:::||:|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db 4 ALDAAAYCFRNVQNCCLRPYIDFKRDLGKWKWIHEPKGYANFCAGACPYLWSSDTHSR 63

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; FILING DATE: 06-OCT-1993
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/063841
; FILING DATE: 18-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/790856
; FILING DATE: 12-NOV-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/401906
; FILING DATE: 01-SEP-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Hasak, Janet E.
; REGISTRATION NUMBER: 28,616
; REFERENCE/DOCKET NUMBER: 597D1C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1896
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 414 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-132-405-2

Query Match 84.4%; Score 535; DB 1; Length 414;
Best Local Similarity 79.5%; Pred. No. 4.le-50;
Matches 89; Conservative 14; Mismatches 9; Indels 0; Gaps 0;

QY 1 ALDTNYCFRNLENCVRLPYIDFRODLGWKWHPEKGYVYANFCGCPYLRSDTTHST 60
Db 303 ALDAAVCFRNVQDNCCLRPYIDFKRDLGWKWHPEKGYVYANFCAGACPYLWSSDTQHRS 362

QY 61 VLGLYNTLNPEASASCCVPQDLEPLTILYVGVTRPKVEQLSNMVKSKCS 112
Db 363 VLSLYNTLNPEASASCCVSDLEPLTILYVGVTRPKVEQLSNMVKSKCS 414

RESULT 64
US-08-395-939A-2
; Sequence 2, Application US/08395939A
; Patent No. 5604204
; GENERAL INFORMATION:
; APPLICANT: Ammann, Arthur J.
; TITLE OF INVENTION: TGF-BETA COMPOSITION FOR INDUCING BONE
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/395,939A
; FILING DATE: 27-FEB-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/132405
; FILING DATE: 12-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/063841
; FILING DATE: 18-MAY-1993
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/790856
; FILING DATE: 12-NOV-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/401906
; FILING DATE: 1-SEP-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Hasak, Janet E.
; REGISTRATION NUMBER: 28,616
; REFERENCE/DOCKET NUMBER: P0597D1C2D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1896
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 414 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-395-939A-2

Query Match 84.4%; Score 535; DB 1; Length 414;
Best Local Similarity 79.5%; Pred. No. 4.le-50;
Matches 89; Conservative 14; Mismatches 9; Indels 0; Gaps 0;

QY 1 ALDTNYCFRNLENCVRLPYIDFRODLGWKWHPEKGYVYANFCGCPYLRSDTTHST 60
Db 303 ALDAAVCFRNVQDNCCLRPYIDFKRDLGWKWHPEKGYVYANFCAGACPYLWSSDTQHRS 362

QY 61 VLGLYNTLNPEASASCCVPQDLEPLTILYVGVTRPKVEQLSNMVKSKCS 112
Db 363 VLSLYNTLNPEASASCCVSDLEPLTILYVGVTRPKVEQLSNMVKSKCS 414

RESULT 65
PCT-US91-01861-2
; Sequence 2, Application PC/TUS9101861
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; TITLE OF INVENTION: Method of Predisposing Mammals to
; TITLE OF INVENTION: Accelerated Tissue Repair
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/01861
; FILING DATE: 19910320
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. Ser. No. 07/504,495
; FILING DATE: 4 April 1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Hasak, Janet E.
; REGISTRATION NUMBER: 28,616
; REFERENCE/DOCKET NUMBER: 637
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/266-1896
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 414 amino acids
; TYPE: AMINO ACID


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; APPLICANT: Schmitz, Albert
; TITLE OF INVENTION: Process for Refolding Recombinantly
; TITLE OF INVENTION: Produced TGF-beta-like Proteins
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Henry P. No. 5650494ak
; STREET: 520 White Plains Road, P.O. Box 2005
; CITY: Tarrytown
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10591-9005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,057B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/201,703
; FILING DATE: 25-FEB-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/960,309
; FILING DATE: 13-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/621,502
; FILING DATE: 03-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 8927546.5
; FILING DATE: 06-DEC-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5650494ak, Henry P.
; REGISTRATION NUMBER: 33200
; REFERENCE/DOCKET NUMBER: 4-17861+/Cont3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 277-5110
; TELEFAX: (908) 277-4306
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 112 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-486-057B-41

Query Match      78.9%; Score 500; DB 1; Length 112;
Best Local Similarity 76.8%; Pred. No. 5.2e-47;
Matches 86; Conservative 11; Mismatches 15; Indels 0; Gaps 0;

OY 1 AIDTNYCFRNLNECCVRLYIDFRQDLGKWKVHEPKGYANFCGSPCYIRSDTTHST 60
    ||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
Db 1 AIDTNYCFSTKNCQVRLYIDFRKDLGKWKIHEPKGYHANFCLGCPYIWSLDTOYSK 60
OY 61 VLGLYNTLNPASASPCVQDLEPLTILYYGRTPKVEQLSNMIVVSKCS 112
    ||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
Db 61 VLALYNQHNPGASAPCCVQALEPLPIYVYGRKPKVEQLSNMIVVSKCS 112

RESULT 72
; US-08-459-850-36
; Sequence 36, Application US/08459850
; Patent No. 5665568
; GENERAL INFORMATION:
; APPLICANT: Anthony J. Mason
; APPLICANT: Peter H. Seeburg
; TITLE OF INVENTION: Nucleic Acid Encoding the Alpha or
; TITLE OF INVENTION: Beta Chains of Inhibin and Method for Synthesizing Polypeptide
; NUMBER OF SEQUENCES: 44
```

```

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,850
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/197792
; FILING DATE: 17-FEB-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/958414
; FILING DATE: 08-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/744207
; FILING DATE: 12-AUG-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/215466
; FILING DATE: 05-JUL-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 06/906729
; FILING DATE: 31-DEC-1986
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 06/827710
; FILING DATE: 07-FEB-1986
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 06/783910
; FILING DATE: 03-OCT-1985
; ATTORNEY/AGENT INFORMATION:
; NAME: Hasak, Janet E.
; REGISTRATION NUMBER: 28,616
; REFERENCE/DOCKET NUMBER: 297P2D5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1896
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 112 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-459-850-36

Query Match      78.9%; Score 500; DB 1; Length 112;
Best Local Similarity 76.8%; Pred. No. 5.2e-47;
Matches 86; Conservative 11; Mismatches 15; Indels 0; Gaps 0;

OY 1 AIDTNYCFRNLNECCVRLYIDFRQDLGKWKVHEPKGYANFCGSPCYIRSDTTHST 60
    ||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
Db 1 AIDTNYCFSTKNCQVRLYIDFRKDLGKWKIHEPKGYHANFCLGCPYIWSLDTOYSK 60
OY 61 VLGLYNTLNPASASPCVQDLEPLTILYYGRTPKVEQLSNMIVVSKCS 112
    ||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
Db 61 VLALYNQHNPGASAPCCVQALEPLPIYVYGRKPKVEQLSNMIVVSKCS 112

RESULT 73
; US-08-459-214-36
; Sequence 36, Application US/08459214
; Patent No. 5716810
; GENERAL INFORMATION:
; APPLICANT: Anthony J. Mason
; APPLICANT: Peter H. Seeburg
```

```

; Patent No. 5800811
; GENERAL INFORMATION:
; APPLICANT: Nimni, Marcel E.
; APPLICANT: Hall, Frederick L.
; APPLICANT: Tuan, Tai-Lan
; APPLICANT: Wu, Lingtao
; APPLICANT: Cheung, David T.
; TITLE OF INVENTION: Transforming Growth Factor B Fusion
; TITLE OF INVENTION: and
; TITLE OF INVENTION: Their Use in Wound Healing
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 11150 Santa Monica Boulevard, Suite 400
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90025-3395
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,837
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharp, Janice A.
; REGISTRATION NUMBER: 34,051
; REFERENCE/DOCKET NUMBER: 30630-IUS01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 310-445-1140
; TELEFAX: 310-445-9031
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 112 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-470-837-30
;
Query Match 78.9%; Score 500; DB 1: Length 112;
Best Local Similarity 76.8%; Pred. No. 5.2e-47;
Matches 86; Conservative 11; Mismatches 15; Indels 0
;
Qy 1 ALDNTYCFRNLEENCCVRPLYIDFRDLGKWKVHEPKGYGVANFCGPGCPYLRSADTT
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 1 ALDNTYCFSSTEKNCVRQLYIDFRDLGKWKVHEPKGYGVANFCGPGCPYLRSADTT
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Qy 61 VLGIYNTLNPEASAPCCVPQDLEPITILYYVGRTPKVEOLSNMVKSCKCS 112
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 61 VLAIYNHNPASAPCCVPQDALEPLIVYVGRKPKVEOLSNMIVRSCKCS 112
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |

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RESULT 75
US-08-789-588-41
; Sequence 41, Application US/08789588
; Patent No. 5922846
; GENERAL INFORMATION:
; APPLICANT: Cerletti, Nico
; APPLICANT: McMaster, Gary K.
; APPLICANT: Cox, David
; APPLICANT: Schmitz, Albert
; APPLICANT: Meyhack, Bernd
; TITLE OF INVENTION: Process for Refolding Recombinantly
; TITLE OF INVENTION: Produced TGF-beta-like Proteins
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Henry P. No. 5922846ak
; STREET: 520 White Plains Road, P.O. Box 2005
; CITY: Tarrytown
;

```

CORRESPONDENCE ADDRESS:
ADDRESSEE: Henry P. No. 5922846ak
STREET: 520 White Plains Road, P.O. Box 2005
CITY: Tarriatown

STATE: New York
COUNTRY: U.S.A.
ZIP: 10591-9005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/789,588
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/486,057
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/201,703
FILING DATE: 25-FEB-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/960,309
FILING DATE: 13-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/621,502
FILING DATE: 03-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 8927546.5
FILING DATE: 06-DEC-1989
ATTORNEY/AGENT INFORMATION:
NAME: No. 5922846ak, Henry P.
REGISTRATION NUMBER: 33200
REFERENCE/DOCKET NUMBER: 4-17861/+Cont3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 277-5110
TELEFAX: (908) 277-4306
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 112 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-789-588-41

Query Match 78.9%; Score 500; DB 2; Length 112;
Best Local Similarity 76.8%; Pred. No. 5.2e-47;
Matches 86; Conservative 11; Mismatches 15; Indels 0; Gaps 0;
Qy 1 ALDNTYCFRNLEENCVRPLYIDFRQDLGKWKVHPEKGYANFCGPGPYLRSADTHTST 60
Db 1 ALDNTYCFSTTEKNCVRQLYIDFRKDLGKWKIHEPKGYHANFCLGPGPYIWSLDTQYSK 60
Qy 61 VLGLYNTLNPEASAPCCVPQDLPLTILYVYVGRTPKVEQLSNMVKSKCS 112
Db 61 VLALYNQHNPGASAPCCVPQALEPLPIVYVYVGRKPKVEQLSNMIVRSCKCS 112

RESULT 76
US-08-410-573-1
Sequence 1, Application US/08410573
Patent No. 5958411
GENERAL INFORMATION:
APPLICANT: LOGAN, ANN
APPLICANT: BAIRD, ANDREW
TITLE OF INVENTION: METHODS OF INHIBITING OR ENHANCING SCAR
TITLE OF INVENTION: FORMATION IN THE CNS
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: PRETTY, SCHROEDER, BRUEGGEMANN & CLARK
STREET: 444 SO. FLOWER STREET, SUITE 2000
CITY: LOS ANGELES
STATE: CALIFORNIA
COUNTRY: UNITED STATES
ZIP: 90071
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/410,573
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/860,704
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: BROWN, THERESA A.
REGISTRATION NUMBER: 32,547
REFERENCE/DOCKET NUMBER: P31 9287
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-535-9001
TELEFAX: 619-535-8949
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 112 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-410-573-1

Query Match 78.9%; Score 500; DB 2; Length 112;
Best Local Similarity 76.8%; Pred. No. 5.2e-47;
Matches 86; Conservative 11; Mismatches 15; Indels 0; Gaps 0;
Qy 1 ALDNTYCFRNLEENCVRPLYIDFRQDLGKWKVHPEKGYANFCGPGPYLRSADTHTST 60
Db 1 ALDNTYCFSTTEKNCVRQLYIDFRKDLGKWKIHEPKGYHANFCLGPGPYIWSLDTQYSK 60
Qy 61 VLGLYNTLNPEASAPCCVPQDLPLTILYVYVGRTPKVEQLSNMVKSKCS 112
Db 61 VLALYNQHNPGASAPCCVPQALEPLPIVYVYVGRKPKVEQLSNMIVRSCKCS 112

RESULT 77
US-09-123-233-2
Sequence 2, Application US/09123233
Patent No. 6057430
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: No. 6057430el process for the production of
TITLE OF INVENTION: biologically active dimeric protein
NUMBER OF SEQUENCES: 14
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/123,233
FILING DATE:
CLASSIFICATION: 530
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 112 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-123-233-2

Query Match 78.9%; Score 500; DB 3; Length 112;
Best Local Similarity 76.8%; Pred. No. 5.2e-47;
Matches 86; Conservative 11; Mismatches 15; Indels 0; Gaps 0;
Qy 1 ALDNTYCFRNLEENCVRPLYIDFRQDLGKWKVHPEKGYANFCGPGPYLRSADTHTST 60
Db 1 ALDNTYCFSTTEKNCVRQLYIDFRKDLGKWKIHEPKGYHANFCLGPGPYIWSLDTQYSK 60


```

; IMMEDIATE SOURCE:
; CLONE: TGF-beta1
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..114
;
US-08-491-835-21

Query Match 78.9%; Score 500; DB 2; Length 114;
Best Local Similarity 76.8%; Pred. No. 5.3e-47;
Matches 86; Conservative 11; Mismatches 15; Indels 0; Gaps 0;

QY 1 ALDNYFCRNLENCNCVRPLYIDFRQDLGKWKWHEPKGYVAFNCSPCYLRSADTTTST 60
DQ 1 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DQ 3 ALDNYFCSFTSKCCVRQLYIDFRKDLGKWKWHEPKGYHANFCLGCPYIWSLDTQYSK 62
QY 61 VLGLYNTLNPEASAPCCVQDPLEPLTLVYVGTRPKVEQLSNMVKSCKCS 112
DQ 63 VLALYNHNPASAAAPCCVQALEPLPIVYVGRKPKVEQLSNMIVRSCKCS 114

RESULT 82
US-09-153-733A-23
; Sequence 23, Application US/09153733A
; Patent No. 6025475
; GENERAL INFORMATION:
; APPLICANT: JOHNS HOPKINS UNIVERSITY
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-3
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SPENSLEY HORN JUBAS & LUBITZ
; STREET: 1880 CENTURY PARK EAST, FIFTH FLOOR
; CITY: LOS ANGELES
; STATE: CALIFORNIA
; COUNTRY: US
; ZIP: 90067
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/153,733A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/481,377
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: WETHERELL, JR. Ph.D., JOHN R.
; REGISTRATION NUMBER: 31,678
; REFERENCE/DOCKET NUMBER: FD2279 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 455-5100
; TELEFAX: (619) 455-5110
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 114 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; IMMEDIATE SOURCE:
; CLONE: TGF-beta 1
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..114
;
US-09-153-733A-23

Query Match 78.9%; Score 500; DB 3; Length 114;
Best Local Similarity 76.8%; Pred. No. 5.3e-47;
Matches 86; Conservative 11; Mismatches 15; Indels 0; Gaps 0;

```


ADDRESSEE: Spensley Horn Jubas & Lubitz
STREET: 1880 Century Park East, Suite 500
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90067
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version 1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/624,635
FILING DATE: 16-AUG-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/134,078
FILING DATE: 08-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Wetherell, Jr., Ph.D., John R.,
REGISTRATION NUMBER: 31,678
REFERENCE/DOCKET NUMBER: PD-3054
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
TELEFAX: (619) 455-5110
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
IMMEDIATE SOURCE:
CLONE: TGF-beta-1
FEATURE:
NAME/KEY: Protein
LOCATION: 1..114
US-08-624-635-22

	Query Match	78.9%	Score 500;	DB 4;	Length 114;
	Best Local Similarity	76.8%;	Pred. No. 5.3e-47;		
	Matches	86;	Conservative 11;	Mismatches 15;	Indels 0;
QY	1	ALDTNYCFRNLENC	CVRPYIYIDFRODLGKWKW	HEPKGYANFC	SGPCPYLRSADTTHT 60
Db	3	ALDTNYCFSSTEKN	CCVRQYIYIDFRODLGKWKI	HEPKGYHANFCL	GPCPYIWSLDTQYSK 62
QY	61	VLGLYNTLNP	EASASCCVPQDLEPTILYVGR	TPKVEQLSNM	VWSKCS 112
Db	63	VLLALYNQHN	PGASAAAPCCPOALEPI	PIVYVGRKPRVEOL	SNMIVRSKCS 114

[illegible]

```

; TOPOLOGY: linear
; MOLECULE TYPE: protein
; IMMEDIATE SOURCE:
; CLONE: TGF-beta1
; FEATURE:
; NAME/KEY: protein
; LOCATION: 1..114
PCT-US94-00685-21

```

Query Match 78.9%; Score 500; DB 5; Length 114;
Best Local Similarity 76.8%; Pred. NO. 5.3e-47;
Matches 86; Conservative 11; Mismatches 15; Indels 0; Gaps 0;

Qy	1	ALDNTNYCFNL	LEENCCV	RPLYLID	PRODLG	WKWHEP	KGYANFC	SGPCPI	RSADTTHST	60
Db	3	ALDNTNYCF	SESTKCCV	RQLYLID	PRODLG	WKWHEP	KGYHANF	CLGCPPI	TWISLDTQYSK	62
Qy	61	VLGIYNTLN	PEASAP	CCVQDLE	PLTILY	VYVGRTP	KEQLSNM	VMVSKCS	112	
Db	63	VLIYLNHNF	GSAAPC	CVQALPE	PLTVTY	VYVGRTP	KEQLSNM	IVRSKCS	114	

```

RESULT 88
US-08-581-529B-19
; Sequence 19, Application US/08581529B
; Patent No. 5770444
;
; GENERAL INFORMATION:
;   APPLICANT: Lee, Se-Jin
;   APPLICANT: Huynh, Thanh
;   TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-6
;   NUMBER OF SEQUENCES: 21
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Fish & Richardson
;   STREET: 4225 Executive Square, Suite 1400
;   CITY: La Jolla
;   STATE: California
;   COUNTRY: USA
;   ZIP: 92037
;

```

```

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/581,529B
FILING DATE: 15-APR-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Lisa A. Haile, Ph.D.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/082001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 678-5070
TELEFAX: (619) 678-5099
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 115 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
IMMEDIATE SOURCE:
CLONE: TGF-beta-1
FEATURE:
NAME/KEY: Protein
LOCATION: 1..115
US-08-581-529B-19

```

Query Match 78.9%; Score 500; DB 1; Length 115;
Best Local Similarity 76.8%; Pred. No. 5.3e-47;
Matches 86; Conservative 11; Mismatches 15; Indels

[illegible]

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RESULT 89
US-08-455-559-25
: Sequence 25, Application US/08455559
: Patent No. 5801014
: GENERAL INFORMATION:
: APPLICANT: LEE, SE-JIN
: APPLICANT: HUYNH, THANH
: TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-5
: NUMBER OF SEQUENCES: 27
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: SPENSLEY HORN JURAS & LUBITZ
: STREET: 1880 CENTURY PARK EAST, FIFTH FLOOR
: CITY: LOS ANGELES
: STATE: CALIFORNIA
: COUNTRY: US
: ZIP: 90067
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/455,559
: FILING DATE: 31-MAY-1995
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/003,144
: FILING DATE: 12-JAN-1993
: ATTORNEY/AGENT INFORMATION:
: NAME: WETHERELL, JR. PH.D., JOHN R.
: REGISTRATION NUMBER: 31,678
: REFERENCE/DOCKET NUMBER: PD2280
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 619/455-5100
: TELEFAX: 619-455-5110
: INFORMATION FOR SEQ ID NO: 25:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 115 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: IMMEDIATE SOURCE:
: CLONE: TGF-beta-1
: FEATURE:
: NAME/KEY: Protein
: LOCATION: 1..115
: US-08-455-559-25

```

```
Query Match          78.9%; Score 500; DB 1; Length 115;
Best Local Similarity 76.8%; Pred. NO. 5.3e-47;
Matches 86; Conservative 11; Mismatches 15; Indels 0; Gaps 0;
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	QY	Db	QY	Db
1	ALDNTNYCPRNLBENCCVRLPYIDFRQDLGWKWHBPKGYANFCSGCPCLYLRADTTTIST	60		
	: : : : : : : : : :			
4	ALDNTNYCFSTPEKCCVRLPYIDFRQDLGWKWHBPKGYANFCSGCPCLYLRADTTTIST	63		
	: : : : : : : : : :			
61	VLGLYNTLNLPASAPCCVPQDLPLTILYVVGRTPKVEQLSNMVKSCCKS	112		
	: : : : : : : : : :			
64	VLALYLNHPGCAAPCCVQALPLPTIVYVVGRTPKVEQLSNMVKSCCKS	115		
	: : : : : : : : : :			

```
RESULT 90
US-08-525-5968-29
; Sequence 29, Application US/08525596B
; Patent No. 5827733
; GENERAL INFORMATION:
; APPLICANT: Huynh, Thanh
; APPLICANT: Lee, Se-Jin
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: US
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/525,596B
; FILING DATE: 19-SEP-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/07762
; FILING DATE: 08-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Wetherell, Jr., Ph.D, John R.
; REGISTRATION NUMBER: 31,678
; REFERENCE/DOCKET NUMBER: 07265/075001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-678-5070
; TELEFAX: 619-678-5099
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 115 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; IMMEDIATE SOURCE:
; CLONE: TGF-beta-1
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..115
US-08-525-5968-29

Query Match 78.9%; Score 500; DB 2; Length 115;
Best Local Similarity 76.8%; Pred. No. 5.3e-47;
Matches 86; Conservative 11; Mismatches 15; Indels 0; Gaps 0;

Qy 1 ALDNTYCFRNLENCVRLPYIDFRDLGKWKVHPEKGYANFCGCPYLRSDTTHST 60
    ||||| : ||||| ||||| ||||| ||||| ||||| ||||| ||||| : || :
Db 4 ALDNTYCFSSSTEKNCCVRLQYIDFRDLGKWKVHPEKGYHANFCLGCPYIWSLDTQYSK 63
    ||||| : ||||| ||||| ||||| ||||| ||||| ||||| ||||| : || :
Qy 61 VLGLYNTLNPEASASCCVPQDLEPLTILYYVGRTPKVEQLSNMVKSKCS 112
    || ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| : |||||
Db 64 VLALYNQHNPGASAAPCCVPQALEPLPIVYVGRKPKVEQLSNMIVRSCKCS 115
    || ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| : |||||

RESULT 91
US-08-581-528A-19
; Sequence 19, Application US/08581528A
; Patent No. 5986058
; GENERAL INFORMATION:
; APPLICANT: Lee, Se-Jin
; APPLICANT: Huynh, Thanh
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-7
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
```

```
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/581,528A
; FILING DATE: 03-Sept-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/089,670
; FILING DATE: 09-JUL-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Lisa A. Halle, Ph.D.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07265/081001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 115 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; IMMEDIATE SOURCE:
; CLONE: TGF-beta-1
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..115
US-08-581-528A-19

Query Match 78.9%; Score 500; DB 2; Length 115;
Best Local Similarity 76.8%; Pred. No. 5.3e-47;
Matches 86; Conservative 11; Mismatches 15; Indels 0; Gaps 0;

Qy 1 ALDNTYCFRNLENCVRLPYIDFRDLGKWKVHPEKGYANFCGCPYLRSDTTHST 60
    ||||| : ||||| ||||| ||||| ||||| ||||| ||||| ||||| : || :
Db 4 ALDNTYCFSSSTEKNCCVRLQYIDFRDLGKWKVHPEKGYHANFCLGCPYIWSLDTQYSK 63
    ||||| : ||||| ||||| ||||| ||||| ||||| ||||| ||||| : || :
Qy 61 VLGLYNTLNPEASASCCVPQDLEPLTILYYVGRTPKVEQLSNMVKSKCS 112
    || ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| : |||||
Db 64 VLALYNQHNPGASAAPCCVPQALEPLPIVYVGRKPKVEQLSNMIVRSCKCS 115
    || ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| : |||||

RESULT 92
US-09-087-616-19
; Sequence 19, Application US/09097616
; Patent No. 6090563
; GENERAL INFORMATION:
; APPLICANT: Lee, Se-Jin
; APPLICANT: Huynh, Thanh
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-6
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: California
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
```

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/097,616
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/581,529
FILING DATE: 15-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Lisa A. Haile, Ph.D.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/082001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 678-5070
TELEFAX: (619) 678-5099
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 115 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
IMMEDIATE SOURCE:
CLONE: TGF-beta-1
NAME/KEY: Protein
LOCATION: 1..115
US-09-097-616-19

Query Match 78.9%; Score 500; DB 3; Length 115;
Best Local Similarity 76.8%; Pred. No. 5.3e-47;
Matches 86; Conservative 11; Mismatches 15; Indels 0; Gaps 0;
QY 1 ALDTNYCFRNLENCVRRPLYIDFRDLGKWKVHPEKGYANFCSPCYLRSADTTHST 60
Db 4 ALDTNYCFSTSKNCCVRQLYIDFRDLGKWKVHPEKGYHANFCLGCPYIWSLDTQYSK 63
QY 61 VLGLYNTLNPEASASPCCVQDLEPLTILYYVGRTPKVEQLSNMIVRSCKCS 112
Db 64 VLALYNQHPGASAAPCCVQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 115

RESULT 93
US-09-177-860A-29
Sequence 29, Application US/09177860A
Patent No. 6096506
GENERAL INFORMATION:
APPLICANT: Huynh, Thanh
APPLICANT: Lee, Se-Jin
TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR GROWTH DIFFERENTIATION FACTOR-8 AN
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSER: Gray Cary Ware & Freidenrich LLP
STREET: 4365 Executive Drive, Suite 1600
CITY: San Diego
STATE: CA
COUNTRY: US
ZIP: 92121
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/177,860A
FILING DATE: 23-OCT-1998
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/525,596
FILING DATE: 19-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Ph.D., Lisa A.

REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/075003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 858-677-1456
TELEFAX: 858-677-1465
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 115 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
IMMEDIATE SOURCE:
CLONE: TGF-beta-1
FEATURE:
NAME/KEY: Protein
LOCATION: 1..115
US-09-177-860A-29

Query Match 78.9%; Score 500; DB 3; Length 115;
Best Local Similarity 76.8%; Pred. No. 5.3e-47;
Matches 86; Conservative 11; Mismatches 15; Indels 0; Gaps 0;
QY 1 ALDTNYCFRNLENCVRRPLYIDFRDLGKWKVHPEKGYANFCSPCYLRSADTTHST 60
Db 4 ALDTNYCFSTSKNCCVRQLYIDFRDLGKWKVHPEKGYHANFCLGCPYIWSLDTQYSK 63
QY 61 VLGLYNTLNPEASASPCCVQDLEPLTILYYVGRTPKVEQLSNMIVRSCKCS 112
Db 64 VLALYNQHPGASAAPCCVQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 115

RESULT 94
US-09-145-060-25
Sequence 25, Application US/09145060
Patent No. 6245896
GENERAL INFORMATION:
APPLICANT: Lee, Se-Jin
APPLICANT: Huynh, Thanh
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-5
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSER: Fish & Richardson, P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/145,060
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/455,559
FILING DATE: 31-MAY-1995
APPLICATION NUMBER: 08/003,144
FILING DATE: 12-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Lisa A. Haile, Ph.D.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/057001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 115 amino acids
TYPE: amino acid
TOPOLOGY: linear

```

; MOLECULE TYPE: protein
; IMMEDIATE SOURCE:
; CLONE: TGF-beta-1
US-09-145-060-25

Query Match      78.9%; Score 500; DB 4; Length 115;
Best Local Similarity 76.8%; Pred. No. 5.3e-47;
Matches 86; Conservative 11; Mismatches 15; Indels 0; Gaps 0;

Qy 1 ALDNTYCFRNLNCCVRPLYIDFRQDLGKWKVHEPKGYANFCSGPCPYLRSADTTHST 60
    ||||| : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 4 ALDNTYCFSSSTKNCVRQLYIDFRKDLGKWKVHEPKGYHANFCLGCPYIWSLDTQYSK 63

Qy 61 VLGLYNTLNPEASAPCCVPQDLEPLTILYVVGRTPKVEQLSNMVKSCKS 112
    || ||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 64 VLALYNQHNPGASAPCCVPQALEPLPIVYVYVGRKPKVEQLSNMIVRSCKS 115

RESULT 95
PCT-US94-00657-25
; Sequence 25, Application PC/TUS9400657
; GENERAL INFORMATION:
; APPLICANT: SE-JIN LEE
; APPLICANT: HUYNH, THANH
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-5
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SPENSLEY HORN JUBAS & LUBITZ
; STREET: 1880 CENTURY PARK EAST, FIFTH FLOOR
; CITY: LOS ANGELES
; STATE: CALIFORNIA
; COUNTRY: US
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/00657
; FILING DATE: 1/12/94
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: WETHERELL, JR. P.H.D., JOHN R.
; REGISTRATION NUMBER: 31,678
; REFERENCE/DOCKET NUMBER: FD3256 CIP OF PD2280
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/455-5100
; TELEFAX: 619-455-5110
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 115 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; IMMEDIATE SOURCE:
; CLONE: TGF-beta-1
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..115
PCT-US94-00657-25

Query Match      78.9%; Score 500; DB 5; Length 115;
Best Local Similarity 76.8%; Pred. No. 5.3e-47;
Matches 86; Conservative 11; Mismatches 15; Indels 0; Gaps 0;

Qy 1 ALDNTYCFRNLNCCVRPLYIDFRQDLGKWKVHEPKGYANFCSGPCPYLRSADTTHST 60
    ||||| : ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 4 ALDNTYCFSSSTKNCVRQLYIDFRKDLGKWKVHEPKGYHANFCLGCPYIWSLDTQYSK 63

Qy 61 VLGLYNTLNPEASAPCCVPQDLEPLTILYVVGRTPKVEQLSNMVKSCKS 112
    || ||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 64 VLALYNQHNPGASAPCCVPQALEPLPIVYVYVGRKPKVEQLSNMIVRSCKS 115

RESULT 96
PCT-US94-07762-19
; Sequence 19, Application PC/TUS9407762
; GENERAL INFORMATION:
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-6
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Spensley Horn Jubas & Lubitz
; STREET: 1880 Century Park East, Suite 500
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/07762
; FILING DATE: 08-JUL-1994
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: TUMARKIN, LISA A. PH.D.
; REGISTRATION NUMBER: P-38,347
; REFERENCE/DOCKET NUMBER: FD2349
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 455-5100
; TELEFAX: (619) 455-5110
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 115 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; IMMEDIATE SOURCE:
; CLONE: TGF-beta-1
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..115
PCT-US94-07762-19

Query Match      78.9%; Score 500; DB 5; Length 115;
Best Local Similarity 76.8%; Pred. No. 5.3e-47;
Matches 86; Conservative 11; Mismatches 15; Indels 0; Gaps 0;

Qy 1 ALDNTYCFRNLNCCVRPLYIDFRQDLGKWKVHEPKGYANFCSGPCPYLRSADTTHST 60
    ||||| : ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 4 ALDNTYCFSSSTKNCVRQLYIDFRKDLGKWKVHEPKGYHANFCLGCPYIWSLDTQYSK 63

Qy 61 VLGLYNTLNPEASAPCCVPQDLEPLTILYVVGRTPKVEQLSNMVKSCKS 112
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Db 64 VLALYNQHNPGASAPCCVPQALEPLPIVYVYVGRKPKVEQLSNMIVRSCKS 115

RESULT 97
PCT-US94-07799-19
; Sequence 19, Application PC/TUS9407799
; GENERAL INFORMATION:
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-7
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Spensley Horn Jubas & Lubitz
; STREET: 1880 Century Park East, Suite 500
```

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Qy 61 VLGLYNTLNPEASAPCCVPQDLEPLTILYVVGRTPKVEQLSNMVKSCKS 112
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Db 64 VLALYNQHNPGASAPCCVPQALEPLPIVYVYVGRKPKVEQLSNMIVRSCKS 115

RESULT 96
PCT-US94-07762-19
; Sequence 19, Application PC/TUS9407762
; GENERAL INFORMATION:
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-6
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Spensley Horn Jubas & Lubitz
; STREET: 1880 Century Park East, Suite 500
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/07762
; FILING DATE: 08-JUL-1994
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: TUMARKIN, LISA A. PH.D.
; REGISTRATION NUMBER: P-38,347
; REFERENCE/DOCKET NUMBER: FD2349
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 455-5100
; TELEFAX: (619) 455-5110
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 115 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; IMMEDIATE SOURCE:
; CLONE: TGF-beta-1
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..115
PCT-US94-07762-19

Query Match      78.9%; Score 500; DB 5; Length 115;
Best Local Similarity 76.8%; Pred. No. 5.3e-47;
Matches 86; Conservative 11; Mismatches 15; Indels 0; Gaps 0;

Qy 1 ALDNTYCFRNLNCCVRPLYIDFRQDLGKWKVHEPKGYANFCSGPCPYLRSADTTHST 60
    ||||| : ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 4 ALDNTYCFSSSTKNCVRQLYIDFRKDLGKWKVHEPKGYHANFCLGCPYIWSLDTQYSK 63

Qy 61 VLGLYNTLNPEASAPCCVPQDLEPLTILYVVGRTPKVEQLSNMVKSCKS 112
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Db 64 VLALYNQHNPGASAPCCVPQALEPLPIVYVYVGRKPKVEQLSNMIVRSCKS 115

RESULT 97
PCT-US94-07799-19
; Sequence 19, Application PC/TUS9407799
; GENERAL INFORMATION:
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-7
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Spensley Horn Jubas & Lubitz
; STREET: 1880 Century Park East, Suite 500
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CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90067
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/07799
FILING DATE: 08-JUL-1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: TUMARKIN, LISA A., PH.D.
REGISTRATION NUMBER: P-38,347
REFERENCE/DOCKET NUMBER: FD-2348
TELEPHONE: (619) 455-5100
TELEFAX: (619) 455-5110
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 115 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
IMMEDIATE SOURCE:
CLONE: TGF-beta-1
FEATURE:
NAME/KEY: Protein
LOCATION: 1..115
PCT-US94-07799-19

Query Match 78.9%; Score 500; DB 5; Length 115;
Best Local Similarity 76.8%; Pred. No. 5.3e-47;
Matches 86; Conservative 11; Mismatches 15; Indels 0; Gaps 0;

QY 1 ALDTNYCFRNLNCCVRPLYIDFRQDLGKWKVHPEKGYANFCSPGYLRSADTTHST 60
||||| : ||||| ||||| ||||| ||||| ||||| ||||| : || :
Db 4 ALDTNYCFSTSEKNCVRLYIDFRKDLGKWKVHPEKGYHANFCLGCPYIWSLDTQYSK 63

QY 61 VLGLYNTLNPEASAPCCVPQDLEPLTILYVYVGRPKVQQLSNMIVRSCKCS 112
|| ||| || ||||| ||||| ||||| ||||| ||||| ||||| : |||||
Db 64 VLALYNQHNPGASAPCCVPQALEPLPIVYVYVGRPKVQQLSNMIVRSCKCS 115

RESULT 98
US-07-669-171-2
; Sequence 2, Application US/07669171
; Patent No. 5304541
; GENERAL INFORMATION:
; APPLICANT: PURCHIO, ANTHONY F.
; APPLICANT: MADISEN, LINDA
; APPLICANT: MERWIN, JUNE RAE
; TITLE OF INVENTION: TGF-b1/b2: A NOVEL CHIMERIC TRANSFORMING
; TITLE OF INVENTION: GROWTH FACTOR-BETA
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS
; STREET: 1155 AVENUE OF THE AMERICAS
; CITY: NEW YORK
; STATE: N.Y.
; COUNTRY: U.S.A.
; ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/669.171

FILING DATE: 19910314
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MISROCK, S. LESLIE
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 5624-159-999
TELEPHONE: 212-790-9090
TELEFAX: 212-869-9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 390 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-669-171-2
Query Match 78.9%; Score 500; DB 1; Length 390;
Best Local Similarity 76.8%; Pred. No. 2.3e-46;
Matches 86; Conservative 11; Mismatches 15; Indels 0; Gaps 0;
QY 1 ALDTNYCFRNLNCCVRPLYIDFRQDLGKWKVHPEKGYANFCSPGYLRSADTTHST 60
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Db 279 ALDTNYCFSTSEKNCVRLYIDFRKDLGKWKVHPEKGYHANFCLGCPYIWSLDTQYSK 338
QY 61 VLGLYNTLNPEASAPCCVPQDLEPLTILYVYVGRPKVQQLSNMIVRSCKCS 112
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Db 339 VLALYNQHNPGASAPCCVPQALEPLPIVYVYVGRPKVQQLSNMIVRSCKCS 390
RESULT 99
US-08-132-405-1
; Sequence 1; Application US/08132405
; Patent No. 5409896
; GENERAL INFORMATION:
; APPLICANT: Ammann, Arthur J.
; APPLICANT: Rudman, Christopher G.
; TITLE OF INVENTION: Method of Inducing Bone Growth Using
; TITLE OF INVENTION: TGF-Beta
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/132.405
FILING DATE: 06-OCT-1993
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/063841
FILING DATE: 18-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/790856
FILING DATE: 12-NOV-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/401906
FILING DATE: 01-SEP-1989
ATTORNEY/AGENT INFORMATION:
NAME: Hasak, Janet E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: 597DIC2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1896

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; ID: 310/371-7108
; INFORMATION FOR SEQ ID NO: 1:
;     SEQUENCE CHARACTERISTICS:
;         LENGTH: 390 amino acids
;         TYPE: amino acid
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Db 121 GCCAACTCTGCTAGGCCCTTGCCCATACCTCCGAGTGCAGACACAAACCCACAGCAG 180
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Db 181 GTCTGGGACTGTACAACTCTGAACCTCTGAACATCTGCCTCGCTTGTCTGCTGCCCC 240
QY 241 caggacctggagccctgacctcctctgtactatgttggaggagcccccaaaagtggagcag 300
Db 241 CAGGACTGGAGCCCTGACCATCTCTGTACTATGTTGGGAGGAGCCCAAAAGTGGAGCAG 300
QY 301 ctctcaacatggtggtgaagtcttgaatgtagctga 339
Db 301 CTCTCAACATGTTGTTGAAGTCTTGTAAATGTAGCTGA 339

RESULT 2
LOCUS A23753 339 bp mRNA PAT 25-JAN-1995
DEFINITION TGF-beta3 coding region.
ACCESSION A23753
VERSION A23753.1 GI:825587
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLES McMaster, G.K., Cox, D., Cerletti, N. and Kuhla, J.
JOURNAL Novel hybrid transforming growth factors
PATENT: EP 0542679-A 3 19-MAY-1993;
CIBA-GEIGY AG
FEATURES
Source 1..339
/db_xref="taxon:9606" 75 t
BASE COUNT 74 a 104 c 86 g 75 t
ORIGIN

Query Match 100.0%; Score 339; DB 9; Length 339;
Best Local Similarity 100.0%; Pred. No. 2.7e-83;
Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gcttggacacaattactctccgaacttgagagaaactgctgtgccccctc 60
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QY 121 gccaactctgtcagcccttgcccatacctccgcagtcagtcagacacacacacagcag 180
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QY 181 gtctgggactgtacaacactctgaacctgaagcatctgcctcgtctgctgccc 240
Db 181 GTCTGGGACTGTACAACTCTGAACCTGGAAGTGGGTCCATGAACCTAAGGGCTACTAT 120
QY 121 gccaactctgtcagcccttgcccatacctccgcagtcagtcagacacacacacagcag 180
Db 121 GCCAACTTCTGCTCAGGCCCTTGCCCATACCTCCGAGTGCAGACACAAACCCACAGCAG 180
QY 181 gtctgggactgtacaacactctgaacctgaagcatctgcctcgtctgctgccc 240
Db 181 GTCTGGGACTGTACAACTCTGAACCTGGAAGTGGGTCCATGAACCTAAGGGCTACTAT 120
QY 241 caggacctggagccctgacctcctctgtactatgttggaggagcccccaaaagtggagcag 300
Db 241 CAGGACTGGAGCCCTGACCATCTCTGTACTATGTTGGGAGGAGCCCAAAAGTGGAGCAG 300
QY 301 ctctcaacatggtggtgaagtcttgaatgtagctga 339
Db 301 CTCTCAACATGTTGTTGAAGTCTTGTAAATGTAGCTGA 339

RESULT 3
LOCUS A48553 339 bp DNA PAT 07-MAR-1997
DEFINITION Sequence 5 from Patent WO9603432.
ACCESSION A48553
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VERSION A48553.1 GI:2302323
KEYWORDS unidentified.
SOURCE unidentified.
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 339)
AUTHORS Cerletti, N.
TITLE NOVEL PROCESS FOR THE PRODUCTION OF BIOLOGICALLY ACTIVE DIMERIC
PROTEI
JOURNAL Patent: WO 9603432-A 5 08-FEB-1996;
COMMENT CIBA GEIGY AG (CH)
FEATURES Other publication AU 3109595 960222.
Source 1..339
Location/Qualifiers
/db_xref="taxon:9606"
/db_xref="taxon:32644"
CDS
1..336
/note="Protein sequence is in conflict with the conceptual
translation"
/codon_start=1
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/db_xref="GI:2302324"
/translation="ALDNYCFRNLENCVVRPLYIDFRODLGKWKWHEPKGYVANFC
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NMVVKSCKS"
BASE COUNT 74 a 104 c 86 g 75 t
ORIGIN

Query Match 100.0%; Score 339; DB 9; Length 339;
Best Local Similarity 100.0%; Pred. No. 2.7e-83;
Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gcttggacacaattactctccgaacttgagagaaactgctgtgccccctc 60
Db 1 GCTTTGGACACCAATTACTCTCCGAACCTTGGAGGAGAACTGCTGTGCGCCCCCTC 60
QY 61 tacattgacttccgacaggatctgggtggaagtgggtccatgaacctaaaggctactat 120
Db 61 TACATTGACTTCGACAGGATCTGGGCTGGAAGTGGGTCCATGAACCTAAGGGCTACTAT 120
QY 121 gccaactctgtcagcccttgcccatacctccgcagtcagtcagacacacacacagcag 180
Db 121 GCCAACTTCTGCTCAGGCCCTTGCCCATACCTCCGAGTGCAGACACAAACCCACAGCAG 180
QY 181 gtctgggactgtacaacactctgaacctgaagcatctgcctcgtctgctgccc 240
Db 181 GTGCTGGGACTGTACAACTCTGAACCTGGAAGTGGGTCCATGAACCTAAGGGCTACTAT 120
QY 241 caggacctggagccctgacctcctctgtactatgttggaggagcccccaaaagtggagcag 300
Db 241 CAGGACTGGAGCCCTGACCATCTCTGTACTATGTTGGGAGGAGCCCAAAAGTGGAGCAG 300
QY 301 ctctcaacatggtggtgaagtcttgaatgtagctga 339
Db 301 CTCTCAACATGTTGTTGAAGTCTTGTAAATGTAGCTGA 339

RESULT 4
LOCUS A48567 339 bp DNA PAT 07-MAR-1997
DEFINITION Sequence 5 from Patent WO9603433.
ACCESSION A48567
VERSION A48567.1 GI:2302337
KEYWORDS
SOURCE unidentified.
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 339)
AUTHORS Cerletti, N.
TITLE NEW PROCESS FOR THE PRODUCTION OF BIOLOGICALLY ACTIVE PROTEIN
JOURNAL Patent: WO 9603433-A 5 08-FEB-1996;
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QY 181 gtctgggactgtacaacactctgaacctctgaagcatctgcctcgcttgcctgctgccc 240
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Db 241 CAGGACCTGGAGCCCTGACCATCTCTGTACTATGTTGGGAGGACCCCAAGTGGAGCAG 300
QY 301 ctctcaacatggtgtgaagctctgtaaatgactga 339
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Db 301 CTCTCCAACATGTTGTGAAGCTCTTGAATGTAGTGA 339
RESULT 7
I56856 I56856 339 bp DNA PAT 07-OCT-1997
LOCUS Sequence 3 from patent US 5650494.
ACCESSION I56856
VERSION I56856.1 GI:2477269
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 339)
AUTHORS Cerletti,N., McMaster,G.Kent, Cox,D., Schmitz,A. and Meyhack,B.
TITLE Process for recombining recombinantly produced TGF-beta-like
proteins
JOURNAL Patent: US 5650494-A 3 22-JUL-1997;
FEATURES Location/Qualifiers
source
1. .339
BASE COUNT 74 a 104 c 86 g 75 t
ORIGIN
Query Match 100.0%; Score 339; DB 10; Length 339;
Best Local Similarity 100.0%; Pred. No. 2.7e-83;
Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 gcttggacacaaattactgcttcgcgaacttgaggagaaactgctgtgccccctc 60
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Db 1 GCCTTGGACACCAATTAAGTCTCCGCAACTTGGAGGAGAACTGCTGTGCGCCCCCTC 60
QY 61 tacattgaacttcgcagagatctggctggagtggtgcctgaacctaaaggctactat 120
Db 61 TACATTGACTTCGCAGAGGATCTGGGCTGGAAGTGGGTCCATGAACCTAAGGGCTACTAT 120
QY 121 gccaaacttctgctcaggcccttgccataacctccgcagtgacagacacacacacagcag 180
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Db 121 GCCAACTTCTGCTCAGGCCCTTGCCCATACCTCCGAGTGCAGACACACACACAGCAG 180
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QY 241 caggacctggagccctcgaccactctgtactatgttggaggagcccccaagtgagcag 300
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Db 241 CAGGACCTGGAGCCCTGACCATCTCTGTACTATGTTGGGAGGACCCCAAGTGGAGCAG 300
QY 301 ctctcaacatggtgtgaagctctgtaaatgactga 339
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Db 301 CTCTCCAACATGTTGTGAAGCTCTTGAATGTAGTGA 339
RESULT 8
HUMTGF3A HUMTGF3A 2529 bp mRNA PRI 14-JAN-1995
LOCUS Human transforming growth factor-beta 3 (TGF-beta3) mRNA, complete
DEFINITION cds.
ACCESSION J03241
VERSION J03241.1 GI:339551
KEYWORDS transforming growth factor.

SOURCE Human placental and umbilical cord (cell line A673), cDNA to mRNA,
from library lambda-gt10.
ORGANISM Homo sapiens
REFERENCE Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Eukaryota; Eutheria; Primates; Catarhini; Homnidae; Homo.
TITLE Identification of another member of the transforming growth factor
type beta gene family
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 85 (13), 4715-4719 (1988)
MEDLINE 88263019
COMMENT Draft entry and computer-readable sequence [1] kindly submitted by
ten Dijke,P., Hansen,P., Iwata,K.K., Pieler,C. and Foulkes,J.G.
C. Pieler 12-SEPT-1988 The authors have found that this transforming
growth factor contains multiple growth inhibitory elements.
FEATURES Location/Qualifiers
source
1. .2529
/organism="Homo sapiens"
/db_xref="taxon:9606"
/map="14q24"
gene 263. .1501
/gene="TGFB3"
CDS 263. .1501
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/protein_id="AAA61161.1"
/db_xref="GI:339552"
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SKRNEQRIELFOILRPDEHIAKORYIGGNLPTGTAELSFSDVTVRWLLRRESN
IGLEISIHCPCHTFQPDGIDLENIHEVMELKFKGVNEDDGHGDLGLKKQKDHNP
HLILMIPPHRLDNPQGGORRKAALDNTFCRNLNLENCVRRPLYIDFRDGLGKWHV
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BASE COUNT 617 a 671 c 660 g 581 t
ORIGIN Chromosome 14.
Query Match 100.0%; Score 339; DB 97; Length 2529;
Best Local Similarity 100.0%; Pred. No. 2.1e-83;
Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 61 tacattgaacttcgcagagatctggctggagtggtgcctgaacctaaaggctactat 120
Db 1223 TACATTGACTTCGCAGAGGATCTGGGCTGGAAGTGGGTCCATGAACCTAAGGGCTACTAT 1282
QY 121 gccaaacttctgctcaggcccttgccataacctccgcagtgacagacacacacacagcag 180
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QY 181 gtctgggactgtacaacactctgaacctctgaagcatctgctcgcttgcctgctgctgccc 240
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Db 1403 CAGGACCTGGAGCCCTGACCATCTCTGTACTATGTTGGGAGGACCCCAAGTGGAGCAG 1462
QY 301 ctctcaacatggtgtgaagctctgtaaatgactga 339
Db 1463 CTCTCCAACATGTTGTGAAGCTCTTGAATGTAGTGA 1501
RESULT 9
HSTGFB3M HSTGFB3M 2574 bp mRNA PRI 12-SEP-1993
LOCUS Human mRNA for transforming growth factor-beta 3 (TGF-beta 3).
DEFINITION

ACCESSION X14149
VERSION X14149.1 GI:37095
KEYWORDS growth factor; transforming growth factor; transforming growth factor-beta 3.
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS 1. (bases 1 to 2574)
JOURNAL Direct Submission
TITLE Submitted (23-MAR-1989) Chen E.Y., Genentech Inc., 460 Pt. San Bruno Blvd., San Francisco, CA 94080, USA
REFERENCE 2. (bases 1 to 2574)
AUTHORS Derynck, R., Lindquist, P.B., Lee, A., Wen, D., Tamm, J., Graycar, J.L., Rhee, L., Mason, A.J., Miller, D.A., Coffey, R.J., Moses, H.L. and Chen, E.Y.
TITLE A new type of transforming growth factor-beta, TGF-beta 3
JOURNAL EMBO J 7 (12), 3737-3743 (1988)
MEDLINE 89091120
COMMENT See <J03241> for alternative sequence of TGF-beta 3.
FEATURES
source Location/Qualifiers
1..2574
/organism="Homo sapiens"
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/chromosome="14q24"
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/cell_line="A172 glioblastoma"
254..1492
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SKRNEQRIELFOILRDEHIAKQRIIGKNLPTRGTAEMLSFDVDTVREMLLRRES
LGLRISHCPTQPNQIDILEHVEYMEIKFGVDNEDHGRGLDKRQKHNP
HLIIMLPPHRLNDPQGQGRKRALDTNYCFRLENCVVRPLYIDFRODLGWKWH
EPKYANFCSGPCPYLRASDTHTSTVLGLYNTLNPEASAPCCVPQDLEPLITLYV
GRTPKEQLSNMVKSCKS"
BASE COUNT 629 a 680 c 666 g 599 t
ORIGIN
Query Match 100.0%; Score 339; DB 93; Length 2574;
Best Local Similarity 100.0%; Pred. No. 2.1e-83;
Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 gcttggacacacattactgtctccgaacttggaggagaactgtgtgccccctc 60
Db 1154 GCTTTGGACACCAATTACTGCTTCGCAACTTGGAGGAGAACTGCTGTGCGCCCTC 1213
QY 61 tacattgacttcgcagagatctggctggaagtgggtccatgaacctaaagggtactat 120
Db 1214 TACATTGACTTCCGACAGCATCTGGGCTGGAAGTGGGTCCATGAACCTAAGGGCTACTAT 1273
QY 121 gcaacttctgctcagcccttgccatacctccagtcagtcagacacacacacagcagc 180
Db 1274 GCCAACTTCTGCTCAGGCCCCCTGGCCATACCTCCAGTCGACAGACACACCCACAGCAG 1333
QY 181 gtgctggagctgtacacactgtgaacctgaagcatctgctcctgtgctgctgccc 240
Db 1334 GTGCTGGGACTGTACAACTCTGAACCTTGAGCATCTGCTCGCCCTGCTGCGTGCCTC 1393
QY 241 caggacctggagccctgaccatctgtactatgtttggaggagacccccaaagtggagcag 300
Db 1394 CAGGACCTGGAGCCCTCACCATCTCTGTACTGTATGTTGGAGGAGACCCCAAGTGGAGCAG 1453
QY 301 ctctccacacatgggtggaagtcttggtaaatgtagctga 339
Db 1454 CTCTCCAAACATGGGTGAAGTCTTGTAAATGTAGCTGA 1492

RESULT 10

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

Location/Qualifiers

BASE COUNT

ORIGIN

Query Match

Best Local Similarity

Matches

Conservative

Mismatches

Indels

Gaps

Length

Pred.

No.

DB

Score

60

60

337.4

DB

10

1899

bp

ss-DNA

PAT

21-MAY-1993

Sequence

11 from Patent

US 4886747

GI:270714

Unknown

Unclassified

1 (bases 1 to 1899)

Derynck, R.M.A. and Goeddel, D.V.

Nucleic acid encoding TGF-beta, and its uses

Patent: US 4886747-A 11 DEC-1989;

Genentech, Inc.;

South San Francisco, CA

Location/Qualifiers

1..1899

/organism="unknown"

515 a

425 c

452 g

507 t

99.5%

Score

337.4

DB

10

Length

1899

99.7%

Pred.

No.

6e-83

0

Mismatches

1

Indels

0

Gaps

0

60

60

337

337

397

180

457

240

517

300

577

RESULT 11

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

Location/Qualifiers

BASE COUNT

ORIGIN

Query Match

Best Local Similarity

Matches

Conservative

Mismatches

Indels

Gaps

Length

Pred.

No.

DB

Score

60

60

337.4

DB

10

Length

1899

99.7%

Pred.

No.

6e-83

0

Mismatches

1

Indels

0

Gaps

0

60

60

337

337

397

180

457

240

517

300

577

PAT

02-DEC-1994

Sequence

2 from Patent

EP 0267463

GI:590974

Unknown

Unclassified

1 (bases 1 to 498)

Iwata, K.K., Gold, L.I. and Stephenson, J.R.

Tissue-derived tumor growth inhibitors, methods of preparation and

uses thereof

Patent: EP 0267463-A2 2 18-MAY-1988;

Location/Qualifiers

1..498

/organism="unknown"

122 a

137 c

129 g

110 t


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Qy 121 gcaacttctgctcagcccttgccatactccgagctcagagcagacacacacacagcagc 180
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Qy 181 gtgctggagctgacacactgaaacctgaagcatctgctcgcttctgctgctgccc 240
Db 181 GTGCTGGGACTGTACACACTCTGAACCCCTGAACCATCTGCCTCGCTTGTGCTGCGGCC 240
Qy 241 caggacctggagcccttgaccatctgtactatgttgggagagaccccccaaaagtggagcag 300
Db 241 CAGGACCTGGAGCCCTTGACCATCTGTACTATGTGGGAGGAGCCCAAAAGTGAGCAG 300
Qy 301 ctctccaaacatggtggtgaagcttctgtaaatgtagc 336
Db 301 CTCTCCAACATGTTGGTGAAGTCTTGTAAATGTAGC 336

RESULT 14
LOCUS A48555 336 bp DNA PAT 07-MAR-1997
DEFINITION Sequence 7 from Patent WO9603432.
ACCESSION A48555
VERSION A48555.1 GI:2302325
KEYWORDS .
SOURCE .
ORGANISM .
REFERENCE 1 (bases 1 to 336)
AUTHORS Cerletti,N.
TITLE NOVEL PROCESS FOR THE PRODUCTION OF BIOLOGICALLY ACTIVE DIMERIC
JOURNAL PROTEI
PATENT: WO 9603432-A 7 08-FEB-1996;
CIBA GEIGY AG (CH)
COMMENT Other publication AU 3109595 960222.
FEATURES
source
1..336
/organism="unidentified"
/db_xref="taxon:32644"
mat_peptide
1..132
/product="N-TERMINAL 44 AMINO ACIDS OF HUMAN TGF-BETA1"
CDS
1..336
/organism="unidentified"
/codon_start=1
/product="HYBRID TGF-BETA NAMED TGF-BETA1-3"
/db_xref="GI:2302326"
/translation="ALDITNYCFSSTEKNCCVRQLYIDFRKDLGKWKIHEPKGYHANFC
SGPCPYLRASADTHTSTVLGTYLNTPASASPCVQDLEPLTILYVYVGRTPKVEQLS
NMVVKSCKS"
mat_peptide
133..336
/product="C-TERMINAL 68 AMINO ACIDS OF HUMAN TGF-BETA3"
BASE COUNT 75 a 109 c 86 g 66 t
ORIGIN
Query Match 87.8%; Score 297.6; DB 9; Length 336;
Best Local Similarity 92.9%; Pred. No. 7.7e-72;
Matches 312; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

Qy 1 gctttggacaccaaattactgtcttcgcaacttgagagagaactgtgtgcgccccctc 60
Db 1 GCCCTGGACACCAACTATTGCTTCAGCTCCACGGAGAGAACTGCTGCTGCGGCGCAGCTG 60
Qy 61 tacattgacttcgacaggaatctgggctggaagtgggtccatgaacctaaagggtactact 120
Db 61 TACATTGACTTCCGCAAGGACCTCGGCTGGAAGTGGATCCACGAGCCCAAGGGCTACCAT 120
Qy 121 gcaacttctgctcagcccttgccatactccgagctcagagcagacacacacacagcagc 180
Db 121 GCCAACTTCTGCTCAGGCCCTTGCCCATACCTCCGCACTGCAGACACAACCCACAGCAGC 180
Qy 181 gtgctggagctgtaacacactctgaacctgaagcatctgctcgcttctgctgctgccc 240
Db 181 GTGCTGGGACTGTACACACTCTGAACCCCTGAACCATCTGCCTCGCTTGTGCTGCGGCC 240
Qy 241 caggacctggagcccttgaccatctgtactatgttgggagagaccccccaaaagtggagcag 300
Db 241 CAGGACCTGGAGCCCTTGACCATCTGTACTATGTGGGAGGAGCCCAAAAGTGAGCAGC 300

RESULT 15
LOCUS A48569 336 bp DNA PAT 07-MAR-1997
DEFINITION Sequence 7 from Patent WO9603433.
ACCESSION A48569
VERSION A48569.1 GI:2302339
KEYWORDS .
ORGANISM .
REFERENCE 1 (bases 1 to 336)
AUTHORS Cerletti,N.
TITLE NEW PROCESS FOR THE PRODUCTION OF BIOLOGICALLY ACTIVE PROTEIN
JOURNAL Patent: WO 9603433-A 7 08-FEB-1996;
CIBA GEIGY AG (CH)
COMMENT Other publication AU 3109695 960222.
FEATURES
source
1..336
/organism="unidentified"
/db_xref="taxon:32644"
mat_peptide
1..132
/product="N-TERMINAL 44 AMINO ACIDS OF HUMAN TGF-BETA1"
CDS
1..336
/organism="unidentified"
/codon_start=1
/product="HYBRID TGF-BETA NAMED TGF-BETA1-3"
/db_xref="GI:2302340"
/translation="ALDITNYCFSSTEKNCCVRQLYIDFRKDLGKWKIHEPKGYHANFC
SGPCPYLRASADTHTSTVLGTYLNTPASASPCVQDLEPLTILYVYVGRTPKVEQLS
NMVVKSCKS"
mat_peptide
133..336
/product="C-TERMINAL 68 AMINO ACIDS OF HUMAN TGF-BETA3"
BASE COUNT 75 a 109 c 86 g 66 t
ORIGIN
Query Match 87.8%; Score 297.6; DB 9; Length 336;
Best Local Similarity 92.9%; Pred. No. 7.7e-72;
Matches 312; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

Qy 1 gctttggacaccaaattactgtcttcgcaacttgagagagaactgtgtgcgccccctc 60
Db 1 GCCCTGGACACCAACTATTGCTTCAGCTCCACGGAGAGAACTGCTGCTGCGGCGCAGCTG 60
Qy 61 tacattgacttcgacaggaatctgggctggaagtgggtccatgaacctaaagggtactact 120
Db 61 TACATTGACTTCCGCAAGGACCTCGGCTGGAAGTGGATCCACGAGCCCAAGGGCTACCAT 120
Qy 121 gcaacttctgctcagcccttgccatactccgagctcagagcagacacacacacagcagc 180
Db 121 GCCAACTTCTGCTCAGGCCCTTGCCCATACCTCCGCACTGCAGACACAACCCACAGCAGC 180
Qy 181 gtgctggagctgtaacacactctgaacctgaagcatctgctcgcttctgctgctgccc 240
Db 181 GTGCTGGGACTGTACACACTCTGAACCCCTGAACCATCTGCCTCGCTTGTGCTGCGGCC 240
Qy 241 caggacctggagcccttgaccatctgtactatgttgggagagaccccccaaaagtggagcag 300
Db 241 CAGGACCTGGAGCCCTTGACCATCTGTACTATGTGGGAGGAGCCCAAAAGTGAGCAGC 300

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unclassified.
REFERENCE 1 (bases 1 to 336)
AUTHORS Carletti,N.
TITLE NEW PROCESS FOR THE PRODUCTION OF BIOLOGICALLY ACTIVE PROTEIN
JOURNAL Patent: WO 9603433-A 9 08-FEB-1996;
CIBA GEIGY AG (CH)
COMMENT Other publication AU 3109695 960222.
FEATURES
    source      Location/Qualifiers
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            /organism="unidentified"
            /db_xref="taxon:32644"
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        /product="N-TERMINAL 44 AMINO ACIDS OF HUMAN TGF-BETA2"
    CDS          1..132
        /product="N-TERMINAL 44 AMINO ACIDS OF HUMAN TGF-BETA2"
        /note="protein sequence is in conflict with the conceptual translation"
        /codon_start=1
        /product="HYBRID TGF-BETA2-3"
        /protein_id="CAA03124.1"
        /db_xref="GI:2302342"
        /translation="ALDAAYCFRNVQDNCLRLPLYIDFKRDLGKWKVHEPRKYNANFC
        SGPCPYLRSDATTHSTVLGLYNTLNPEASASPCCPQDLEPLTILYVGRTPKVEQLS
        NMVVKCKCS"
    mat_peptide 133..336
        /product="C-TERMINAL 68 AMINO ACIDS OF HUMAN TGF-BETA3"
    BASE COUNT 81 a 94 c 84 g 77 t
    ORIGIN

Query Match      81.7%; Score 276.8; DB 9; Length 336;
Best Local Similarity 89.0%; Pred. No. 4.3e-66;
Matches 299; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

Qy 1 gcttggacacaaattactgcttcgcgaacttgaggagaaactgctgtgccccctc 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 GCTTGGATGGCGCTATTGCTTTAGAAATGTGCGAGGATATTGCTGCTACGTCACATT 60

Qy 61 tacattgactccagacaggtatggctggagtggtggtccatgaacctaaagggtactat 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 TACATTGATTTCAAGAGGATCTAGGGTGGAAATGGATACACAGAACCCCAAGGGTACAA 120

Qy 121 gcaactctctcagggccctggccatacctccgcagtcagtcagacacacacagacag 180
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 121 GCCAATCTCTGCTCAGGCGCTTGCCCATACCTCCGACAGACACAAACCCACAGCAG 180

Qy 181 gtgctggagactgtcaaacactgaacctgaagcatctgctgcctgtgctgctgccc 240
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 181 GTGCTGGGACTGTACACACTCTGNACCCTGNAGCATCTGCTCGCCTTGTCTGCTGCC 240

Qy 241 caggacctggagccctgaccatcctgtactatgttggaggagaccccccaagtggagcag 300
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 241 CAGGACCTGGAGCCCTGACCATCCTGTACTATGTGGAGGAGACCCCAAGTGAGCAG 300

Qy 301 ctctcccaacatggtggtagaagtcttggtaaatgtagc 336
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 301 CTCCTCAACATGGTGGTGAAGTCTTGTAAATGTAGC 336

RESULT 23
CHKGFB      2187 bp mRNA VRT      28-APR-1993
LOCUS       Chicken transforming growth factor beta (TGF-beta-3) mRNA, complete cds.
DEFINITION
ACCESSION  M31154
VERSION    M31154.1 GI:212758
KEYWORDS   transforming growth factor-beta.
SOURCE     Chicken embryo chondrocyte, cDNA to mRNA.
ORGANISM   Gallus gallus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
            Phasianinae; Gallus.
REFERENCE  1 (bases 1 to 2187)
AUTHORS   Jakowlew,S.B., Dillard,P.J., Kondalish,P., Sporn,M.B. and

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Roberts,A.B.
TITLE       Complementary deoxyribonucleic acid cloning of a novel transforming
            growth factor-beta messenger ribonucleic acid from chick embryo
            chondrocytes
JOURNAL     Mol. Endocrinol. 2, 747-755 (1988)
MEDLINE     89096966
FEATURES    Location/Qualifiers
            source      1..2187
                /organism="Gallus gallus"
                /db_xref="taxon:9031"
            CDS          40..1278
                /note="transforming growth factor beta precursor"
                /codon_start=1
                /protein_id="AAA49089.1"
                /db_xref="GI:212759"
                /translation="MKMYAQRALVLLSLFSFATVSLALSCTTLDLEHIKKKVEAIR
                GOILSKRLTSPSPVGAHPVQIILALYNSTRELLEEMEEKEESCQONTSESYVA
                KEIHFDMIOGIPHEHNELCICPKGVTSNVRFNVSSAEKNSNLFRAEFRLVLPNPS
                SKRSQRIELFOILRDEHIAKQYLSGRNVQTRGSPWLSFDVDTVRWLLHRESN
                LGLEISIHCPCHTFQPNGDILHLEHVEIKFKGIDSEDDYRGDLGRLLKQDLHNP
                HLILMLPPHRLSEPTLGQRKKRALDTNYCFRNLEENCVRPLYIDFKQDLGKWKVH
                EPKGYFANFGSGCPYLRSDATTHSTVLGLYNTLNPEASASPCCPQDLEPLTILYV
                GRTPKVEQLSNMVVKCKCS"
            sig_peptide  40..108
                /note="transforming growth factor beta signal peptide
                (pot.); putative"
            sig_peptide  40..93
                /note="transforming growth factor beta signal peptide
                (pot.); putative"
            mat_peptide  940..1275
                /note="transforming growth factor beta (5' end could be at
                109)"
    BASE COUNT 525 a 587 c 608 g 467 t
    ORIGIN

Query Match      79.7%; Score 270.2; DB 8; Length 2187;
Best Local Similarity 87.3%; Pred. No. 2.2e-64;
Matches 296; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

Qy 1 gcttggacacaaattactgcttcgcgaacttgaggagaaactgctgtgccccctc 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 940 GCCCTGGATACCAACTACTGCTTCCGGAACCTGGAGGAGAACTGCTGTGCGCTCTT 999

Qy 61 tacattgactccagacaggtatggctggagtggtggtccatgaacctaaagggtactat 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1000 TACATTGACTTCGACAGGACCTGGCGTGGAAATGGTCCATGAGCCTAAAGGCTACTT 1059

Qy 121 gcaactctctcagggccctggccatacctccgcagtcagtcagacacacacagacag 180
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1060 GCAAACTTCTGTTGGGCGCATGTCGTACCTCCGAGTGCAGACACCACTACAGCAG 1119

Qy 181 gtgctggagactgtcaaacactgtgaacctgaagcatctgctgcctgtgctgctgcc 240
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1120 GTGCTGGGCTTGTACAAACACGCTGAACCCCGAGGCACTGCTTACCCCTGCTGTGCCA 1179

Qy 241 caggacctggagccctgaccatcctgtactatgttggaggagaccccccaagtggagcag 300
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1180 CAGGACCTGGAGCCACTGACGATCTTGTACTATGTGGGAGGACACCCCAAGTGGAGCAG 1239

Qy 301 ctctcccaacatggtggtagaagtcttggtaaatgtagctga 339
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1240 CTCTCCAATATGTTGGTGAATCTCTGCAAGTGCAGCTGA 1278

RESULT 24
LOCUS       A23758      336 bp mRNA PAT
DEFINITION TGF-beta3(44/45)beta1 hybrid coding region.
ACCESSION  A23758
VERSION    A23758.1 GI:825592
KEYWORDS   human.
SOURCE     human.

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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 336)
AUTHORS McMaster,G.K., Cox,D., Cerletti,N. and Kuhla,J.
TITLE Novel hybrid transforming growth factors
JOURNAL Patent: EP 0542679-A 8 19-MAY-1993;
CIBA-GEIGY AG

FEATURES
source Location/Qualifiers
1..336
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 63 a 109 c 98 g 66 t
ORIGIN
Query Match 70.8%; Score 240; DB 9; Length 336;
Best Local Similarity 82.1%; Pred. No. 6.5e-56;
Matches 276; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

Qy 1 gctttggacaccaattactcttcgcgaacttgaggagagaactgtgtgccccctc 60
Db 1 GCTTTGGACACCAATTAAGTCTCCGCAACTTGGAGGAGAACTGCTGTGCGCCCTC 60
Qy 61 tacattgacttcgcagcaggtctggctggaagtgggtccatgaacccaaggtactat 120
Db 61 TACATTGACTTCGCACAGATCTGGGCTGGAGTGGTCCATGAACCTTAAGGGCTACTAT 120
Qy 121 gccaaactctgctcagcagcttgcacacacttgaaacctgcagctcagacacacacagcagc 180
Db 121 GCGCAACTTCTGCTCGGGCCCTGCGCCCTACATTTGGAGCTGGACGCTGACAGCAAG 180
Qy 181 gtgctggagactgtacaaactctgaacctgaagcatctgctccttgcgtgcccc 240
Db 181 GTCTGGCCCTGTACAAACAGCATATAAGCTGGAGCGGCTCGGCGCCGCTGCTGCGTCCG 240
Qy 241 caggacctggagccctgacctctgtactatgttgaggagaccccccaagtggagcag 300
Db 241 CAGGCGCTGGAGCCCTGCCCATCTGTACTACGTGGCCGCGGCGGCGGCGGCGGCGG 300
Qy 301 ctctccaacatggtggtgaagtcttgaatgtagc 336
Db 301 CTGTCCACATGATCGTGGCTGCTGCTGCAAGTGCAGC 336

RESULT 25
A23759 LOCUS A23759 336 bp mRNA PAT 25-JAN-1995
DEFINITION TGF-beta3(44/45)beta2 hybrid coding region.
ACCESSION A23759
VERSION A23759.1 GI:825593
KEYWORDS human.
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 336)
AUTHORS McMaster,G.K., Cox,D., Cerletti,N. and Kuhla,J.
TITLE Novel hybrid transforming growth factors
JOURNAL Patent: EP 0542679-A 9 19-MAY-1993;
CIBA-GEIGY AG

FEATURES
source Location/Qualifiers
1..336
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 88 a 87 c 71 g 90 t
ORIGIN
Query Match 70.8%; Score 240; DB 9; Length 336;
Best Local Similarity 82.1%; Pred. No. 6.5e-56;
Matches 276; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

Qy 1 gctttggacaccaattactcttcgcgaacttgaggagagaactgtgtgccccctc 60
Db 1 GCTTTGGACACCAATTAAGTCTCCGCAACTTGGAGGAGAACTGCTGTGCGCCCTC 60
Qy 61 tacattgacttcgcagcaggtctggctggaagtgggtccatgaacccaaggtactat 120
Db 61 TACATTGACTTCGCACAGATCTGGGCTGGAGTGGTCCATGAACCTTAAGGGCTACTAT 120
Qy 121 gccaaactctgctcagcagcttgcacacacttgaaacctgcagctcagacacacacagcagc 180
Db 121 GCGCAACTTCTGCTCGGGCCCTGCGCCCTACATTTGGAGCTGGACGCTGACAGCAAG 180
Qy 181 gtgctggagactgtacaaactctgaacctgcagcatctgctccttgcgtgcccc 240
Db 181 GTCTGGAGCTTATATATACCATTAATCCAGAAAGCATCTGCTTCTCTCTGCTGCTGCC 240
Qy 241 caggacctggagccctgacctctgtactatgttgaggagaccccccaagtggagcag 300
Db 241 CAAGATTAGAACCTCTAACCATTTCTACTACATTGGCAAAACACCAAGATTGAACAG 300
Qy 301 ctctccaacatggtggtgaagtcttgaatgtagc 336
Db 301 CTTTCTAATATGATTGATTAAAGTCTTGCAATGCGAGC 336

RESULT 26
A48559 LOCUS A48559 336 bp DNA PAT 07-MAR-1997
DEFINITION Sequence 11 from Patent WO9603432.
ACCESSION A48559
VERSION A48559.1 GI:2302329
KEYWORDS unidentified.
SOURCE unidentified.
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 336)
AUTHORS Cerletti,N.
TITLE NOVEL PROCESS FOR THE PRODUCTION OF BIOLOGICALLY ACTIVE DIMERIC PROTEIN
JOURNAL Patent: WO 9603432-A 11 08-FEB-1996;
CIBA GEIGY AG (CH)
COMMENT Other publication AU 3109595 960222.
FEATURES Location/Qualifiers
source 1..336
/organism="unidentified"
/db_xref="taxon:32644"
1..132
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CDS 1..336
/note="protein sequence is in conflict with the conceptual translation"
/codon_start=1
/product="HYBRID TGF-BETA3-2"
/protein_id="CAA03118.1"
/db_xref="GI:2302330"
mat_peptide /translation="ALDITNYCFRNLEENCVRPLYIDFRODLGKWKVHPKGYANFC
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NMIVSKCS"
133..336
BASE COUNT 88 a 87 c 71 g 90 t
ORIGIN

Query Match 70.8%; Score 240; DB 9; Length 336;
Best Local Similarity 82.1%; Pred. No. 6.5e-56;
Matches 276; Conservative 0; Mismatches 60; Indels 0; Gaps 0;
Qy 1 gctttggacaccaattactcttcgcgaacttgaggagagaactgtgtgccccctc 60
Db 1 GCTTTGGACACCAATTAAGTCTCCGCAACTTGGAGGAGAACTGCTGTGCGCCCTC 60
Qy 61 tacattgacttcgcagcaggtctggctggaagtgggtccatgaacccaaggtactat 120

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Db 61 TACATTGACCTCCAGAGGATCTGGGCTGGAGTGGGTCCTAATGAACCTAAGGGCTACTAT 120
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Db 121 GCCAACTTCTGCTGGAGCATGCCGCTATTATGGAGTTCAGACACTCAGACAGCAGG 180
Qy 181 gtgctggagctgtacaactctgaacccctgaagcatctgctgccttgcctgtgcgtgcc 240
Db 181 GTCTGAGCTTATATAATACATAAATCCAGAAGCATCTGCTTCTCTTGTGCTGGGTGCC 240
Qy 241 caggacctgagccctgacacactctgactctatctgtggagagaccccccaagtgagagcag 300
Db 241 CTTCTAGCTTATATAATACATAAATCCAGAAGCATCTGCTTCTCTTGTGCTGGGTGCC 240
Qy 241 caggacctgagccctgacacactctgactctatctgtggagagaccccccaagtgagagcag 300
Db 241 CAAGATTTAGAACCTCTAACCATTTCTTACTACATTTGCAAAACACCCCAAGATTGAACAG 300
Qy 301 ctctcccaacatggtggaagtctgttaaatgtagc 336
Db 301 CTTTCTAATATGATGTAAGTCTTTGCAATGCAGC 336

RESULT 27
A48573
LOCUS A48573 336 bp DNA PAT 07-MAR-1997
DEFINITION Sequence 11 from Patent WO9603433.
ACCESSION A48573
VERSION A48573.1 GI:2302343
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
COMMENT
FEATURES
source
1..336
/organism="unidentified"
/db_xref="taxon:32644"
mat_peptide
1..132
/product="N-TERMINAL 44 AMINO ACIDS OF HUMAN TGF-BETA3"
CDS
1..336
/notes="Protein sequence is in conflict with the conceptual
translation"
/codon_start=1
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/protein_id="CAA03125.1"
/db_xref="GI:2302344"
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AGACPVLWSDDTQHSRVLSLYNTINPEASAPCCVQDLEPLTILYIGKTPKIEQLS
NMIVKSKCS"
mat_peptide
133..336
/product="C-TERMINAL 68 AMINO ACIDS OF HUMAN TGF-BETA2"
BASE COUNT 88 a 87 c 71 g 90 t
ORIGIN

Query Match 70.8%; Score 240; DB 9; Length 336;
Best Local Similarity 82.1%; Pred. No. 6.5e-56;
Matches 276; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

Qy 1 gcttggacacaaatctactcttccgaacttgagagaaactctgtgagcccccctc 60
Db 1 GCTTTGGACACCAATTAATCTGCTTCCGCAACTTGGAGGAGAACTGCTGTGCGCCCCCTC 60
Qy 61 tabattgacttccgacagagatctgggtggaagtgggtcccatgaacctaagggtactat 120
Db 61 TACATTGACTTCGACAGGATCTGGGCTGGAGTGGGTCCATGAACCTAAGGGCTACTAT 120
Qy 121 gccaaattctgctagcccttggccataccctccgcagtcagacacaaacccacagcagc 180
Db 121 GCCAACTTCTGCTGGAGCATGCCGCTATTATGGAGTTCAGACACTCAGACAGCAGG 180

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Qy 181 gtgctggagctgtacaacactgtgaacccctgaagcatctgcctgccttgcctgtgcgtgcc 240
Db 181 GTCTGAGCTTATATAATACATAAATCCAGAAGCATCTGCTTCTCTTGTGCTGGGTGCC 240
Qy 241 caggacctgagccctgacacactctgactctatctgtggagagaccccccaagtgagagcag 300
Db 241 CAAGATTTAGAACCTCTAACCATTTCTTACTACATTTGCAAAACACCCCAAGATTGAACAG 300
Qy 301 ctctcccaacatggtggaagtctgttaaatgtagc 336
Db 301 CTTTCTAATATGATGTAAGTCTTTGCAATGCAGC 336

RESULT 28
AF152592
LOCUS AF152592 244 bp mRNA MAM 28-MAR-2001
DEFINITION Capreolus capreolus transforming growth factor beta 3 (TGF-b3)
mRNA, partial cds.
ACCESSION AF152592
VERSION AF152592.1 GI:8132130
KEYWORDS
SOURCE roe deer.
ORGANISM Capreolus capreolus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervioidea;
Cervidae; Odocoileinae; Capreolus.
REFERENCE
AUTHORS Wagener,A., Blottner,S., Goeritz,F. and Fickel,J.
TITLE Detection of growth factors in the testis of roe deer (Capreolus capreolus)
JOURNAL Anim. Reprod. Sci. 64 (1-2), 65-75 (2000)
MEDLINE 20532861
PUBMED 11078967
REFERENCE
AUTHORS Wagener,A. and Fickel,J.
TITLE Direct Submission
JOURNAL Submitted (19-MAY-1999) Evolutionary Genetics, Institute for Zoo
Biology and Wildlife Research, Alfred-Kowalke-Str. 17, Berlin
D-10315, Germany
FEATURES
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/gene="TGF-b3"
<1..>244
/gene="TGF-b3"
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/db_xref="GI:8132131"
/translation="EENCVRPLYIDFRQDLGKWWHEPKGYANFCGCPYLRRSSD
TTHSTVLGLYNTLNPEASAPCCVQDLEPLTILYV"
BASE COUNT 52 a 84 c 57 g 51 t
ORIGIN

Query Match 65.4%; Score 221.6; DB 7; Length 244;
Best Local Similarity 94.3%; Pred. NO. 8.2e-51;
Matches 230; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Qy 34 gagagaactctgtgtgcgccccctctacattgacttccgacagatctggctggaag 93
Db 1 GAGGAGAACTGCTGTGCGCCCTCTCTATATTCTCCGACAGATCTGGCGTGA 60
Qy 94 tgggtccatgaactaagggtactatcgcaactctgtcagcgccttgcctacacctc 153
Db 61 TGGGTCCATGAACCTAAGGGCTACTATGCCAACTTCTGCTCAGGCCCATGCCATACCTC 120
Qy 154 cgcagtgcagacacaaacccacagcagcgtgctggtgactgtacaacactctgaacctgaa 213

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/product="HUMAN TGF-BETA1"
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NMIVRSCKKS"

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BASE COUNT	66 a	114 c	100 g	59 t
ORIGIN				

Query Match	60.4%	Score	204.6	DB	9	Length	339
Best Local Similarity	75.2%	Pred. No.	3.9e-46				
Matches	255	Conservative	0	Mismatches	84	Indels	0
						Gaps	0

Qy	1	gctttgacacaaattactcttccgcaacttgagagagaactgctgtgtgagcccccctc	60
Db	1	gccctgacacacaaattactcttccgcaacttgagagagaactgctgtgtgagcccccctc	60
Qy	61	tacattgacttcgcagcaggatctggctggaatgggtccatgaacctaaaggctactact	120
Db	61	tacattgacttcgcagcaggatctggctggaatgggtccatgaacctaaaggctactact	120
Qy	121	gcaaaccttcctcagggcccttgccataacctccgcagtcgagacacaaccacacagcag	180
Db	121	gccaaacttcctcagggcccttgccataacctccgcagtcgagacacaaccacacagcag	180
Qy	181	gtctgtggactgtacaacactctgaacccctgaagcatctgctcgcctgtctgtcgtgcgc	240
Db	181	gtctgtgcctgtgacacacactctgaacccctgaagcatctgctcgcctgtctgtcgtgcgc	240
Qy	241	caggaactggaagccctcgacactctgtactatgttggagagacccccaaagtggagacag	300
Db	241	cagggcttgagccgcctgcccactgtgtactgtacgtggggccgcaagccccaaagtggagacag	300
Qy	301	ctctcccaacatggtgggtgaagctctgttaaatgtagctga	339
Db	301	ctgtcccaacatggtgggtgaagctctgttaaatgtagctga	339

RESULT	38		
A48563			
LOCUS	A48563	339 bp	DNA
DEFINITION	Sequence 1 from Patent WO9603433.		
ACCESSION	A48563		
VERSION	A48563.1	GI:2302333	
KEYWORDS	.		
SOURCE	unidentified.		
ORGANISM	unidentified		
REFERENCE	1 (bases 1 to 339)		
AUTHORS	Carletti,N.		
TITLE	NEW PROCESS FOR THE PRODUCTION OF BIOLOGICALLY ACTIVE PROTEIN		
JOURNAL	Patent: WO 9603433-A 1 08-FEB-1996;		
	CIBA GEIGY AG (CH)		
COMMENT	Other publication AU 3109695 960222.		
FEATURES	Location/Qualifiers		
source	1..339		

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CDS
1..336
/db_xref=taxon:32044
/notes="Protein sequence is in conflict with the conceptual
translation"
/codon_start=1
/product="HUMAN TGF-BETA1"
/protein_id="CAA03120.1"
/db_xref="GI-2302334"
/translation="ALDITCFSSSTKNCVRLYIDFRKDLGKWKIHDPKGYHANFC
LGPCPYIWSLDITYSKVLALYNHNPNGSAAPCCVQALEPLPIVYVVGRRKPKVEQLS
NMTVRSCKGS"
66 a      114 c      100 g      59 t
BASE COUNT
ORIGIN

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Query Match	60.48;	Score	204.6;	DB	9;	Length	339;
Best Local Similarity	75.2;	Pred.	No.	3.9e-46;			
Matches	255;	Conservative	0;	Mismatches	84;	Indels	0;
Gaps	0;						
Qy	1	gcttggacacccaattactgcttcgcgaactgtgagagaaactgctgtgtgcgccccctc	60				
Db	1	GCCTTGGACACCACTATTGCTTCAGCTCCACGGAGAGAACTGCTGCGTGGCGACGTG	60				
Qy	61	tacattgactctccgacaggatctggctgggaagtgggtccatgaacctaaagggctactat	120				
Db	61	TACATTGACTTCCGCAAGGACCTCGGTGGAAGTGGATCCACGAGCCCAAGGGCTACCAT	120				
Qy	121	gccaaactctgctcaggcccttgcccatactccgcagtcgagacacacccccacagcacg	180				
Db	121	GCCAACTTCTGCCCTCGGSCCTTGCCCCCTACATTTTGGAGCCTTGGACACGACAGTACAGCAAG	180				
Qy	181	gtgtggagactgtacaacactctgaacctgaacctgaacatctgcctcgcttgcgtgcgcc	240				
Db	181	GTCTTGGCCCCGTGTACACACAGCATTAACCCGGCGCGCTCGGCGGCGCGTGTGTCGTGCCG	240				
Qy	241	caggacctggagcccttgaccactctgtactatgttgggagagacccccaaagtggagcag	300				
Db	241	CAGGCGTGGAGCGCTGCCCATCTGCTGTACTACGTGGSCCGCAAGCCCAAGTGGAGCAG	300				
Qy	301	ctctccacaatctgttgggtgaagctctgttaaatgtagtcta	339				
Db	301	CTGTCCCAACATGATCGTGCCTCTCTGCAAGTGCAGCTGA	339				

RESULT 39

LOCUS	I56854	339 bp	DNA	PAT	07-OCT-1997
DEFINITION	Sequence 1 from patent US 5650494.				
ACCESSION	I56854				
VERSION	I56854.1	GI:2477267			
KEYWORDS	.				
SOURCE	Unknown.				
ORGANISM	Unknown.				

REFERENCE	1 (bases 1 to 339)
AUTHORS	Carletti,N., McMaster,G.Kent, Cox,D., Schmitz,A. and Meyhack,B.
TITLE	Process for refolding recombinantly produced TGF-.beta.-like proteins
JOURNAL	Patent: US 5650494-A 1 22-JUL-1997;
FEATURES	Location/Qualifiers
source	1..339
	/organism="unknown"
BASE COUNT	66 a 114 c 100 g 59 t
ORIGIN	

Query Match	60.4%	Score	204.6;	DB	10;	Length	339;
Best Local Similarity	75.2%	Pred. NO.	3.9e-46;				
Matches	255;	Conservative	0;	Mismatches	84;	Indels	0;
						Gaps	0;

Qy	1	gcttggacacccaattactgcttcgcgaacttgaggaggaactgctgtgacgcccctc	60
Db	1	GCCTGGACACCAACTATGTCTCAGCTCCACGGAGAAGAACTGCTGGTGGCAGCTG	60
Qy	61	tacattgacttccgacaggatctggctgggaagtgggtccatgaacctaaagggctactat	120
Db	61	TACATTGACTTCCGCAAGGACCTCGCTGGGAAGTGGATCCACGAGCCCAAGGGTACCAT	120
Qy	121	gcgaactctgctcaggcccttgcccatlacctccgcagtgacacacaacccaagacagc	180
Db	121	GCCAACTTCTGGCTCGGGCCCTGCCCTTACATTGGAGCCTGGACACGCAGTACAGCAAG	180
Qy	181	gtctgtggactgtatacaacactctgaacctgaagcatctgctgcctgtgctgctgccc	240
Db	181	GTCTGTGGCCCTGTATCAACACCATAAACCCGGCGCCTCGGGGGCGCGTGTGGTGGCG	240
Qy	241	caggacctggagcccctgaccatcctgtactatgttggaggaacccccaaagtggagcag	300

ORIGIN

[illegible]

RESULT 43

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BOVTFGB 1117 bp mRNA MAM 27-APR-1993
LOCUS Bovine transforming growth factor-beta-1 (TGF beta-1) mRNA, 3' end.
DEFINITION
ACCESSION M36271
VERSION M36271.1 GI:163747
KEYWORDS transforming growth factor-beta 1.
SOURCE Bovine fibropapilloma, cDNA to mRNA, (library of Okayama and Berg).
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae.
Bovidae; Bovinae; Bos.
1 (bases 1 to 1117)
Van Obberghen-Schilling, E., Kondaiah, P., Ludwig, R.L., Sporn, M.B.
and Baker, C.C.
TITLE Complementary deoxyribonucleic acid cloning of bovine transforming
growth factor-beta-1
JOURNAL Mol. Endocrinol. 1, 693-698 (1987)
MEDLINE 91042552
FEATURES
source Location/Qualifiers
1. .1117
/organism="Bos taurus"
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/note="transforming growth factor-beta-1 precursor"
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/db_xref="GI:163748"
/translation="AIALYLNSTRDRVAGESAETEPEADYYAKEVTRVLMVEYGNK
IDYKMSSESHITFMFTSELRAQPEPVLLSRADVKRLKLKVEQHVLEYQKYSNN
SWRLNRLILAPSDPEWLSFDVTGVVQWLTRRETEGFLSAHSCDSKDTLQYNN
INGFSRRGRDLAT IHGMNRPKYLLMATPLERAQHLSRHRRLADNTNYCFSTSEKKA
CVROLYIDFKDLGKWKWIKHPKGYHANFCIGPCPYIWSLDTQYSKVLALYNQHNPFQAS
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mat_peptide 612..947
/note="transforming growth factor-beta-1"
BASE COUNT 244 a 379 c 301 g 193 t
ORIGIN

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Query Match

60.48: Score 204.6: DB 7: Length 1117:

Best Local Similarity 75.2%; Pred. No. 3.4e-46;									
Matches 255; Conservative 0; Mismatches 84; Indels 0; Gaps 0;									
Qy	1	gctttgacaccaattactgtcttcgcgaacttggagagaaactgtgtgtgcgccctc	60						
Db	612	GCCTGGACACCACTACTGCTTTCAGCTCCACAGAAAGAACTGCTGTGTCTGTCGACTC	671						
Qy	61	tacattgacttcgcagcaggatctgggtggaagtgggtccatgaacctaaagggctactat	120						
Db	672	TACATTGACTTCGGGAAGGACCTGGGCTGGAAGTGGATTTCATGAACCAACCAAGGGGTACCAC	731						
Qy	121	gcaacttcgtctcagggcccttggccatactccgcagtcgcagtcagacacacccacagcag	180						
Db	732	GCCAAATTTCTGCTGGGGCCCTGCGCTTACATCTGGAGCCCTGGATACACAGTACAGCAAG	791						
Qy	181	gtctgagactgtacaacactctgaacctgaacctgaacatctgcctcgccttccttggtgccc	240						
Db	792	GTCTGGCCCTGTACAACACAGACACACCGGCGCTTCGGCGGCGCGCTGCTGGTGCCT	851						
Qy	241	cagcactggagcccttgacctctgacctctgactatgttggaggaccccaagtggagcag	300						
Db	852	CAGCGCTGGAGCCCTGCCATGCTGCTACTACGTGGCGCGCAAGCCCAAGGTGGAGCAG	911						
Qy	301	ctctcaacatggtggtgaagttcttgaatgtagtga	339						
Db	912	TTGTCCAACATGATGCTGCGCTCTCGAAGTGCAGCTCA	950						
RESULT 44									
OATGFB1									
LOCUS									
DEFINITION									
ACCESSION									
VERSION									
KEYWORDS									
SOURCE									
ORGANISM									
Ovis aries									
Ovis aries									
O. aries mRNA for transforming growth factor-beta 1.									
X76916									
X76916.1 GI:496648									
TGF-beta 1; transforming growth factor-beta 1.									
sheep.									
REFERENCE									
AUTHORS									
TITLE									
JOURNAL									
MEDLINE									
REFERENCE									
AUTHORS									
TITLE									
JOURNAL									
FEATURES									
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/translation="MPSPGLRLPLPLPLPLWLMLTPGRPVAGLSTCKTIDMELVKR									
GIPATKQILSKURLASPQSGDPPGLPEALILYNSTRVAGESATETPEPDA									
YKAEVTVLMVLYQYKNIYDKMSSHSIYFFNTSELREAVPEPVLISRADYRLIK									
KLKVEHVELYQYKNSRILNRLAPSDPEWLSTGTGVVROWLTHREIEGR									
LSACSDCSKDNLTQYDINGFSSGRGLDITIGHMNPFLMLMATPLERAQHLHSSRH									
RALDNYCFSTSEKCCVQRLVYIDFKDLGKWKIHEPKGYHANFCLGCPYIWSLDT									
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ORIGIN									

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Best Local Similarity 75.2%; Pred. No. 3.3e-46;
Matches 255; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

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QY 61 tacattgacttcgacagatctggctggagtggttccatgaacctaaagggtactat 120
DB 895 TACATTGACTTCCGGAAGACCTGGCTGGAGTGGATTCCAGAACCCCAAGGCTACAC 954

QY 121 gccaaactctgtcagggcccttgcccatatctcccgagtcgagacacacacacagcag 180
DB 955 GCCAATTTCTGCTGGGCGCTGTCCCTACATCTGGAGCCTGGACACACAGTACAGCAAG 1014

QY 181 gtctggagactgtacacacactgtgaacctgaagcatctgctccttctgtgtgccc 240
DB 1015 GTCTGGGCGCTGTACACACAGACACACCCGGCGCATCGCGCGCCGCTGCTGCTGCCT 1074

QY 241 caggacctggagccctgaccatctgtactatgttgaggagaccccccaaaagtggagcag 300
DB 1075 CAGGCGCTGGAAACCCCTGCCCATCTGTACTACGTGGGCGCCGACGCCAAGTGGAGCAG 1134

QY 301 ctctccaaatggtgtgaagtctgttaaatgtactga 339
DB 1135 TTGTCCAACATGATGTGCGTCTCTGCAAGTGCAGCTGA 1173

RESULT 45
DOGTGFB1A 1369 bp mRNA MAM 30-OCT-1994
LOCUS Canine transforming growth factor-beta 1 (TGFB1) mRNA, complete cds
DEFINITION L34956
VERSION L34956.1 GI:516071
KEYWORDS homologue; transforming growth factor-beta 1.
SOURCE Canis familiaris adult jugular vein endothelial CDNA to mRNA.
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE 1 (bases 1 to 1369)
AUTHORS Manning,A.M., Auchampach,J.A., Drong,R.F. and Slightom,J.L.
TITLE Cloning of a canine cDNA homologous to human transforming growth factor-beta 1 (TGFBeta1)
JOURNAL Unpublished (1994)
FEATURES
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            /tissue_type="jugular vein endothelial"
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            /gene="TGFB1"
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            /function="anti-inflammatory agent"
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            /protein_id="AAA51458.1"
            /db_xref="GI:516072"
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            RIFAIRGQILSKLRLSPSQGEVPPVPLPEAVLALYNSTRDVRVAGSAEPEPEAD
            YYAKEVTVLMQENTNIIYKVKSPHSIYMLFNTSELREAVPEVLLSRAELRLRL
            KLAQEVRLKYISNDWRYLNLRLAPDTPWLSFDVTGVVROWLSHGGEVEGER
            LSAHSCDSKNDLQVDINGFSSRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRQ
            RRALDTNYCFSSTEKNCQVRQLYIDFRKDLGKWKWIHEPKGYHANFCLGPGPIYWSLDT

mat_peptide
/gene="TGFB1"
/product="transforming growth factor-beta 1"
1231..1369
/gene="TGFB1"

BASE COUNT 264 a 473 c 415 g 216 t 1 others
ORIGIN

Query Match 60.4%; Score 204.6; DB 7; Length 1369;
Best Local Similarity 75.2%; Pred. No. 3.3e-46;
Matches 255; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

QY 1 gctttggacacaaattactgtctccgcaacttggaggagaaactgtgtgtgccccctc 60
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QY 61 tacattgacttcgacagatctggctggagtggttccatgaacctaaagggtactat 120
DB 952 TACATTGACTTCCGGAAGGATCTGGGCTGGAGTGGATCCATGAGCCCAAGGTTACAC 1011

QY 121 gccaaactctgtcagggcccttgcccatatctcccgagtcgagacacacacacagcag 180
DB 1012 GCTAATTCTGCTGGGCGCTGCCCTACATTTGGAGCCTGGACACGAGTACAGCAAG 1071

QY 181 gtctggagactgtacacacactgtgaacctgtgaagcatctgctccttctgtgtgccc 240
DB 1072 GTCTGGGCGCTGTACACACAGCACAACCCGGCGCGCTGCGCGCGCTGCTGCTGCGC 1131

QY 241 caggacctggagccctgaccatctgctgtactatgttgaggagaccccccaaaagtggagcag 300
DB 1132 CAGGCGCTGGAGCCACTGCCCATCTGTACTACGTGGGCGCCGACGCCAAGTGGAGCAG 1191

QY 301 ctctccaaatggtgtgaagtctgttaaatgtactga 339
DB 1192 CTGTGCAACATGATGTGCGTCTCTGCAAGTGCAGCTGA 1230

RESULT 46
I08268
LOCUS I08268 1560 bp PAT 02-DEC-1994
DEFINITION Sequence 2 from Patent EP 0373994.
ACCESSION I08268
VERSION I08268.1 GI:589017
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1560)
AUTHORS Purchio,A.F., Gentry,L., Twardzik,D. and Brunner,A.M.
TITLE Cloning and expression of simian transforming growth factor-beta 1
JOURNAL Patent: EP 0373994-A1 20-JUN-1990;
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ORIGIN

Query Match 60.4%; Score 204.6; DB 10; Length 1560;
Best Local Similarity 75.2%; Pred. No. 3.2e-46;
Matches 255; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

QY 1 gctttggacacaaattactgtctccgcaacttggaggagaaactgtgtgtgccccctc 60
DB 1095 GCCCTGGACACCAACTACTGCTTCAAGCTCCACAGAGAAGAACTGCTGCTGCGCGCAGCTG 1154

QY 61 tacattgacttcgacagatctggctggagtggttccatgaacctaaagggtactat 120
DB 1155 TATATTGACTTCCGGAAGACCTTCGCTGGAAGTGGATCCAGAGCCCAAGGCTACCAT 1214

QY 121 gccaaactctgtcagggcccttgcccatatctcccgagtcgagacacacacacagcag 180
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Db 1215 GCCAACTTCTGCTGGGGCCCTGTCCCTACATTGGAGCCTGGACACGACGATACAGCAAG 1274
QY 181 gtgttgagactgtacaacactgtgaacctgaagcatctgctcgccctgtgctgctgccc 240
Db 1275 GTCTGCGCCCTGTACACACGACATACCCGGCGCCCTCGGGCGCCGTGCTGCGTGCCG 1334
QY 241 caggacctggagccctgaccatctgtactatgttgaggagaccccccaagtgagcag 300
Db 1335 CAGCGCTGGAGCCACTGCCCATCGTGTACTAGCTGGCGCGCAAGCCCAAGGTGGACGAG 1394
QY 301 ctctccaacatggtggtgaagtctttaaattagctga 339
Db 1395 CTGTCCAACATGATCGTGCCTCTCTGAAATGCAAGTGA 1433

RESULT 47
AGMTGFB
LOCUS AGMTGFB 1561 bp mRNA PRI 27-APR-1993
DEFINITION Simian transforming growth factor-beta (TGF) mRNA, complete cds.
ACCESSION M16658
VERSION M16658.1 GI:176552
KEYWORDS growth factor; transforming growth factor-beta.
SOURCE African green monkey cells (cell line BSC-40), cDNA to mRNA, clone pTGF-beta-2.
ORGANISM Cercopithecus aethiops
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
Cercopithecinae; Cercopithecus.
REFERENCE
AUTHORS Sharples,K., Plovman,G.D., Rose,T.M., Twardzik,D.R. and
Purchio,A.F.
TITLE Cloning and sequence analysis of simian transforming growth
factor-beta cDNA
JOURNAL DNA 6, 239-244 (1987)
MEDLINE 87246074
FEATURES
source Location/Qualifiers
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262..1095
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262..1434
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CDS
262..1434
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YIAKEVTRVLVETHNEIYDKFKQSTHSIYFNTSELREAVPVLGRALRLRL
KLKVEQHVLYQKSNWSRYLSNRLIAPSNPEWLSFDVTGVYRWLRGGEIEGR
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RRALDPTNCFSSKTCCKVQRLYIDFKDLGWKWIHEPKYHANFCIGPCPYIWSLDT
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Best Local Similarity 75.2%; Pred. No. 3.2e-46;
Matches 255; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

QY 1 gctttgacacaaactactgtctccgaacttgagagagaaactgtgtgcccctc 60
Db 1096 GCCCTGGACACCACTACTGCTTACGCTCCAGGAGAGAACTGCTGCTGGCGCAGCTG 1155
QY 61 tacattgactccgacaggaatctgggctggaagtgggtccatgaacacaaagggctactat 120
Db 1156 TATATTGACTCCGCAAGGACCTCGGCTGGAAGTGGATCCAGGACCCCAAGGGCTACCAT 1215
QY 121 gccaaacttctgctcaggcccttgccctactctcactcctcgagctgcagacacacacagcag 180

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Db 1216 GCCAACTTCTGCTGGGGCCCTGTCCCTACATTGGAGCCTGGACACGACGATACAGCAAG 1275
QY 181 gtgttgagactgtacaacactgtgaacctgaagcatctgctcgccctgtgctgctgccc 240
Db 1275 GTCTGCGCCCTGTACACACGACATACCCGGCGCCCTCGGGCGCCGTGCTGCGTGCCG 1335
QY 241 caggacctggagccctgaccatctgtactatgttgaggagaccccccaagtgagcag 300
Db 1335 CAGCGCTGGAGCCACTGCCCATCGTGTACTAGCTGGCGCGCAAGCCCAAGGTGGACGAG 1395
QY 301 ctctccaacatggtggtgaagtctttaaattagctga 339
Db 1395 CTGTCCAACATGATCGTGCCTCTCTGAAATGCAAGTGA 1434

RESULT 48
BC000125
LOCUS BC000125 1780 bp mRNA PRI 16-MAR-2001
DEFINITION Homo sapiens, similar to transforming growth factor, beta 1, clone MGC:3119, mRNA, complete cds.
ACCESSION BC000125
VERSION BC000125.1 GI:12652748
KEYWORDS MGC.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Strausberg,R.
TITLE Direct Submission
JOURNAL Submitted (03-NOV-2000) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Rubin Laboratory
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
Info@bcsc.bc.ca
Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,
Leticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo
Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven
Ness, Pawan Pandoh, Anna-Liisa Prabh, Parvaneh Saeedi, Jacqueline
Schein, Duane Smalius, Michael Smith, Lorraine Spence, Jeff Stott,
Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,
George Yang, Scott Zuyderduyn, Marco Marra.
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LNL at: http://image.llnl.gov
Series: IRAL Plate: 6 Row: e Column: 11.
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447..1619
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LSAHCSDSDNTLQVDINGTTGRGLDIAIHGMNRPFLLLMATPLERAOHLQSSRH
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BASE COUNT 341 a 648 c 493 g 298 t
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BASE COUNT 341 a 648 c 493 g 298 t
ORIGIN

Query Match 60.4%; Score 204.6; DB 91; Length 1780;
Best Local Similarity 75.2%; Pred. No. 3.2e-46;
Matches 255; Conservative 0; Mismatches 84; Indels 0; Gaps 0;
Qy 1 gctttggacacaaattactgttcgcgaacttggaggagaactgtgtgtgcgccccctc 60
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Qy 61 tacattgacttcgcagacatctgggctggaagtggctgaactgaacctgaagggctactat 120
Db 1341 TACATTGACTTCGCGAAGGACCTCGGCTGGAAGTGGATCCACGAGCCCAAGGCTACCAT 1400

Qy 121 gcaacttctgtcagggcccttgcccatcctccgcagtcgagacacacacacagcacg 180
Db 1401 GCCAACTTCTGCTCGGGCCCTGCCCTACATTGGAGCTGGACACGCGAGTACAGCAAG 1460

Qy 181 gtgctggagactgtacaaactctgaacctctgaagcactgtcctgcctgtcgtgcgcc 240
Db 1461 GTCTCTGGCCCTGTACAAACGAGCATAAACCGGGCGCTCGGGCGGCGCTGCTGCTGCGCG 1520

Qy 241 caggaaccttgagcccttgaccatcctgtactatgtttggaggagcccccaagtggagcag 300
Db 1521 CAGGCGCTGGAGCCGCTGCCCATCGTGTACTACGTGGCGCGCAAGCCCAAGGTGGAGCAG 1580

Qy 301 ctctcacaactgtgtggaagtcttgaatgtagctga 339
Db 1581 CTGTCCACATGATCGTGGCTCCTGCAAGTGCAGCTGA 1619

Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,
George Yang, Scott Zuyderduyn, Marco Marra.
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAL plate: 6 Row: e Column: 10.
Location/Qualifiers

FEATURES source
1..1780
/organism="Homo sapiens"
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/clone="MGC:2323 IMAGE:3356605"
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/lab_host="DH10B-R"
/note="Vector: pOTB7"
447..1619
/codon_start=1
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/protein_id="AAH01180.1"
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BASE COUNT 341 a 648 c 493 g 298 t
ORIGIN

Query Match 60.4%; Score 204.6; DB 91; Length 1780;
Best Local Similarity 75.2%; Pred. No. 3.2e-46;
Matches 255; Conservative 0; Mismatches 84; Indels 0; Gaps 0;
Qy 1 gctttggacacaaattactgttcgcgaacttggaggagaactgtgtgtgcgccccctc 60
Db 1281 GCCCTGGACACCAACTATTGCTTCAGCTCCACGGAGAAGAACTGCTGCGGCGAGCTG 1340

Qy 61 tacattgacttcgcagacatctgggctggaagtggctgaactgaacctgaagggctactat 120
Db 1341 TACATTGACTTCGCGAAGGACCTCGGCTGGAAGTGGATCCACGAGCCCAAGGCTACCAT 1400

Qy 121 gcaacttctgtcagggcccttgcccatcctccgcagtcgagacacacacacagcacg 180
Db 1401 GCCAACTTCTGCTCGGGCCCTGCCCTACATTGGAGCTGGACACGCGAGTACAGCAAG 1460

Qy 181 gtgctggagactgtacaaactctgaacctctgaagcactgtcctgcctgtcgtgcgcc 240
Db 1461 GTCTCTGGCCCTGTACAAACGAGCATAAACCGGGCGCTCGGGCGGCGCTGCTGCTGCGCG 1520

Qy 241 caggaaccttgagcccttgaccatcctgtactatgtttggaggagcccccaagtggagcag 300
Db 1521 CAGGCGCTGGAGCCGCTGCCCATCGTGTACTACGTGGCGCGCAAGCCCAAGGTGGAGCAG 1580

Qy 301 ctctcacaactgtgtggaagtcttgaatgtagctga 339
Db 1581 CTGTCCACATGATCGTGGCTCCTGCAAGTGCAGCTGA 1619

RESULT 50
LOCUS E03028 1821 bp RNA PAT 29-SEP-1997
DEFINITION DNA encoding human prepro TGF-beta1.
ACCESSION E03028
VERSION E03028.1 GI:2171250
KEYWORDS JP 19911180192-A/1.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1821)
AUTHORS Ohashi,H., Ishii,Y., Miyata,Y., Miyazono,K., Miyagawa,K. and

YKAEVTRVLMVEKENELIKYIVETGSHSIYMFNASELRAAVDPDMLLSRAELRLRL
LSVQEVHLYQKYSNSWRYLSNRLITPDSPEWLSFDVTGVVYRQMLSQGMEGLR
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BASE COUNT 230 a 395 c 361 g 201 t
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Query Match 59.4%; Score 201.4; DB 7; Length 1187;
Best Local Similarity 74.6%; Pred. No. 2.6e-45;
Matches 253; Conservative 0; Mismatches 86; Indels 0; Gaps 0;
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Qy 61 tacattgaacttcgacaggaactgtggctgggaagtgggtccatgaacctaaaggctactat 120
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Qy 121 gccaaactctgctcagggcccttgccataacctccgcagtcgagacacacacacagcagc 180
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Qy 241 cagacactgagccctgacacactctgtactatgtatgtggagagacccccaaagtggagcag 300
Db 1089 CAGGTGTGGAGCGCTGCCCTCGTACTACGTGTGCTGGTGGCAAGCCCAAGTGGAGCAG 1148
Qy 301 ctctcccaacatggtggaagtctgttaaatgtagctga 339
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RESULT 61
AF153013 2796 bp mRNA ROD 24-JUL-2000
LOCUS Rattus norvegicus TGF-beta 2 short form precursor (TGF-beta2) mRNA,
DEFINITION complete cds.
ACCESSION AF153013
VERSION AF153013.1 GI:4929797
KEYWORDS Norway rat.
SOURCE Rattus norvegicus
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 2796)
AUTHORS Koishi,K., Dalzell,K.G. and McLennan,I.S.
TITLE The expression and structure of TGF-beta2 transcripts in rat
muscles
JOURNAL Biochim. Biophys. Acta 1492 (2-3), 311-319 (2000)
MEDLINE 20461836
REFERENCE 2 (bases 1 to 2796)
AUTHORS Koishi,K., Dalzell,K.G.B. and McLennan,I.S.
TITLE Direct Submission
JOURNAL Submitted (18-MAY-1999) Anatomy & Structural Biology, University of
Otago, Dunedin PO Box 913, New Zealand

FEATURES
Source 1..2796
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CDS

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GFKTLLHLLPSYRLESQSSRRRRKALDAAYCFRNVQDNCLRLPYIDFKRDLGKWK
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2077..2082
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Best Local Similarity 74.6%; Pred. No. 2.3e-45;
Matches 253; Conservative 0; Mismatches 86; Indels 0; Gaps 0;
Qy 1 gctttggacacaaattactgttcgcgaacttgaggagaaactgtgtgccccctc 60
Db 1214 GCTTTGGATGCGCCCTATTGCTTTAGGAATGTGCAGGATAATTGCTGCCCTCGCCCTCTT 1273
Qy 61 tacattgaacttcgacaggaactgtggctgggaagtgggtccatgaacctaaaggctactat 120
Db 1274 TACATTGATTTTAAGAGGGATCTTGGATGGAATGATCCATGAACCCAAAGGATACAAT 1333
Qy 121 gccaaactctgctcagggcccttgccataacctccgcagtcgagacacacacacagcagc 180
Db 1334 GCTAACTTCTGCTGGGCGCATGCCCTTATCTGTGGAGTTCAGACACACACACACAAA 1393
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Qy 301 ctctcccaacatggtggaagtctgttaaatgtagctga 339
Db 1514 CTTTCCAACATGATCGTCAAGTCTTGTAAATGCAGCTAA 1552

RESULT 62
AF153012 2880 bp mRNA ROD 24-JUL-2000
LOCUS Rattus norvegicus TGF-beta 2 long form precursor (TGF-beta2) mRNA,
DEFINITION complete cds.
ACCESSION AF153012
VERSION AF153012.2 GI:4980482
KEYWORDS Norway rat.
SOURCE Rattus norvegicus
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 2880)
AUTHORS Koishi,K., Dalzell,K.G. and McLennan,I.S.
TITLE The expression and structure of TGF-beta2 transcripts in rat
muscles
JOURNAL Biochim. Biophys. Acta 1492 (2-3), 311-319 (2000)
MEDLINE 20461836
REFERENCE 2 (bases 1 to 2880)

AUTHORS Koishi,K., Dalzell,K.G.B. and McLennan,I.S.
 TITLE Direct Submission
 JOURNAL Submitted (18-MAY-1999) Anatomy & Structural Biology, University of
 Otago, Dunedin PO Box 913, New Zealand
 COMMENT On Jun 3, 1999 this sequence version replaced gi:4929795.
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polyA_signal

BASE COUNT 824 a 684 c 604 g 768 t
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Query Match 59.4%; Score 201.4; DB 94; Length 2880;
 Best Local Similarity 74.6%; Pred. No. 2.3e-45;
 Matches 253; Conservative 0; Mismatches 86; Indels 0; Gaps 0;

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RESULT 63
 AF135598
 LOCUS AF135598 1255 bp mRNA ROD 11-APR-1999

DEFINITION Rattus norvegicus transforming growth factor beta 2 precursor,
 mRNA, complete cds.
 ACCESSION AF135598
 VERSION AF135598.1 GI:4580714
 KEYWORDS
 SOURCE Norway rat.
 ORGANISM
 Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.
 REFERENCE 1 (bases 1 to 1255)
 AUTHORS Plisov,S.Y., Ivanov,S.V., Plisova,T.M., Lerman,M. and
 Perantoni,A.O.
 TITLE Rat transforming growth factor-beta2, complete coding sequence
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 1255)
 AUTHORS Plisov,S.Y., Ivanov,S.V., Plisova,T.M., Lerman,M. and
 Perantoni,A.O.
 TITLE Direct Submission
 JOURNAL Submitted (18-MAR-1999) Laboratory of Comparative Carcinogenesis,
 National Cancer Institute, FCRDC, Bldg.538, Room 206, Frederick, MD
 21702, USA
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 BASE COUNT 334 a 353 c 299 g 269 t
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QY 1 gctttgacaccaatactgcttcgcaacttggaggagaactgctgtgtgccccctc 60
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 Db 908 GCTTTGGATGCCGCTATTGCTTTAGGAATGTGCAGATAATTGCTGCTCGCCCTCTT 967
 QY 61 tacattgactccgacagatctggctggaagtgggtccatgaacctaaaggctactat 120
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 Db 968 TACATTGATTTTAAGAGGATCTTGATGGAATGGATGCATGAACCCAAAGGATACAAT 1027
 QY 121 gcaactctgctcaggcccttggccataacctccgcagtcgagacacacacacagcacg 180
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 Db 1028 GCTAACTTCTGTGTGGGCATGCCCTTATCTGTGAGTTTCAGACACACACACACAAA 1087
 QY 181 gtgctgggactgtacaacactctgaacctgaagcatctgcctcgctgtgctgcccc 240
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 Db 1088 GTCTCAGCCTGTACAACACCATAAACCCGGAAGCTTCTGCTTCCCTTGTGTGTGTC 1147
 QY 241 caggacctggagccctcgacctctgtactatgttggaggagacccccaaagtggagcag 300
 ||||| || ||||| || ||||| || ||||| || ||||| || ||||| ||
 Db 1148 CAGGATCTGGACCACTGACCATCTCTACTTACATTGGCAATACGCCCAAGATCGAACAA 1207
 QY 301 ctctccacatggtggtggaagtctttaaattagctga 339
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 Db 1208 CTTTCCACATGATCGTCAAGTCTTGTAAATGCAGCTAA 1246

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RESULT 64
RN0132718      1274 bp      mRNA      ROD      21-OCT-2000
LOCUS          Rattus norvegicus mRNA for TGF-beta2 protein.
DEFINITION     AJ132718
ACCESSION      AJ132718
VERSION        AJ132718.1 GI:4753895
KEYWORDS       tgfbeta2 gene; TGF-beta2 protein.
SOURCE         Norway rat.
ORGANISM       Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE      1 (bases 1 to 1274)
AUTHORS        Konrad, L., Albrecht, M., Renneberg, H. and Amuller, G.
TITLE          Transforming growth factor-beta2 mediates mesenchymal-epithelial
               interactions of testicular somatic cells
JOURNAL        Endocrinology 141 (10), 3679-3686 (2000)
MEDLINE        20466150
REFERENCE      2 (bases 1 to 1274)
AUTHORS        Konrad, L.
TITLE          Direct Submission
JOURNAL        Submitted (02-FEB-1999) Konrad L., Anatomy and Cell Biology,
               University, Robert-Koch-Str. 6, 35033 Marburg, GERMANY
               Location/Qualifiers
FEATURES       1..1274
               /organism="Rattus norvegicus"
               /strain="Wistar"
               /db_xref="taxon:10116"
               /sex="male"
               /dev_stage="19-days-old"
               /cell_type="peritubular myoid primary cells"
gene           16..1260
               /gene="tgfbeta2"
CDS            16..1260
               /gene="tgfbeta2"
               /codon_start=1
               /product="TGF-beta2 protein"
               /protein_id="CAB42003.1"
               /db_xref="GI:4753896"
               /db_xref="SPTREMBL:Q9R2B8"
               /translation="MHYCVLRTEFLHLVVALSLSCSTLMDQFMKRIEATRGQI
               LSKLITSPEDPEPEVPEVSIYNSTRDLLOEKASRRACERERDEEYCAKE
               VYKIDMSPHSPENAPPTFYRFRVFRDVTMEKNALNVAEYFVRLQNPKE
               VAGQRELYQLKSLDPTQRIIDSKVVKVRAEGWLSFDVTDVHVELHKKRNL
               GFKISHCPCTTIPNNYIIPNKQSELEAFIDGTSTYASGDQRTIKSTRKSSG
               KTHLLMLLSYRLSQSSRRKRALDAAYCFRNVOHNCRLRLPYIDFKRLGKW
               IHEPKGVANFCAGACPYLWSSDTQHTKVLSTNTINPEASAPCCVSDLEPLILY
               YIGNTPKIEQLSNVVKSKCS"
               YIGNTPKIEQLSNVVKSKCS"
BASE COUNT    339 a 354 c 303 g 278 t
ORIGIN

Query Match      58.9%; Score 199.8; DB 95; Length 1274;
Best Local Similarity 74.3%; Pred. No. 7e-45;
Matches 252; Conservative 0; Mismatches 87; Indels 0; Gaps 0;

Qy 1 gctttgacaccaattactgcttcgcaacttgaggagaactgctgtgctgcgccctc 60
Db 922 GCTTTGGATGCCGCTATTGCTTAGGAATGTGCAGCATATTGCTGCTTCGCCCTCTT 981

Qy 61 taacattgacttcgacaggaatctggctgggaagtgggtcccatgaacctaaagggtactat 120
Db 982 TACATTGATTTAAGAGGGATCTTGGATGGAATGGATCCATGATCAACCAAGGGGTACAAT 1041

Qy 121 gcaactctgctcaggcccttgccatactccgactcgagtcagacacacccacagcag 180
Db 1042 GCTAACCTCTGCTGCTGGGGATGCCCTTATCTGTGGAGTTCAGACACACACACACAAA 1101

Qy 181 gtgctggagactgtacaaactctgaacctgaagcatctgcctgccttactgctgctccc 240
Db 1102 GTCTAGCTGTACACACACATAAACCCGAGACTTCTGCTCCCCCTGCTGTGTGCTCC 1161

Qy 241 caggacctggagccccctgaaccatctgtactatgttggaggagcccccaagtggagcag 300
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Db 1162 CAGGATCTGGAACCACTGACCATCTCTACTATTGGTAATACGCCCAAGATCGAACAA 1221
Qy 301 ctctccaaatggtggtgaagtctttaaagttagctga 339
Db 1222 CTTTCCAACATGATGTCAGTCAAGTCTTGTAAATGCAGCTAA 1260

RESULT 65
I08275      1561 bp      PAT      02-DEC-1994
LOCUS          I08275
DEFINITION     Sequence 3 from Patent EP 0374044.
ACCESSION      I08275
VERSION        I08275.1 GI:589015
KEYWORDS       Unknown.
SOURCE         Unknown.
ORGANISM       Unclassified.
REFERENCE      1 (bases 1 to 1561)
AUTHORS        Purchio, A.F. and Madisen, L.
TITLE          TGF-beta 1 / beta 2 : a novel chimeric transforming growth
               factor-beta
JOURNAL        Patent: EP 0374044-A2 3 20-JUN-1990;
               Location/Qualifiers
FEATURES       1..1561
               /organism="unknown"
BASE COUNT    304 a 544 c 442 g 271 t
ORIGIN

Query Match      57.5%; Score 195; DB 10; Length 1561;
Best Local Similarity 73.5%; Pred. No. 1.5e-43;
Matches 249; Conservative 0; Mismatches 90; Indels 0; Gaps 0;

Qy 1 gctttggacaccaattactgcttcgcaacttgaggagaactgctgtgctgcgccctc 60
Db 1096 GCCCTGGACCACTACTGCTTCAGAAATGTGCAGGATAATGCTGCTTACGTCGCTT 1155

Qy 61 tacattgacttcgacaggaatctggctgggaagtgggtccatgaacctaaagggtactat 120
Db 1156 TACATTGACTCAAGAGGACCTCGCTGGAAGTGGATCCACAGGCCCAAGGGCTACCAT 1215

Qy 121 gcaactctgtctcaggcccttgccatactccctcgcagtcgacacacacccacagcag 180
Db 1216 GCCAACTTCTGCTGGGGCCCTGTCCCTACATTGGAGCTGGACACGCGTAGACGCAAG 1275

Qy 181 gtgctggagactgtacaaactctgaacctgaagcatctgcctgccttactgctgctccc 240
Db 1276 GTCTGGGCCCTGTCAACACAGCATAAACCGGGCGCTCGGGCGCGCTGCTGCTGCCG 1335

Qy 241 caggacctggagccccctgaaccatctgtactatgttggaggagcccccaagtggagcag 300
Db 1336 CAGGGCTGGAGCCACTGCCCATGCTGTACTACGTGGGGCGGCAAGCCCAAGGTGGAGCAG 1395

Qy 301 ctctccaaatggtggtgaagtctttaaagttagctga 339
Db 1396 CTGTCCAACATGATGTCGCGCTCCGTCAGTCAAAATGCAGCTGA 1434

RESULT 66
MNTGFB2      4267 bp      mRNA      ROD      14-JUN-1991
LOCUS          MNTGFB2
DEFINITION     Mouse mRNA for transforming growth factor-beta2.
ACCESSION      X57413
VERSION        X57413.1 GI:54772
KEYWORDS       cell proliferation; transforming growth factor-beta2.
SOURCE         Mus musculus.
ORGANISM       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE      1 (bases 1 to 4267)
AUTHORS        Miller, D.A., Lee, A., Pelton, R.W., Chen, E.Y., Moses, H.L. and
               Derynck, R.
```

TITLE Murine transforming growth factor-beta 2 cDNA sequence and expression in adult tissues and embryos
JOURNAL Mol. Endocrinol. 3 (7), 1108-1114 (1989)
MEDLINE 90014832
FEATURES Location/Qualifiers
source 1..4267
/organism="Mus musculus"
/db_xref="taxon:10090"
/dev_stage="embryonic"
/cell_type="carcinoma"
/cell_lines="PCC3"
gene 1218..2462
/gene="TGF-beta2"
CDS 1218..2462
/gene="TGF-beta2"
/codon_start=1
/product="transforming growth factor-beta2 precursor"
/protein_id="CAA40672.1"
/db_xref="GI:54773"
/translation="MHYCVLSFLLHLVVALSLSTCTLDMDQFMKRIEIRGOI LSKLITSPEDYPPPEVPIVSIINSTROLLOEKASRRRAACERSEOEYFAKE VKIDMPSLSENAIPTEFYRIVRFVSTMEKNASNLVKAERFRLQNPKEAR VAEQRIEYLKSKDLSPQRYIDSKVVKTRAEGLWISFDVDAVQEWLHKDKNL GFKISLHPCCTFVPSNNKIIIPNKSEELERAGIDGTSYASGDKQYIDKPRKTSI KTHPLLMLPSYLESOSSRRKRALDAVCFRNVODNCLRLYIDFKRDLGKWK HEPKGYANPCAGNCPYLWSSDQHTKVLSLYNTINPEASAPCCVSDLEPLILY XIGNPKIEQLSNMIVRSKCS"
mat_peptide 2124..2459
/gene="TGF-beta2"
/product="transforming growth factor-beta2"
polysite 4260
BASE COUNT 1139 a 1036 c 989 g 1103 t
ORIGIN
Query Match 57.1%; Score 193.4; DB 94; Length 4267;
Best Local Similarity 73.2%; Pred. No. 3.5e-43;
Matches 248; Conservative 0; Mismatches 91; Indels 0; Gaps 0;
QY 1 gctttggacacaaattactgtctccgcaacttggaggagaactgctgtgtgccccctc 60
Db 2124 GCCTTGGATGCTGCTACTGCTTTAGAAATGTGCAGGATAATTGCTGCTGCTGCTCTT 2183
QY 61 tacattgacttcgacagatctggctggaagtgggttcacataagggctactat 120
Db 2184 TACATTGATTTTAAAGAGGATCTGGATGGAATGGATCCATGAACCCAAAGGATACAAT 2243
QY 121 gcaactctgtcagcccttgccataacctcccgagtcagacacacacacagcag 180
Db 2244 GCTAACTTCTGTGCTGGGCGATGCCCATATCTATGAGTTTCAGACACTCAACACACAAA 2303
QY 181 gtgctgggactgtacacactctgaacctgaagcatctgctcgcttgcctgtgctgccc 240
Db 2304 GTCTCAGCTGTACACACACATAATCCGAGCTTCGCTTCCCTTGCCTGTGTGTC 2363
QY 241 caggacctggagcccttgaccactctgtactatgttggaggaccacccaaagtggagcag 300
Db 2364 CAGGATCTGGACCACTGACCATCTCTATTACATTGGAATACGCCCAAGATCGAAGCAG 2423
QY 301 ctctcaacatggtggaagtctgtaaatgtagctga 339
Db 2424 CTTTCCAATATGATGTCGAAGTCTTGTAAATGCAGCTAA 2462
RESULT 67
RNTGFB1 RNTGFB1 1585 bp mRNA ROD 23-MAR-1995
LOCUS Rat mRNA for transforming growth factor-beta 1.
DEFINITION X52498
ACCESSION X52498.1 GI:57341
VERSION growth factor; TGF-beta 1; transforming growth factor-beta 1.
KEYWORDS Norway rat.

ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE 1 (bases 1 to 1585)
AUTHORS Su Wen, Q.
TITLE Direct Submission
JOURNAL Submitted (01-MAR-1990) Su Wen Q., National Cancer Institute NIH, Bldg 41 Room C629, Laboratory of Chemoprevention, NCI Bethesda MD 20892, U S A
REFERENCE 2 (bases 1 to 1585)
AUTHORS Qian, S.W., Kondaliah, P., Roberts, A.B. and Sporn, M.B.
TITLE cDNA cloning by PCR of rat transforming growth factor beta-1
JOURNAL Nucleic Acids Res. 18 (10), 3059 (1990)
MEDLINE 90272425
FEATURES Location/Qualifiers
source 1..1585
/organism="Rattus norvegicus"
/strain="Sprague Dawley"
/db_xref="taxon:10116"
/dev_stage="adult"
/tissue_type="heart"
sig_peptide 413..481
/product="signal peptide (AA -23 to -1)"
CDS 413..1585
/note="prepro-TGF-beta 1 (AA -23 to 367)"
/codon_start=1
/protein_id="CAA36741.1"
/db_xref="GI:57342"
/translation="MPPSGRLRLPLPLPWLVLTPGRPAAGLSTCKTIDMELVRRK RIEAIRGOILSKLRASPPSGVEPPGLPEAVLALYNSDRVAGSADPEPEPEAD YYAKEVTRVLMDRNNAIYDKDTHSIYMFNTSDIREAVPEPPLLSRAELRLQRF KSTVEOVELYQYISNNRWYLGNNRLTPTDPELWISFDVTVVVRQWLNOGDGQGER FSAHCSKSDKNVLHVEINGISPKRRDLGTIDMNRPLLLMLAERQHLHLSRH RRALDTNYCFSSSTEKNCCVRLYIDFKDLGKWIHEPKGYHANFCLGPGCPYIWSLDT QYSKVALYNOHNPAGASAPCCVPQALEPLIVYVYGRKPKVEQLSNMIVRSKCS"
misc_feature 482..1582
/note="pro-TGF-beta 1 (AA 1 to 367)"
mat_peptide 1247..1582
/product="mature TGF-beta 1 (AA 255 to 367)"
BASE COUNT 337 a 538 c 403 g 307 t
ORIGIN
Query Match 56.6%; Score 191.8; DB 95; Length 1585;
Best Local Similarity 72.9%; Pred. No. 1.1e-42;
Matches 247; Conservative 0; Mismatches 92; Indels 0; Gaps 0;
QY 1 gctttggacacaaattactgtctccgcaacttggaggagaactgctgtgtgccccctc 60
Db 1247 GCCTTGGATACCAACTACTGCTTTCAGCTCCACAGAGAAGAACTGCTGTGTACGCAGCTG 1306
QY 61 tacattgacttcgacagatctggctggaagtgggtccatgaacctaaaggtactat 120
Db 1307 TACATTGACTTTAGGAAGGACCTGGGTGGAAGTGGATCCACGAGCCCAAGGCTACCAT 1366
QY 121 gcaactctgtcagcccttgccataacctcccgagtcagacacacacacacagcag 180
Db 1367 GCCAACTCTGTCTGGGGCCCTGCCCTTACATTGAGCCCTGGACACACACAGTACAGCAAG 1426
QY 181 gtgctgggactgtacacactctgaacctgaagcatctgctcgcttgcctgtgctgccc 240
Db 1427 GTCTTTCCTCTACAAACCAACACACCCGGGTGCTTCCGCATCCCGTGTGTGCTGCCG 1486
QY 241 caggacctggagcccttgaccactctgtactatgttggaggaccccccaaggtgagcag 300
Db 1487 CAGCTTTGGAGGCACCTGCCCATCTGCTACTACGTGGTTCGCAAGCCCAAGTGGAGCAG 1546
QY 301 ctctcccaacatggtggtggaagtcttgaatgttagctga 339
Db 1547 TTGTCCAAACATGATCGTGGCGCTCTCTGCAAGTGCAGCTGA 1585

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RESULT 68
MUSTGFRNA 1579 bp mRNA 27-APR-1993
LOCUS transforming growth factor beta mRNA (TGF-beta), complete
DEFINITION cds.
ACCESSION M13177
VERSION M13177.1 GI:201952
KEYWORDS growth factor.
SOURCE Mouse monocytic cell, cDNA to mRNA.
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1579)
Derynck, R., Jarrett, J.A., Chen, E.Y. and Goeddel, D.V.
TITLE The murine transforming growth factor-beta precursor
JOURNAL J. Biol. Chem. 261, 4377-4379 (1986)
MEDLINE 86168129
FEATURES
Location/Qualifiers
Source 1..1579
/organism="Mus musculus"
/db_xref="taxon:10090"
1..1579
/note="TGF-beta mRNA"
353..1525
/note="TGF-beta precursor"
/codon_start=1
/protein_id="AAA40423.1"
/db_xref="GI:201953"
/translation="MPPSGRLRLPLLPWLLVLTGPRPAAGLSTCKTIDMELVKRK
RIRAEKQILSKLRASPPSQGVEPPGPELVAVLYNSTRDRVAGESADPEPEAD
YYAKEVTVLMVDNRNNAIYEKTKDISHIYMFNTSDIREAVPEPILLSRAELRLQRL
KSSVEQVELYQKYSNNRWYLGNNRLTPTDPEWLSFDVTGVVROWLNGDDGIQGRF
FSACSDSKDNKLHVEINGISPKRRDGLGTIDHMRPFLLLMATPLERAOHLHSSRH
RRALDYNVCFSSTEKNCVRLYIDFRKDLGKWIHEPKGYHANFCLGPCPYIWSLDT
QYSKVLALYNQHNPGASASPCCPVQALEPLPIVYVGRKPKVEQLSNMIVRSCKS"
BASE COUNT 330 a 540 c 410 g 299 t
ORIGIN

Query Match 56.1%; Score 190.2; DB 94; Length 1579;
Best Local Similarity 72.6%; Pred. No. 3.1e-42;
Matches 246; Conservative 0; Mismatches 93; Indels 0; Gaps 0;

Qy 1 gctttggacacaaattactgtctccgcaactggaggagaactgctgtgtgcgccccctc 60
Db 1187 GCCCTGGATACCAACTATTGCTTCAGCTCCACAGAGAGAAGTGTGTGTGCGGCGAGTG 1246

Qy 61 tacattgactccgacaggatctgggctggaagtgggtccatgaacctgctgcctgtgctgctc 120
Db 1247 TACATTGACTTTAGGAGGACCTGGGTGGAAGTGATGATCCACGAGCCCAAGGGCTACCAT 1306

Qy 121 gccaaacttgctcaggcccttgccataacctccgcaagtgcagacacaaacccacagcag 180
Db 1307 GCCAACTTCTGCTGGGACCTGCCCTTATATTGGAGCCCTGGACACACAGTACAGCAAG 1366

Qy 181 gtgctgggaactgtacaacactctgaacctgaagcatctgctgcctgtgctgctgctgccc 240
Db 1367 GTCCCTGCCCTCTACACCAACACACACCCGGCGCTTCGGGCTCACCGTGTGCTGCGCG 1426

Qy 241 caggacctggagcccttgaccatctgtactatgttgaggagaccccccaagtgagcag 300
Db 1427 CAGGCTTTGGAGCCACTGCCCATGCTTACTACGTGGGTGCGAAGCCCAAGGTGGAGCAG 1486

Qy 301 ctctccaaatggtgggaagtcttgtaaatgtagctga 339
Db 1487 TTGTCCAAACATGATGTGCGCTCCTGCAAGTGCAGCTGA 1525

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RESULT 69
MMU009862 2094 bp mRNA 01-OCT-1998
LOCUS Mus musculus mRNA for transforming growth factor-beta 1.
DEFINITION

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ACCESSION AJ009862
VERSION AJ009862.1 GI:3688423
KEYWORDS TGF beta 1 gene; transforming growth factor-beta 1.
SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 2094)
Poirrot, L.
TITLE Direct Submission
JOURNAL Submitted (07-AUG-1998) Poirrot L., Department of Immunology,
I.G.B.M.C., BP 163, 67404 Illkirch, FRANCE
2 (bases 1 to 2094)
Poirrot, L., Benoist, C. and Mathis, D.
REFERENCE Transforming growth factor-beta 1 sequence and expression: no
AUTHORS difference between NOD/Lt and C57Bl/6 mouse strains
TITLE
JOURNAL Unpublished
FEATURES
Location/Qualifiers
Source 1..2094
/organism="Mus musculus"
/strain="NOD/Lt"
/strain="C57Bl/6"
/db_xref="taxon:10090"
/tissue_type="spleen"
868..2040
/feature="TGF beta 1"
868..2040
/feature="TGF beta 1"
/codon_start=1
/product="transforming growth factor-beta 1"
/protein_id="CAA08900.1"
/db_xref="GI:3688424"
/translation="MPPSGRLRLPLLPWLLVLTGPRPAAGLSTCKTIDMELVKRK
RTEARGTGILSKLRASPPSQGVEPPGPELVAVLYNSTRDRVAGESADPEPEAD
YYAKEVTVLMVDNRNNAIYEKTKDISHIYMFNTSDIREAVPEPILLSRAELRLQRL
KSSVQHVLYQKYSNNRWYLGNNRLTPTDPEWLSFDVTGVVROWLNGDDGIQGRF
FSACSDSKDNKLHVEINGISPKRRDGLGTIDHMRPFLLLMATPLERAOHLHSSRH
RRALDYNVCFSSTEKNCVRLYIDFRKDLGKWIHEPKGYHANFCLGPCPYIWSLDT
QYSKVLALYNQHNPGASASPCCPVQALEPLPIVYVGRKPKVEQLSNMIVRSCKS"
1702..2037
/mat_peptide
/feature="TGF beta 1"
/product="transforming growth factor-beta 1"
BASE COUNT 421 a 734 c 574 g 365 t
ORIGIN

Query Match 56.1%; Score 190.2; DB 94; Length 2094;
Best Local Similarity 72.6%; Pred. No. 3e-42;
Matches 246; Conservative 0; Mismatches 93; Indels 0; Gaps 0;

Qy 1 gctttggacacaaattactgtctccgcaactggaggagaactgctgtgtgcgccccctc 60
Db 1702 GCCCTGGATACCAACTATTGCTTCAGCTCCACAGAGAAGTGTGTGTGCGGCGAGTG 1761

Qy 61 tacattgactccgacaggatctgggctggaagtgggtccatgaacctgaagggctactat 120
Db 1762 TACATTGACTTTAGGAGGACCTGGGTGGAAGTGATGATCCACGAGCCCAAGGGCTACCAT 1821

Qy 121 gccaaacttgctcaggcccttgccataacctccgcaagtgcagacacaaacccacagcag 180
Db 1822 GCCAACTTCTGCTGGGACCTGCCCTTATATTGGAGCCCTGGACACACAGTACAGCAAG 1881

Qy 181 gtgctgggaactgtacaacactctgaacctgaagcatctgctgcctgtgctgctgccc 240
Db 1882 GTCCCTGCCCTCTACACCAACACACACCCGGCGCTTCGGGCTCACCGTGTGCTGCGCG 1941

Qy 241 caggacctggagcccttgaccatctgtactatgttgaggagaccccccaagtgagcag 300
Db 1942 CAGGCTTTGGAGCCACTGCCCATGCTTACTACGTGGGTGCGAAGCCCAAGGTGGAGCAG 2001

Qy 301 ctctccaaatggtgggaagtcttgtaaatgtagctga 339
Db 2002 TTGTCCAAACATGATGTGCGCTCCTGCAAGTGCAGCTGA 2040

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RESULT 70
LOCUS AF097509 358 bp DNA ROD 09-DEC-1998
DEFINITION Cavia porcellus interleukin TGF beta gene, partial cds.
ACCESSION AF097509
VERSION AF097509.1 GI:3983112
KEYWORDS domestic guinea pig.
SOURCE Cavia porcellus
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
REFERENCE 1 (bases 1 to 358)
AUTHORS Wicher,V., Scarozza,A.M., Ramsingh,A.I. and Wicher,K.
TITLE Cytokine gene expression in skin of susceptible guinea-pig infected
with Treponema pallidum
JOURNAL Immunology 95 (2), 242-247 (1998)
MEDLINE 99069279
REFERENCE 2 (bases 1 to 358)
AUTHORS Scarozza,A.M., Ramsingh,A.I., Wicher,V. and Wicher,K.
TITLE Spontaneous cytokine gene expression in normal guinea pig blood and
tissues
JOURNAL Cytokine 10 (11), 851-859 (1998)
MEDLINE 99144670
REFERENCE 3 (bases 1 to 358)
AUTHORS Scarozza,A.M., Ramsingh,A.I., Wicher,V. and Wicher,K.
TITLE Direct Submission
JOURNAL Submitted (05-OCT-1998) New York State Dept of Health, David
Axelrod Institute, Wadsworth Center for Laboratories & Research,
120 New Scotland Ave, Albany, NY 12208, USA
FEATURES
source
1..358
/organism="Cavia porcellus"
/db_xref="taxon:10141"
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/codon_start=3
/product="interleukin TGF beta"
/protein_id="AAC83807.1"
/db_xref="GI:3983113"
/translation="LERAQHLHSHRRRLDPTNYCSSSTERNCCVRLQYIDFRKDLGW
EWIHPKGYHANFRILGPCPYIWSLDTOYSKVLALYNQHPGSAAPCCVPOALEPLPI
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BASE COUNT 76 a 120 c 103 g 59 t
ORIGIN
Query Match 55.1%; Score 186.8; DB 94; Length 358;
Best Local Similarity 75.2%; Pred. No. 3.3e-41;
Matches 233; Conservative 0; Mismatches 77; Indels 0; Gaps 0;
QY 5 tggacaccaattactgtctccgaacttgaggagaaactgtgtgtgccccctctaca 64
Db 49 TGCACACCAACTATTGCTCCAGCTCCACGGAAGAAGCTGCTGTGTGGCGAGCTCTACA 108
QY 65 ttgaacttcgacagagatctgggtggaagtgggtccatgaacctaaaggctactatgcc 124
Db 109 TTGACTTCGCAAGGACCTTAGGATGGAGTGGATCCACGAGGCCAAGGCGCTACCAATGCCA 168
QY 125 actctgtcaggcccttgcctacacctccgcagtgagacacacccacagcaggtgc 184
Db 169 ACTTCGGCTGGGGCCCTGCGCCCTACATTTGGAGCCTGGACACACAGTACAGCAAGGTCC 228
QY 185 tgggactgtacacactctgaacctgaagcatctgcctgccttgctgctgccccag 244
Db 229 TGGCCCTGTACAAACAGCAACACCCGGGGTTTCGGGGCGCTTGTCTGTGTGCCGAGC 288
QY 245 acctggagccctgacctcctgtactatgttgggagagaccccccaaaagtggagcagctct 304
Db 289 CGTTGGAGCACTGGCCACTCGTGTACTACGTGGGGCGCCAAAGCAAGGTGGAGCAGCTCT 348
QY 305 ccaacatggt 314
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Db 349 CCAACATGAT 358
RESULT 71
LOCUS PIGTGF2A 1427 bp mRNA MAM 15-JUL-1996
DEFINITION Sus scrofa transforming growth factor beta 2 mRNA, 3' end.
ACCESSION L08375
VERSION L08375.1 GI:1421492
KEYWORDS transforming growth factor beta 2.
SOURCE Sus scrofa (strain crossbreed) male adult Lung cDNA to mRNA.
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE 1 (bases 1 to 1427)
AUTHORS Zhou,Y.
TITLE Cloning and expression of porcine transforming growth factor beta 2
in immune cells
JOURNAL Unpublished (1993)
COMMENT On Jul 16, 1996 this sequence version replaced gi:164688.
FEATURES
source
1..1427
/organism="Sus scrofa"
/strain="crossbreed"
/db_xref="taxon:9823"
/cell_type="alveolar macrophage cells"
/dev_stage="adult"
/sex="male"
/tissue_type="Lung"
<1..1305
/feature="precursor"
/codon_start=1
/product="transforming growth factor beta 2"
/protein_id="AA03850.1"
/db_xref="GI:164689"
/translation="HYCVLSAFLLHLVTVALSLSTCIDMDQFMKRRIEARGQL
SKLTLSPEDYPEPEVPEVPEVSIYNSRDLLOEKASRAAAERERSDEEYAKV
YKIDMPPEPSENAIPPTFYRFRIVRFDVSAMEKNASNLVAERFVRLONPKRV
AEORIELYQILKSLDLSPTQRYIDSKVYKTRAEGLWFSFDVDAVHWHKDRNLG
FKISLHCPCTFVPSNNYIIPNKESELEAFAGIDGTSTYSGDKMTKTRKNSG
TPHLLMLPSYGLSQSRRKRALDAAYCFRNVDNCCRLPLYIDFKRDLGKWI
HBPGLMNAFCAGACPYLWSSDTHSRVLSLYNTINPEASAPCCVSDLEPLTILY
ICKTPKIEOLSNMIVKSCSKTKLAAFAARLYHSHNLGSET"
mat_peptide 904..1302
BASE COUNT 389 a 395 c 336 g 307 t
ORIGIN
Query Match 54.7%; Score 185.6; DB 7; Length 1427;
Best Local Similarity 72.0%; Pred. No. 5.8e-41;
Matches 242; Conservative 0; Mismatches 94; Indels 0; Gaps 0;
QY 1 gctttggacaccaattactgtctccgaacttgaggagaaactgtgtgtgccccctc 60
Db 904 GCTTTGGATGCACCTATTGCTTTAGAAATGTCAGAGATAATTGCTGCTGCGTCCACTT 963
QY 61 tacattgacttcgacagagatctgggctggaagtgggtccatgaacctaaagggtactat 120
Db 964 TACATTGATTTCAAGAGGGATCTTGGTGGAAATGGATACATGAGCCTAAAGGCTACAAT 1023
QY 121 gcaacttctgtcagggcccttgccataacctccgagtagtcagacacacccacagcag 180
Db 1024 GCCAACTTCTGTGCGGGGGGTGCCCGTACCTGTGGAGCTCTGACACCCAGCATAGCAGG 1083
QY 181 gtctgggactgtacacactctgaacctgaacctgaagcatctgcctgccttgcctgctgctgccc 240
Db 1084 GTTCTCAGCTTATATACACCATAAACCCAGAGACTTCTGCTTCCCTTGTGCTGGTGTC 1143
QY 241 caggacctggagcccttgacctcctgtactatgttgggagagaccccccaaaagtggagcag 300
Db 1144 CAGGATTTAGAACCGTCACTATCTCTACTACATCGGCAAAAGCCCAAGATCGAGCAG 1203

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QY 301 ctctccacatggtgtaagtcttgaatgtagc 336
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Db 1204 CTTTCTAATGATCGTAAAGTCTTGCAATGACG 1239

RESULT 72
SOURCE SSTGFB2 477 bp mRNA MAM 30-JUN-1993
LOCUS S. scrofa mRNA for transforming growth factor beta 2.
DEFINITION X70142 S48994
ACCESSION X70142.1 GI:312949
VERSION TGF-beta 2; transforming growth factor-beta2.
KEYWORDS pig.
SOURCE Sus scrofa
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE 1 (bases 1 to 477)
AUTHORS Mulherson, G.W., Mulherson, J.G., Danielpour, D. and Schomberg, D.W.
TITLE Porcine granulosa cells do not express transforming growth
factor-beta 2 (TGF-beta 2) messenger ribonucleic acid: molecular
basis for their inability to produce TGF-beta activity comparable
to that of rat granulosa cells
JOURNAL Endocrinology 131 (6), 2609-2614 (1992)
MEDLINE 93076683
FEATURES Location/Qualifiers
source 1..477
/organism="Sus scrofa"
/db_xref="taxon:9823"
/cell_type="1-3mm size follicles"
<1..>477
/product="Transforming Growth Factor-beta 2"
primer_bind 1..20
primer_bind 458..477
BASE COUNT 129 a 124 c 108 g 116 t
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Query Match 54.3%; Score 184; DB 7; Length 477;
Best Local Similarity 71.7%; Pred. NO. 1.9e-40;
Matches 241; Conservative 0; Mismatches 95; Indels 0; Gaps 0;
QY 1 gcttggacacaaattactgtccgaacttggaggagaactgtgtgtgccccctc 60
Db 142 GCTTTGGATGACGCTATGCTTTTGAAGATGTCAGGATAATTGCTGCTCCGCTT 201
QY 61 tacattgacttcgcacagagatctggctgggaagtgggtccatgaacctaaaggctactat 120
Db 202 FACATTGATTTCAAGAGGATCTTGGGTGGAATGGATACATGAGCCTAAAGGGTACAT 261
QY 121 gcaacttctgcacagagcttgccttgcacatacctccgcagtgacagacacacagcagc 180
Db 262 GCCAACTTCTGTGCGGGCGGTGCGCGTACCTGTGGAGCTCTGGCACCAGCATAGCAGG 321
QY 181 gtgtgggactgtacacacttgaacctgaacctgaagcatctgctcgtcgtgtgccc 240
Db 322 GTTCTACGCTTATATACACCAATAAACAGAAAGCTTGTCTTCCCTTGTCTGCGTGTCC 381
QY 241 caggacctggagccctgacctctgtactatgttgtagagagaccccaaaagtggagcag 300
Db 382 CAGGATTTAGAACCCCTCCTATCTCTACTACATCGCGCAAAACGCCCAAGATCGAGCAG 441
QY 301 ctctccacatggtggtgaagtcttgaatgtagc 336
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Db 442 CTTTCTAATGATCGTCAAGTGTGTGTAATGACG 477

RESULT 73
SOURCE AGMGBSC1 1585 bp mRNA PRI 27-APR-1993
LOCUS African green monkey BSC-1 cell growth inhibitor, complete cds.
DEFINITION J03585
ACCESSION J03585
VERSION BSC-1 cell growth inducing factor B;
KEYWORDS
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polyergin; transforming growth factor-beta 2.
African green monkey kidney epithelium, cDNA to mRNA.
Cercopithecus aethiops
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Cercopithecus.
1 (bases 1 to 1585)
Hanks, S., Armour, R., Baldwin, J.H., Maldonado, F., Spiess, J. and
Holley, R.W.
Amino acid sequence of the BSC-1 cell growth inhibitor (polyergin)
deduced from the nucleotide sequence of the cDNA
Proc. Natl. Acad. Sci. U.S.A. 85, 79-82 (1988)
88124824
COMMENT Draft entry and computer-readable sequence for [1] kindly provided
by S.Hanks, 03-DEC-1987.
FEATURES Location/Qualifiers
source 1..1585
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/db_xref="taxon:9534"
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200..1444
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VPEQRIELYQILKSKDLSTPTORYIDSKVVKTRAESEWLSFDVDAVHWHKDRNL
GFKSLHPCCTTFVPSNNIIPNKSEELRAEDAGIDGTSTYRSDQKTKSTRKNSG
KTPHLLMLLPYSRLESQOTNRKRKALDAAYCFRNVQDNCCLRPYIDFKRLGKWK
IHEPKYNAFCAGACPYLWSDDTQHSRVSLSYNTINPEASAPSCVCSODLEPLTILY
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BASE COUNT 487 a 367 c 334 g 397 t
ORIGIN
Query Match 54.2%; Score 183.8; DB 89; Length 1585;
Best Local Similarity 71.4%; Pred. NO. 1.8e-40;
Matches 242; Conservative 0; Mismatches 97; Indels 0; Gaps 0;
QY 1 gcttggacacaaattactgtccgaacttggaggagaactgtgtgtgccccctc 60
Db 1106 GCTTTGGATGACGCTATGCTTTTGAAGATGTCAGGATAATTGCTTACGCTTCCGCTT 1165
QY 61 tacattgacttcgcacagagatctggctgggaagtgggtccatgaacctaaaggctactat 120
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QY 121 gcaacttctgcacagagcttgccttgcacatacctccgcagtgacagacacacagcagc 180
Db 1226 GCCAACTTCTGTGCGGGCGGTGCGCGTATTTATGGAGTCTCAGACACTCAGCAGCAGG 1285
QY 181 gtgtgggactgtacacacttgaacctgaacctgaagcatctgctcgtcgtgtgccc 240
Db 1286 GTTCTGAGCTTATATACCAATAATCCAGAGCATCTGCTTCTCTCTGCTGGTGTCC 1345
QY 241 caggacctggagccctgacctctgtactatgttgtagagagaccccaaaagtggagcag 300
Db 1346 CAAGACTTAGAACCTCTAACCATTCCTACTACTATGTCGCAAAACACCCAAAGATTGAACAG 1405
QY 301 ctctccacatggtggtgaagtcttgaatgtagc 339
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Db 1406 CTTTCTAATGATGTTAAAGTCTTGCAATGACGCTAA 1444

RESULT 74
SOURCE CCU66874 1083 bp mRNA VRT 14-JUL-1997
LOCUS Cyprinus carpio transforming growth factor-beta 2 mRNA, partial
DEFINITION
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cds.
ACCESSION U66874
VERSION U66874.1 GI:1519488
KEYWORDS
SOURCE common carp.
ORGANISM Cyprinus carpio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Cyprininae; Cyprinus.
REFERENCE
AUTHORS Sumathy,K., Desai,K.V. and Kondalah,P.
TITLE Isolation of transforming growth factor-beta2 cDNA from a fish,
JOURNAL Cyprinus carpio by RT-PCR
MEDLINE Gene 191 (1), 103-107 (1997)
97354301
REFERENCE
AUTHORS Sumathy,K., Desai,K.V. and Kondalah,P.
TITLE Direct Submission
JOURNAL Submitted (14-AUG-1996) Center for Reproductive Biology and
Molecular Endocrinology, Indian Institute of Science, Bangalore,
Karnataka 560 012, India
FEATURES
source Location/Qualifiers
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BASE COUNT 282 a 310 c 281 g 210 t
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Best Local Similarity 74.0%; Pred. No. 4.6e-40;
Matches 231; Conservative 0; Mismatches 81; Indels 0; Gaps 0;
QY 1 gctttggacaccaattactgcttcgcgaacttggagagaactgctgtgtgccccctc 60
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Db 772 GCTCTGGACGCGCCTTCGCTCAGAAATGTGCAGGACAACTGCTGTTCAGCTCTC 831
QY 61 tacattgactccgacaggaatctggctggaagtgggtccatgaacctaaaggctactat 120
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Db 832 TACATCGACTTCAAGAAGGATCTGGTTGGAAGTGGATCCAGAACCCCAAGGATATAAC 891
QY 121 gcaacttctcagcccttgccatactccgcagtcgagacacacacacacagcag 180
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Db 892 GCCAAGCTTCTGCGGGAGCCCTGCGTATCTGTGGAGTGCAGACACCCAGCAGCAAT 951
QY 181 gtgctgggactgtacaaactctgaacctgaagcatcgctcgctgtgctgctgccc 240
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Db 952 ATCCCTGGGCTCTACAAACCACTTAATCCAGAGCATCCGCATCTCCTTGTGTGTCT 1011
QY 241 caggacctggagccctgacctctgactatgtttggagagacccccaaagtggagcag 300
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Db 1012 CAGGATCTGGAACCCCTTACATCCTTTACTACATCGGAAAAACGCCCAAAATCGAACAA 1071
QY 301 ctctccaacatg 312
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Db 1072 CTGCTCAACATG 1083
RESULT 75
A18279
LOCUS A18279 339 bp mRNA PAT 17-MAY-1994
DEFINITION TGF-beta 2 peptide seq ID No.2.
ACCESSION A18279
VERSION A18279.1 GI:513239
KEYWORDS
SOURCE synthetic construct.
ORGANISM artificial construct.
REFERENCE 1 (bases 1 to 339)
AUTHORS Cerletti,N., McMaster,G.K., Cox,D., Schmitz,A. and Meyhack,B.
TITLE Process for the production of biologically active protein (e.g.
TGF)
JOURNAL Patent: EP 0433225-A 3 19-JUN-1991;
CIBA-GEIGY AG
FEATURES
source Location/Qualifiers
1..339
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/db_xref="taxon:32630"
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/notes="Protein sequence is in conflict with the conceptual
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BASE COUNT 98 a 77 c 70 g 94 t
ORIGIN
Query Match 53.7%; Score 182.2; DB 9; Length 339;
Best Local Similarity 71.1%; Pred. No. 6.2e-40;
Matches 241; Conservative 0; Mismatches 98; Indels 0; Gaps 0;
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Db 1 GCTTTGGATGCGCCTATTGCTTTAGAAATGTGCAGGATAATTGCTGCTACGTCACCTT 60
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Db 61 TACATTGATTTCAAGAGGATCTAGGGTGAATGGATACAGAACCCAAAGGGTACAAT 120
QY 121 gcaacttctcagcccttgccatactccgcagtcgagacacacacacacagcag 180
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Db 121 GCCAAGCTTCTGCTGGAGCATGCCGTATTTATGGAGTTCAGACACTCAGCACAGCAGG 180
QY 181 gtgctgggactgtacaaactctgaacctgaagcatcgctcgctgtgctgctgccc 240
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Db 181 GTCTTGAGCTTATATAATACCATTAATAATCCAGAGCATCTGCTTCTCTTGTGCGTGTCC 240
QY 241 caggacctggagcccttgacctctgactatgtttggagagacccccaaagtggagcag 300
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Db 241 CAAGATTTAGAACCTCTAACCATTTCTCTACTACATTTGGCAAAACACCCCAAGATTGAACAG 300
QY 301 ctctccaacatggtggtagagcttctgtaaatgtagctga 339
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Db 301 CTTTCTAATATGATGTGTAAGTCTTTGCAATGCAGCTAA 339
RESULT 76
A23752
LOCUS A23752 339 bp mRNA PAT 25-JAN-1995
DEFINITION TGF-beta2 coding region.
ACCESSION A23752
VERSION A23752.1 GI:825586
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 339)
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AUTHORS	McMaster,G.K., Cox,D., Cerletti,N. and Kuhla,J.									
TITLE	Novel hybrid transforming growth factors									
JOURNAL	Patent: EP 0542679-A 2 19-MAY-1993;									
FEATURES	CIBA-GEIGY AG									
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Best Local Similarity	71.1%; Pred. No. 6.2e-40;									
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Db	1	GCTTTGGATGGGGCTATTGCTTTAGAAAATGTCAGAGTAATTTGCTGCCTAGTCCACTT	60							
Qy	61	tacattgacttcgcacaggaattctgggtggaagtgggtccatgaacctaaagggctactat	120							
Db	61	TACATTGATTTCAGAGGGATCTAGGTGGAAATGGATACACGAACCCAAAGGTACAAT	120							
Qy	121	gcaactctctgcagagcccttgcccatctccgcagtcgagacacacccacagacag	180							
Db	121	GCCAACTTCTGTGTGAGCATGCCCCGCTATTATTATGGAGTTTCAGACACTCAGCAGCAGG	180							
Qy	181	gtctgagactgtacaacactctgaacccctgaagcatctgcctgcctgtcgctgctg	240							
Db	181	GTCCTGAGCTTATATATACATTAATTCAGAGCACTCTGCTTCTCTGCTGGTGTCC	240							
Qy	241	caggaacctggagcccttgacatcctgtactatgttgggagagaccccaagtgagcag	300							
Db	241	CAAGATTTAGAACCTCTAACCATTCCTACTACATTGGCAAAACACCAAGATTGAACAG	300							
Qy	301	ctctcaacatggtggtggaagtcttgttaaatgtagtcta	339							
Db	301	CTTTCTAATATGATTGTAAGTCTTTGCAAAATGCAGCTAA	339							
RESULT	77									
A48551										
LOCUS	A48551 339 bp DNA PAT 07-MAR-1997									
DEFINITION	Sequence 3 from Patent WO9603432.									
ACCESSION	A48551									
VERSION	A48551.1 GI:2302321									
KEYWORDS	unidentified.									
SOURCE	unidentified									
ORGANISM	unclassified.									
REFERENCE	1. (bases 1 to 339)									
AUTHORS	Cerletti,N									
TITLE	NOVEL PROCESS FOR THE PRODUCTION OF BIOLOGICALLY ACTIVE DIMERIC PROTEIN									
JOURNAL	Patent: WO 9603432-A 3 08-FEB-1996;									
COMMENT	CIBA GEIGY AG (CH)									
FEATURES	Other publication AU 3109595 960222.									
source	Location/Qualifiers									
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BASE COUNT	98 a 77 c 70 g 94 t									


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QY 301 ctctcaacatggtggtgaagtcttgtaaatgtactga 339
Db 1388 CTTTCTAATATGATTGTAAGTCTTGCAAAATGCAGCTAA 1426

RESULT 84
LOCUS All1709 1695 bp DNA PAT 10-DEC-1993
DEFINITION H.sapiens G-TsF gene precursor.
ACCESSION All1709
VERSION All1709.1 GI:490100
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1695)
AUTHORS De Martin,R., Fontana,A., Hofer,E., Hofer-Warbinek,R. and Wrann,M.
TITLE Production and use of a novel T-cell suppressor factor
JOURNAL Patent: EP 0268561-A 8 25-MAY-1988;
SANDOZ AG; SANDOZ-PATENT-GMBH; SANDOZ-ERFINDUNGEN
Verwaltungs-gesellschaft m.b.H
FEATURES
location/Qualifiers
source 1..1695
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BASE COUNT 523 a 386 c 354 g 432 t
ORIGIN
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Best Local Similarity 71.1%; Pred. No. 5e-40;
Matches 241; Conservative 0; Mismatches 98; Indels 0; Gaps 0;
QY 1 gctttggacaccaattactgctccgcaacttggaggagaactgctgtgtgccccctc 60
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QY 61 tacattgactccgacagatcggtggaagtgggtccatgaacctaaagggctactat 120
Db 1148 TACATTGATTTCAAGAGGATCTAGGGTGAATGGATACACAGAACCCAAAGGGTACAAT 1207
QY 121 gcaactctgtcaggcccttgccatccactccgcagctgcagacacacccacagcag 180
Db 1208 GCAACTCTGTGCTGGAGCATGCCGTATTTATGGAGTTCAGACACTCAGCACAGCAGG 1267
QY 181 gtctgggactgtacaacactgaacctgaacctgaagcatctgcctgcctgtcgtgccc 240
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Db 1328 CAAGATTTAGACCTTACCAATCTCTACTACATGTCGGAACACCCCAAGATTGACAG 1387
QY 301 ctctcaacatggtggtgaagtcttgtaaatgtactga 339
Db 1388 CTTTCTAATATGATTGTAAGTCTTGCAAAATGCAGCTAA 1426
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RESULT 85

HSGTsf

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

CDS

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mat_peptide

BASE COUNT

ORIGIN

Query Match

Best Local Similarity

Matches

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Db

QY

Db

QY

Db

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HSGTsf 1695 bp mRNA PRI 27-MAR-1995
Human mRNA for glioblastoma-derived T-cell suppressor factor G-TsF
(transforming growth factor-beta2, TGF-beta2).
Y00083
X00083.1 GI:31959
T-cell suppressor factor; transforming growth factor-beta2.
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1695)
AUTHORS Hofer,E.
TITLE Direct Submission
JOURNAL Submitted (02-NOV-1987) Hofer, E., Sandoz AG, Department for
Biotechnology, Preclinical Research, Building 386/328, Sandoz AG,
CH-4002 Basel
REFERENCE 2 (bases 1 to 1695)
AUTHORS de Martin,R., Haendler,B., Hofer-Warbinek,R., Gaugitsch,H.,
Wrann,M., Schlusener,H., Seifert,J.M., Bodmer,S., Fontana,A. and
Hofer,E.
TITLE Complementary DNA for human glioblastoma-derived T cell suppressor
factor, a novel member of the transforming growth factor-beta gene
family
JOURNAL EMBO J. 6 (12), 3673-3677 (1987)
MEDLINE 8811555
FEATURES
location/Qualifiers
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/clone_lib="lambda gt10"
/clone="lambda SUP25, lambda SUP40, lambda SUP42"
182..1426
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/codon_start=1
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/db_xref="SWISS-PROT:P08112"
/translation="MHYCVLSAFILHLVTVALSSTCLDMDQFMRKRTEAIRGOI
LSKLKLTSPEDYPEPEVPEVPEVSIYNSTRDLLOEKASRAAACERSDSEYVAK
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VPEQRIELYILKSLDTSPTQYIDSKVVKRAEGLWLSFDVDAVHEWLHKKDRNL
GFKISLHCPCTFVPSNNYIIPNKSELEAFIDGTSTYTGDKTIFSKRKNNG
KTPHLLMLLPLPSYRLSQOTNRKRKRALDAAYCFRNQDNCCLRLPYIDFKRLGKW
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1088..1423
/product="put. mature G-TsF"
BASE COUNT 523 a 386 c 354 g 432 t
ORIGIN
Query Match 53.7%; Score 182.2; DB 93; Length 1695;
Best Local Similarity 71.1%; Pred. No. 5e-40;
Matches 241; Conservative 0; Mismatches 98; Indels 0; Gaps 0;
QY 1 gctttggacaccaattactgctccgcaacttggaggagaactgctgtgtgccccctc 60
Db 1088 GCTTTGGATGCGCCCTATTGCTTTAGAAATGTCAGGATAATTGCTGCTCCACTT 1147
QY 61 tacattgactccgacagatcggtggaagtgggtccatgaacctaaagggctactat 120
Db 1148 TACATTGATTTCAAGAGGATCTAGGGTGAATGGATACACAGAACCCCAAGGGTACAAT 1207
QY 121 gcaactctgtcaggcccttgccatccactccgcagctgcagacacacccacagcag 180
Db 1208 GCAACTCTGTGCTGGAGCATGCCGTATTTATGGAGTTCAGACACTCAGCACAGCAGG 1267
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Db	1578	GCCAACTTCTGTGCTGGAGCATGCCGTATTATGGAGTTAGACACTCAGACAGCAGG	1637
Qy	181	gtgctgggactgcaacacactctgaacccctgaagcatctgctcgccttgcgtgccc	240
Db	1638	GTCCGTGAGCTTATAATAATACCAATAATCCAGAAGCATCTGCTTCTCCTTGCTGCTGCTGC	1697
Qy	241	caggacctggagccctgacacctctgactatgtgtggagagacccccaaagtggagcag	300
Db	1698	CAAGATTTAGAACCTCTAACCATTTCTACTACATTTGCCAAACACCCCAAGATTGAACAG	1757
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RESULT	88		
LOCUS	A23756	336 bp mRNA	PAT 25-JAN-1995
DEFINITION	TGF-beta2(44/45)beta1 hybrid coding region.		
ACCESSION	A23756		
VERSION	A23756.1	GI:825590	
KEYWORDS			
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
TITLE	McMaster, G.K., Cox, D., Cerletti, N. and Kuhla, J.		
JOURNAL	Novel hybrid transforming growth factors		
FEATURES	Patent: EP 0542679-A 6 19-MAY-1993;		
source	CIBA-GEIGY AG		
location/Qualifiers			
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71 a	99 c	97 g	69 t
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Query Match	53.3%;	Score 180.8;	DB 9; Length 336;
Best Local Similarity	71.1%;	Pred. No. 1.5e-39;	
Matches 239;	Conservative 0;	Mismatches 97;	Indels 0; Gaps 0;
Qy	1	gctttggacacaaattactgctccgcgaacttgaggagaaactgctgtgctgccccctc	60
Db	1	GCTTTGGATGGCGCTATTGCTTTAGAATGTGCAGGATAATTGCTGCTAGCTCACTT	60
Qy	61	tacattgactccgacagatctgggctggaagtgggtccatgaacccaagggctactat	120
Db	61	TACATTGATTTCAAGAGGGATCTAGGGTGGAAATGGATACACGAACCCAAAGGGTACAAAT	120
Qy	121	gcaactctctcagcccttgcccatcacctcccgagtgagacacacacccacagcagc	180
Db	121	GCCAACTTCTGCTCGGCGCTGCGCCCTGACATTTTGAGAGCTGGACACGAGTACAGCAAG	180
Qy	181	gtgctgggactgcaacacactctgaacccctgaagcatctgctcgccttgcgtgccc	240
Db	181	GTCTTGGCCCTGTACAAACAGCATACCCGGCGGCTCGGGCGGCGGCTGCTGCTGCGG	240
Qy	241	caggacctggagccctgacacctctgactatgtgtggagagacccccaaagtggagcag	300
Db	241	CAGGCGCTGGAGCCCTGCCCATCTGTTACGTACGTGGGCGGCGCAAGCCCAAGTGGAGCAG	300
Qy	301	ctctccaacatgggtgaagtcttgtaaatgtagc	336
Db	301	CTGTCCAACATGATGCTGCGCTCTGCAAGTGCAGC	336
RESULT	89		

XLTFB2	2724 bp	mRNA	VRT	08-NOV-1993
LOCUS	Xenopus laevis TGF-beta2 mRNA for transforming growth factor-beta2.			
DEFINITION				
ACCESSION	X51817			
VERSION	X51817.1	GI:414789		
KEYWORDS	growth factor; transforming growth factor.			
SOURCE	African clawed frog.			
ORGANISM	Xenopus laevis			
REFERENCE	Amphibia; Batrachia; Chordata; Craniata; Vertebrata; Euteleostomi;			
AUTHORS	Xenopodinae; Xenopus.			
TITLE	1 (bases 1 to 2724)			
JOURNAL	Rebbert, M.L.			
REMARK	Direct Submission			
REFERENCE	Submitted (07-FEB-1990) Rebbert M.L., Laboratory of Molecular			
AUTHORS	Genetics, National Institute of Child, Health and Human			
TITLE	Development, Bldg 6 Rm 324, Bethesda MD 20892, U S A			
JOURNAL	sequence revised by [3]			
REMARK	2 (bases 1 to 2724)			
REFERENCE	Rebbert, M.L., Bhatia-Dey, N. and Dawid, I.B.			
AUTHORS	The sequence of TGF-beta 2 from Xenopus laevis			
TITLE	Nucleic Acids Res. 18 (8), 2185 (1990)			
JOURNAL	90245678			
MEDLINE	3 (bases 1 to 2724)			
REFERENCE	Rebbert, M.L.			
AUTHORS	Direct Submission			
TITLE	Submitted (08-NOV-1993) Rebbert M.L., Laboratory of Molecular			
JOURNAL	Genetics, National Institute of Child, Health and Human			
REMARK	Development, Bldg 6 Rm 324, Bethesda MD 20892, U S A			
REFERENCE	On Nov 9, 1993 this sequence version replaced gi:65136.			
AUTHORS	Data kindly reviewed (16-AUG-1990) by Rebbert .M.L.			
TITLE	Location/Qualifiers			
JOURNAL	1..2724			
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	LSKLKLNPPEDYPEGEVSQDVISYINSTRDLLOKANERATSCERESEDEYYAKE			
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	YSEQRILEYQILKSKDLASPTQYIDSKVVKTRAEGLWISFDVTEAVNEWLHKKRNL			
	GFKISLHPCCTTFIPSNYYIIPNKSELETFRAGIDDAVMYAGDSKSKTKGRKHTGR			
	TPLLMLLPSYRLESQQSSRRKKRALDAAYCFRNQDNCCLRLPLYIDPKKDLGWKI			
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	136..1317			
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	/protein_id="CAA36117.1"			
	/db_xref="GI:1334690"			
	/db_xref="SWISS-PROT:PI7247"			
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	TPQYIDSKVVKTRAEGLWISFDVTEAVNEWLHKKRNLGFKISLHPCCTTFIPSNYY			
	IIPNKSELETFRAGIDDAVMYAGDSKSKTKGRKHTGRTPHLLMLLPSYRLESQQS			
	SRKKRALDAAYCFRNQDNCCLRLPLYIDPKKDLGWKIHEPKGNANFCAGACPYLW			
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BASE COUNT				
ORIGIN				


```

Sekizawa, K.
Direct Submission
Submitted (16-JUL-1999) Department of Pulmonary Medicine, Institute
of Clinical Medicine, University of Tsukuba, 1-1-1 Tennoudai,
Tsukuba, Ibaraki 305-8575, Japan
FEATURES
  source      Location/Qualifiers
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      /db_xref="taxon:10141"
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      /note="Obtained from injured tissue"
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      /translation="PLETNVCFSTSEKNCVRLYIDFRKDLGKWKIHEPKGYHANFC
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BASE COUNT      56 a      92 c      77 g      53 t
ORIGIN
Query Match      50.1%; Score 170; DB 94; Length 278;
Best Local Similarity 76.3%; Pred. No. 1.5e-36;
Matches 209; Conservative 0; Mismatches 65; Indels 0; Gaps 0;
QY 5 tggacaccaattactgtctccgaacttggaggaactgtgtgtgcgccctctaca 64
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DB 5 TGGACACCAACTATTGCTTCAGCTCCACGGAGAGAACTGCTGTGCGGAGCTCTACA 64
QY 65 ttgacttcgcagagcttggtggctgaagtgggtccatgaacctaaaggctactatgcc 124
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DB 65 TTGACTTCGCGAAGACCTAGTAGTGGAGTGGATCCACGAGCCGACGCTACCATGCCA 124
QY 125 acttctgcaggcccttgcacatactccgcagtcagtcagacacacccacagcaggtgc 184
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DB 125 ACTTGTGCTGGGGCCCTGCGCCCTACATTTGGAGCGCTGGACACACAGTACAGCAAGGTCC 184
QY 185 tggactatacaactctgaacctgaagcatctgcctgccttgcgtgccccagg 244
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DB 185 TGGCCCTGTAAACAGACACACCCCGGCTTGGCGGCGCCTTGCTGTGTGCGCGCAG 244
QY 245 acctggagcccttgaccatctgtactatgttg 278
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DB 245 CGTTGGAGCCACTGCCCATCTGTACTACGTGGG 278

RESULT 94
AF140363
LOCUS      AF140363      1514 bp      mRNA      VRT      18-FEB-2000
DEFINITION Morone chrysops x Morone saxatilis transforming growth factor-beta
precursor (TGF-beta) mRNA, complete cds.
ACCESSION AF140363
VERSION    AF140363.1 GI:5690245
KEYWORDS   white bass x striped bass.
SOURCE     Morone chrysops x Morone saxatilis
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
  Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes;
  Percoidae; Moronidae; Morone.
  1 (bases 1 to 1514)
REFERENCE 1 (bases 1 to 1514)
AUTHORS   Harms,C.A., Kennedy-Stoskopf,S., Horne,W.A., Fuller,F.J. and
  Tompkins,W.A.
  Cloning and sequencing hybrid striped bass (Morone saxatilis x M.
  chrysops) transforming growth factor-beta (TGF-beta), and
  development of a reverse transcription quantitative competitive
  polymerase chain reaction (RT-qPCR) assay to measure TGF-beta mRNA
  of teleost fish
JOURNAL    Fish Shellfish Immunol. 10 (1), 61-85 (2000)
MEDLINE    20394636
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REFERENCE      2 (bases 1 to 1514)
AUTHORS        Harms,C.A., Kennedy-Stoskopf,S., Horne,W.A., Fuller,F.J. and
  Tompkins,W.A.F.
TITLE          Direct Submission
JOURNAL        Submitted (05-APR-1999) MPP, College of Veterinary Medicine, North
  Carolina State University, 4700 Hillsborough St., Raleigh, NC
  27606, USA
FEATURES
  source      Location/Qualifiers
    1..1514
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      /db_xref="taxon:45352"
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      /translation="MRLAFLMLVVVTVGVNVSMTCKTLDLEMKKKRIAIRSQIL
      SKLRLPKPEPDQAGDEBEIPTPLSLNSTKEMLKEQOTEVQTDISTQBEERFPAK
      VLHKFMTRKNNNTDTTKRMFFNISEIRSVGDYRLTLTSAELRMLIKTKTIYDEQRVEL
      YSGLDSPRYLASRFTITNKDKWLSFDVTKTLDMLKGTDDQGLRFLFCECNKVS
      AGETIFKFGISIDPGRGTGPMQLITQOPPYILTMSIPQNTSSPSTSRKKSTETKD
      VCTAOTETCCVRSRLYIDFRKDLGKWKIHKPTGYNANCYMGCTYTINWANKYSQILAL
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      143..898
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      /note="encodes transforming growth factor-beta preprotein"
      791..799
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      /note="Region: RGD integrin binding site"
      887..898
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      /note="Region: RKRR tetrabasic cleavage site"
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      /product="transforming growth factor-beta"
BASE COUNT    448 a    359 c    378 g    329 t
ORIGIN
Query Match    47.8%; Score 162.2; DB 8; Length 1514;
Best Local Similarity 71.0%; Pred. No. 1.7e-34;
Matches 215; Conservative 0; Mismatches 88; Indels 0; Gaps 0;
QY 37 gagaactgtgtgcgccccctctacattgactccgacagatctgggctggaagtgg 96
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DB 935 GAGACCTGTGCTGGGAGCTGTACATCGACTTCAGGAAGATCTGGATGGAAGTGG 994
QY 97 gtccatgaacctaaaggctactatgccaaactctgtctcaggcccttgcacatacctccgc 156
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DB 995 ATACATAAGCCAAACGGCTTACAAATGCCAACTACTGCGATGGGGTCTCGACCTACATCTGG 1054
QY 157 aqtcagacacacacccacagcagtgctggactgtacaacactctgaacctgaagca 216
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DB 1055 AATGCTGAAAACAATAATTCTCAGATTTTGGCCCTTTATTAAGCATCACACCCAGAGGCC 1114
QY 217 tctgcctgccttgcgtgcgccaggacctggagccctgagccctctgtactatgtt 276
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DB 1115 TCTGCCAGCCCTGTGTGTTCCCGAGGACCTGGAGCCACTGCCAATCCTCTACTATGTG 1174
QY 277 gggaggaccccccaagtggagcagctctctccaacatgggtgaagtcttgaatagtagc 336
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Db	167	CCAGGACCTGGAGCCCTGACCATCTGTACTATGTGGGAGGACCCCAAAAGTGGAGCA	226
QY	300	gctctcccaacatggtggaagtctgtgtaaaatgtagctga	339
Db	227	GCTCTCCAACATGGTGGTGAAGCTCTGTGAAGTGA	266
RESULT	97		
LOCUS	DJ270M14	192126 bp	DNA
DEFINITION	Homo sapiens chromosome 14q24.3 clone BAC270M14 transforming growth factor-beta 3 (VGF-beta 3) gene, complete cds; and unknown genes.		
ACCESSION	AF107885		
VERSION	AF107885.2	GI:5468516	
KEYWORDS			
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiinae; Homo.		
AUTHORS	Madan,A., Rowen,L., Qin,S., Dickhoff,R., Shaffer,T., James,R., Abbasi,N., Loretz,C., Madan,A., Dors,M., Dahl,T., Hall,J., Lasky,S. and Hood,L.		
TITLE	Complete genomic sequence of human transforming growth factor-beta 3		
JOURNAL	Unpublished		
REFERENCE	2 (bases 1 to 192126)		
AUTHORS	Madan,A.		
TITLE	Direct Submission		
JOURNAL	Submitted (20-NOV-1998) Department of Molecular Biotechnology, Box 357730 University of Washington, Seattle, WA 98195, USA		
COMMENT	On Jul 14, 1999 this sequence version replaced gi:3928926. Sequence methodology: High Redundant shotgun sequence using plasmid subclones. Interspersed Repeats were identified with RepeatMasker (available from http://ftp.genome.washington.edu/RM/RepeatMasker.html).		
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	/clone="BAC270M14"		
	/clone_lib="P. de Jong RPC11"		
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repeat_region	/rpt_family="AluY"		
repeat_region	complement(689..713)		
repeat_region	/rpt_family="AT-rich"		
repeat_region	complement(968..1277)		
repeat_region	/rpt_family="AluSg"		
repeat_region	1407..1646		
repeat_region	/rpt_family="MIR"		
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Best Local Similarity	96.4%;	Pred. No. 2.3e-33;				
Matches	162;	Conservative	0;	Mismatches 6;	Indels 0;	Gaps 0;
QY	15	ttactgtcttcgcaacttgagagaaactgctgtgtgccccctctacattgactctcg	74			
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QY	75	acaggatctgggtggaagtgggtccatgaacctaaaggtactactatgccaaactctgtctc	134			
Db	155	ACAGGATCTGGCTGGAGTGGTCCATGAACCTAAGGGCTACTATGSCCAACTTCTGCTC	214			
QY	135	agcccttgccctacatctccgagtcgagacacacacacacacagcacgct	182			
Db	215	AGGCCCTTGCCCATCTCCGAGTGCAGACACAACCCACAGACCGGT	262			
RESULT 100						
AB020217						
LOCUS	AB020217	298 bp	mRNA	MAM	09-JAN-1999	
DEFINITION	Oryctolagus cuniculus mRNA for transforming growth factor beta-1, partial cds.					
ACCESSION	AB020217					
VERSION	AB020217.1	GI:4127220				
KEYWORDS	TGF-beta-1; transforming growth factor beta-1.					
SOURCE	Oryctolagus cuniculus cDNA to mRNA.					
ORGANISM	Oryctolagus cuniculus					
REFERENCE	Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi; Inoue,K., Kawabe,Y. and Kodama,T.					
AUTHORS	1 (bases 1 to 298)					
TITLE	Direct Submission					
JOURNAL	Submitted (18-NOV-1998) to the DDBJ/EMBL/GenBank databases. Kenji Inoue, Research Center for Advanced Science and Technology, University of Tokyo, Molecular Biology and Medicine; 4-6-1, Komaba, Meguro, Tokyo 153-8904, Japan (E-mail: keinoue-tky@umin.u-tokyo.ac.jp, Tel:81-3-3481-4560, Fax:81-3-3481-4560)					
REFERENCE	2 (bases 1 to 298)					
AUTHORS	Inoue,K., Kawabe,Y. and Kodama,T.					
TITLE	Rabbit TGF-beta-1 cDNA, partial					
JOURNAL	Published Only in DataBase (1999) In press					
FEATURES	Location/Qualifiers					
source	1. .298					
	/organism="Oryctolagus cuniculus"					
	/db_xref="taxon:9986"					
gene	1. .298					
	/gene="TGF-beta-1"					
CDS	<1. .>298					
	/codon_start=2					
	/product="transforming growth factor beta-1"					
	/protein_id="BAA36950.1"					
	/db_xref="GI:4127221"					
	/translation="FSTNYCFSTSEKNCVRLYIDFRKDLGKWKIHPKGYHANPCLGPCPYIWSLDTQYSKVLALYNHNPASAAPCCVPQALEATHRVTLTRGPKPVE"					
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ORIGIN						
Query Match	44.2%;	Score 150;	DB 7;	Length 298;		
Best Local Similarity	75.2%;	Pred. No. 5e-31;				
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Db	2	TTCTCCACCACTACTGTCTCAGCTCCACAGAGAAGAACTGTGTGTGGCGGAGCTGTAC	61			
QY	64	attgacttcgacagatctgggtcggaagtgggtccatgaacctaaaggtactatgcc	123			

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|||||
Db 62 ATGACTTCCGCAAGGACCTGGGCTGGAGTGGATCCACGAGCCCAAGGGCTACCCACGCC 121
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Db 122 RACTTCTGCTGGGACCCCTGCCCCCTACATCTGGAGCCTGGACACCCAGTACAGCAAGGTC 181
Qy 184 ctgggactgtacaacactctgaacctgaacctgaagcatctgcctgcctgtgtgcgtgccccag 243
Db 182 CTGGCCCTGTACACACAGCAGCACAAACCCGGCGGTCTGCAGCGCCGTGCTGTGTGCCACAG 241
Qy 244 gacctgg-agccccctgaccatcctgt 268
Db 242 GCGCTGGAAGCCACTGCCCATCGTGT 267
```

Search completed: October 30, 2001, 11:17:46
Job time: 6184 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: October 30, 2001, 09:13:52 ; Search time 76.31 Seconds
(without alignments)
2789.394 Million cell updates/sec

Title: TGFB3N

Perfect score: 339

Sequence: 1 gcttggacaccaattactg.....agtcttgaatagtatgta 339

Scoring table:

IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 730101 seqs, 313950809 residues

Total number of hits satisfying chosen parameters: 1460202

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

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13: /SIDSI/gcgdata/geneseq/geneseq/NA1992.DAT.*
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22: /SIDSI/gcgdata/geneseq/geneseq/NA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	339	100.0	339	12	AAQ11995
2	339	100.0	339	14	AAQ41601
3	339	100.0	339	17	AAAT17234
4	339	100.0	339	17	AAAT15464
5	339	100.0	339	18	AAAT80110
6	339	100.0	339	20	AAAT42773
7	339	100.0	339	20	AAAT15247
8	339	100.0	339	20	AAV99377
9	339	100.0	609	11	AAQ05774
10	339	100.0	2529	13	AAQ20576
11	339	100.0	2574	19	AAV63209

12	337.4	99.5	2157	15	AAQ56926	Human TGF-beta-3.
13	337.4	99.5	2157	19	AAV52935	Human transforming
14	337.4	99.5	2158	11	AAQ02820	cDNA sequence enco
15	333	98.2	1239	13	AAQ22229	Mutant transformin
16	332.6	98.1	498	17	AAQ06496	Tissue-derived tum
17	326.2	96.2	2530	11	AAQ06845	Sequence encoding
18	315	92.9	2676	11	AAQ02819	cDNA sequence enco
19	302.2	89.1	2639	19	AAV52934	Pig transforming g
20	302.2	89.1	2669	15	AAQ56925	Pig TGF-beta-3. S
21	302.2	89.1	2671	11	AAQ03303	Entire porcine tra
22	297.6	87.8	336	14	AAQ41603	Transforming Growt
23	297.6	87.8	336	17	AAAT17237	Hybrid TGF-beta 1-
24	297.6	87.8	336	17	AAAT15465	cDNA encoding huma
25	291	85.8	4382	22	AAF55131	Nucleotide sequenc
26	276.8	81.7	336	14	AAQ41605	Transforming Growt
27	276.8	81.7	336	17	AAAT17238	Hybrid TGF-beta 2-
28	276.8	81.7	336	17	AAAT15466	cDNA encoding huma
29	240	70.8	336	14	AAQ41606	Transforming Growt
30	240	70.8	336	14	AAQ41607	Transforming Growt
31	240	70.8	336	17	AAAT17239	Hybrid TGF-beta 3-
32	240	70.8	336	17	AAAT15467	cDNA encoding huma
33	206.2	60.8	339	18	AAAT42771	TGF-beta1 active f
34	206.2	60.8	339	20	AAV99375	cDNA encoding a tr
35	204.6	60.4	339	17	AAAT17235	Human TGF-beta 1 c
36	204.6	60.4	339	20	AAAT15245	Sequence encoding
37	204.6	60.4	1303	11	AAQ09317	Monkey transforming
38	204.6	60.4	1559	13	AAQ02089	Sequence encoding
39	204.6	60.4	1560	9	AAAT1084	Seeding sequence of
40	204.6	60.4	1560	11	AAQ03508	Simian Transformin
41	204.6	60.4	1561	11	AAQ03268	Simian Transformin
42	204.6	60.4	1569	11	AAQ03509	Human Transforming
43	204.6	60.4	1571	11	AAQ03269	Human transforming
44	204.6	60.4	1821	12	AAQ13392	Human pro-TGF-beta
45	204.6	60.4	2537	7	AAAT0972	Sequence encoding
46	204.6	60.4	2537	11	AAQ03301	cDNA encoding huma
47	204.6	60.4	2537	11	AAQ02814	Sequence of pre-TG
48	204.6	60.4	2537	15	AAQ56923	Human pre-TGF-beta
49	204.6	60.4	2537	17	AAAT15720	Pre-transforming g
50	204.6	60.4	2537	19	AAV52933	Human pre-transfor
51	204.6	60.4	2745	16	AAAT05876	cDNA encoding tran
52	204.6	60.4	3541	17	AAAT16516	Collagen A1/TGF-be
53	204.6	60.4	3541	21	AAAT12498	cDNA encoding a ch
54	204.6	60.4	4105	15	AAQ55624	TGFbeta1 5'-UTR-CD
55	203	59.9	339	12	AAQ11993	Transforming Growt
56	203	59.9	339	17	AAAT15462	Human transforming
57	203	59.9	1569	9	AAAT1085	Coding sequence of
58	201.6	59.5	336	14	AAQ41602	Transforming Growt
59	200.4	59.1	345	14	AAQ41599	Mature human Trans
60	195	57.5	1561	11	AAQ04908	Sequence encoding
61	195	57.5	1561	13	AAQ29177	TGF-beta 1/beta 2
62	182.2	53.7	339	12	AAQ11994	Encodes Transformi
63	182.2	53.7	339	14	AAQ41600	Mature human Trans
64	182.2	53.7	339	17	AAAT17236	Human TGF-beta 2 c
65	182.2	53.7	339	17	AAAT15463	Human transforming
66	182.2	53.7	339	18	AAAT42772	TGF active fragmen
67	182.2	53.7	339	20	AAAT15246	cDNA encoding the
68	182.2	53.7	339	20	AAV99376	cDNA encoding a tr
69	182.2	53.7	1695	16	AAAT05877	cDNA encoding tran
70	182.2	53.7	2208	13	AAQ20291	Sequence encoding
71	182.2	53.7	2568	10	AAAT09067	Sequence of human
72	182.2	53.7	2569	11	AAQ05126	Human TGF-Beta2-44
73	182.2	53.7	2569	13	AAQ20290	Sequence encoding
74	182.2	53.7	2592	16	AAAT04116	Human transforming
75	180.8	53.3	336	14	AAQ41604	Transforming Growt
76	180.6	53.3	2206	11	AAQ03510	Human Transforming
77	180.6	53.3	2207	11	AAQ03511	Hybrid Transformin
78	180.6	53.3	2207	11	AAQ05127	Human TGF-Beta1/TG
79	180.6	53.3	2217	10	AAAT09068	Sequence of human
80	177.4	52.3	2200	16	AAAT04115	Simian-human hybri
81	176.2	52.0	1565	13	AAQ29178	TGF-beta 1. Homo
82	161.2	47.6	2754	21	AAAG3944	cDNA encoding a pa
83	134.2	39.6	852	12	AAQ11774	Encodes Pb-Pb-trun
84	96.8	28.6	975	7	AAAT0973	Genomic sequence e

Qy	1	gctttggacaccaattactgtcttcgcgaacttgaggagaaactgctgtgtgcgccccctc	60
Db	1	gctttggacaccaattactgtcttcgcgaacttgaggagaaactgctgtgtgcgccccctc	60
Qy	61	tacattgaacttcgcacaggaatctggctggaagtgggtccatgaaccttaagggtacttat	120
Db	61	tacattgaacttcgcacaggaatctggctggaagtgggtccatgaaccttaagggtacttat	120
Qy	121	gccaaactcttctcagagcccttgcaccatactccgcagtgtagacacaaccccagcacg	180
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Qy	181	gtcgtcggaactgtacaacacttgaacctgaagcatctgcctcgccotctctcggtgcc	240
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Qy	241	caggacatggagcccccgacaactctactatgtttggaggagcccccaagaatggagcag	300
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Query Match      100.0%; Score 339; DB 12; Length 339;
Best Local Similarity 100.0%; Pred. No. 3.3e-87;
Matches 339; Conservative 0; Mismatches 0; Indels 0
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The invention covers hybrid TGF-beta molecules consisting of parts of the human isoforms TGF-beta1, TGF-beta2 and TGF-beta3 (see AAQ11599, AAQ11600 and AAQ11601, respectively). The hinge points between parts derived from different parent isoforms are pref. between amino acids 44 and 45, 56 and 57, 79 and 80, 90 and 91, or 22 and 23. The hybrid molecules promote cell migration, inhibit the growth of A375 melanoma cells, accelerate the healing of partial-thickness burn wounds and full-thickness incisional wounds and increase formation

CC of fibrous granular tissue. See e.g. AAQ41602-Q41607 for pref. hybrids.
 XX Sequence 339 BP; 74 A; 104 C; 86 G; 75 T; 0 other;
 SQ

Query Match 100.0%; Score 339; DB 14; Length 339;
 Best Local Similarity 100.0%; Pred. No. 3.3e-87;
 Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gcttggacacacaaattactgtctccgcaacttgagagaaactgctgtgccccctc 60
 |||||
 DB 1 gcttggacacacaaattactgtctccgcaacttgagagaaactgctgtgccccctc 60
 |||||
 QY 61 tacattgacttcacagagatcgtggctggaagtgggtccatgaacctaaaggctactat 120
 |||||
 DB 61 tacattgacttcacagagatcgtggctggaagtgggtccatgaacctaaaggctactat 120
 |||||
 QY 121 gccaaacttctgcagggcccttgcacatacctccgagtcagtcagacacacacacagcag 180
 |||||
 DB 121 gccaaacttctgcagggcccttgcacatacctccgagtcagtcagacacacacacagcag 180
 |||||
 QY 181 gtgctggagactgtacacactctgaaccttgaaacctgaagcatctgcctcgtcgtgccc 240
 |||||
 DB 181 gtgctggagactgtacacactctgaaccttgaaacctgaagcatctgcctcgtcgtgccc 240
 |||||
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 |||||
 DB 241 caggacctgagccctgacctgacctgtactatgttggaggagacccccaaagtggagcag 300
 |||||
 QY 301 ctctccaaacatggtggtgaagtctttaaagttagctga 339
 |||||
 DB 301 ctctccaaacatggtggtgaagtctttaaagttagctga 339
 |||||

RESULT 3

AAT17234
 ID AAT17234 standard; cDNA to mRNA; 339 BP.
 XX
 AC
 XX
 AAT17234;

DT 17-JUL-1996 (first entry)

XX Human TGF-beta 3 cDNA.

DE Transforming growth factor type beta; TGF-beta 3;
 KW protein renaturation; protein folding; ds.
 KW
 XX

OS Homo sapiens.

XX

XX WO9603433-A1.

XX PD 08-FEB-1996.

XX PF 12-JUL-1995; 95WO-EP02719.

XX PR 25-JUL-1994; 94EP-0810439.

XX PA (CIBA) CIBA GEIGY AG.

XX PI Cerletti N;

XX DR WPI; 1996-117000/12.

XX DR P-PSDB; AAR92772.

XX Prodn. of dimeric biologically active transforming growth factor -

PT by refolding denatured monomer in detergent-free folding buffer

PT contg. specific organic solvent to improve yield

XX Example 1B; Page 34; 54pp; English.

XX The coding sequence (AAT17234) of human transforming growth factor

CC TGF-beta 3 (AAR92772) was cloned into plasmid pGEM-52F(+) (Promega)

CC and the construct used to transform E. coli Y1090. Subcloning in

CC pPLMu yielded plasmid pPLMu.HTGF-beta 3. Non-soluble, monomeric
 CC TGF-beta 3 was recovered from E. coli LC 137/pPLMu.HTGF-beta 3 (DSM
 CC 5658) transformants. A biologically active, dimeric form of
 CC TGF-beta 3 was obtd. by refolding this monomer in detergent-free
 CC buffer contg. DMSO and/or DMF. Dimers of TGF-beta 1 (AAR92773) and
 CC TGF-beta 2 (AAR92774), and hybrid dimers (see also AAR92775-77), were
 CC also produced.

XX Sequence 339 BP; 74 A; 104 C; 86 G; 75 T; 0 other;
 SQ

Query Match 100.0%; Score 339; DB 17; Length 339;
 Best Local Similarity 100.0%; Pred. No. 3.3e-87;
 Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gcttggacacacaaattactgtctccgcaacttgagagaaactgctgtgccccctc 60
 |||||
 DB 1 gcttggacacacaaattactgtctccgcaacttgagagaaactgctgtgccccctc 60
 |||||
 QY 61 tacattgacttcacagagatcgtggctggaagtgggtccatgaacctaaaggctactat 120
 |||||
 DB 61 tacattgacttcacagagatcgtggctggaagtgggtccatgaacctaaaggctactat 120
 |||||
 QY 121 gccaaacttctgcagggcccttgcacatacctccgagtcagtcagacacacacacagcag 180
 |||||
 DB 121 gccaaacttctgcagggcccttgcacatacctccgagtcagtcagacacacacacagcag 180
 |||||
 QY 181 gtgctggagactgtacacactctgaaccttgaaacctgaagcatctgcctcgtcgtgccc 240
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 DB 181 gtgctggagactgtacacactctgaaccttgaaacctgaagcatctgcctcgtcgtgccc 240
 |||||
 QY 241 caggacctgagccctgacctgacctgtactatgttggaggagacccccaaagtggagcag 300
 |||||
 DB 241 caggacctgagccctgacctgacctgtactatgttggaggagacccccaaagtggagcag 300
 |||||
 QY 301 ctctccaaacatggtggtgaagtctttaaagttagctga 339
 |||||
 DB 301 ctctccaaacatggtggtgaagtctttaaagttagctga 339
 |||||

RESULT 4

AAT15464
 ID AAT15464 standard; cDNA to mRNA; 339 BP.
 XX
 AC
 XX
 AAT15464;

DT 10-JUN-1996 (first entry)

XX Human transforming growth factor beta 3 encoding cDNA.

DE Transforming growth factor beta; TGF; regulator; method;

KW proliferation; differentiation; wound healing; solvent; ds.

KW
 KW
 XX

OS Homo sapiens.

XX

XX Key Location/Qualifiers

FT CDS 1..339

FT /*tag= a

FT /product= human_TGF-beta-3

XX WO9603432-A1.

XX XX 08-FEB-1996.

XX PF 12-JUL-1995; 95WO-EP02718.

XX XX 25-JUL-1994; 94EP-0810438.

XX PA (CIBA) CIBA GEIGY AG.

XX PI Cerletti N;

XX DR WPI; 1996-116999/12.

```

DR P-PSDB; AAR91958.
XX
XX Prodn. of dimeric, biologically active transforming growth factor
PT beta - by refolding denatured monomer in buffer contg. mild
PT detergent and specific organic solvents to improve yields
XX
XX Example 1; Page 36-37; 59pp; English.
XX
XX AAT15462-T15464 encode transforming growth factor (TGF) beta-1,
CC TGF beta-2 and TGF beta-3 which are produced using recombinant
CC DNA technology and used to produce TGF beta-like proteins in
CC dimeric form. The TGF beta-like proteins produced are hybrids of
CC 2 different types of TGF beta e.g. TGF beta-1-3, TGF beta-2-3, etc.,
CC or bone morphogenic proteins e.g. BMP-2. The TGF beta hybrids were
CC made using a new process of producing dimeric, biologically active
CC TGF beta-like proteins. The new process involves treating denatured
CC TGF beta monomers with folding buffer contg. a mild detergent (CHAPS,
CC CHAPSO or digitonin) and at least one of the solvents DMSO (dimethyl
CC sulphoxide), DMSO2 (dimethylsulphone) and DMF (dimethyl formamide).
CC The detergent allows folding of the monomer such that, after
CC dimerisation, the TGF beta-like protein retains biological activity
CC and remains in soluble form. The method allows relatively high yields
CC of biologically active TGF beta-like proteins in their native dimeric
CC form. TGF-beta like proteins are multifunctional regulators of
CC cellular activity and a typical use is to stimulate wound healing.
XX
XX Sequence 339 BP; 74 A; 104 C; 86 G; 75 T; 0 other;
SQ
Query Match 100.0%; Score 339; DB 17; Length 339;
Best Local Similarity 100.0%; Pred. No. 3.3e-87;
Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 gctttggacacaaattactgttcgcgaacttgaggagaactgctgtgccccctc 60
QY 61 tacattgacttcgcagagatctggctggaagtgggtccatgaacctaaagggtactat 120
DB 61 tacattgacttcgcagagatctggctggaagtgggtccatgaacctaaagggtactat 120
QY 121 gccaaactctgctcaggcccttgcccatccctcgcagtcagacacacacacagcag 180
DB 121 gccaaactctgctcaggcccttgcccatccctcgcagtcagacacacacacagcag 180
QY 181 gtgctggagactgtacacactctgaacctctgaagcatctgctcgccttgctgctgcc 240
DB 181 gtgctggagactgtacacactctgaacctctgaagcatctgctcgccttgctgctgcc 240
QY 241 caggaacctggagccctcgaccatctgtactatgttggaggagaccccccaagtgagcag 300
DB 241 caggaacctggagccctcgaccatctgtactatgttggaggagaccccccaagtgagcag 300
QY 301 ctctccaaacatggtggaagtcttggtaaatgtagctga 339
DB 301 ctctccaaacatggtggaagtcttggtaaatgtagctga 339
RESULT 5
AAT80110
ID AAT80110 standard; cDNA to mRNA; 339 BP.
XX
XX AC AAT80110;
XX
XX 28-NOV-1997 (first entry)
XX
XX Mature transforming growth factor beta3 coding sequence.
XX
XX Transforming growth factor beta3; TGF-beta3; human; mature protein;
KW acid-stable; heat-stable; homodimer; mitogenesis; cell proliferation;
KW cell growth; wound; oral mucositis; intestinal mucositis; osteoarthritis;
KW bone disease; bone repair; therapy; ds.
XX

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```

OS Homo sapiens.
XX
XX WO9705166-A1.
XX
XX PD 13-FEB-1997.
XX
XX PF 17-JUL-1996; 96WO-EP03140.
XX
XX PR 25-JUL-1995; 95EP-0810484.
XX
XX PA (CIBA ) CIBA GEIGY AG.
XX
XX PI Arvinte T, Grutter M, Mittl P;
XX
XX DR WPI; 1997-145621/13.
XX
XX P-PSDB; AAW26173.
XX
XX Crystalline form of transforming growth factor beta-3 - useful in
PT compns. as slow release form of TGF, e.g. for wound healing, and
PT for structure determ. in rational drug design
XX
XX Example 1; Page 25-26; 34pp; English.
XX
XX This sequence represents the coding sequence for human transforming
CC growth factor beta3 (TGF-beta3). TGF-beta3 is one of five distinct
CC homodimeric TGFbeta's. TGF-beta3 is an acid-stable and heat-stable
CC disulphide linked homodimer. All the TGF-beta's are produced as 390-412
CC amino acid precursors, which undergo proteolytic cleavage to produce
CC mature forms which consist of the C-terminal 112 amino acids. Depending
CC upon cell and tissue type, and the presence of other growth factors,
CC TGF-beta may either stimulate mitogenesis, cell proliferation and growth,
CC or inhibit these processes. Many of the actions of TGF-beta are related
CC to the response of cells or tissues to stress or injury, and to the
CC repair of resultant damage. A crystalline form of TGF-beta3 can be
CC produced by a method of the invention. Crystalline TGF-beta3 is useful in
CC slow release compositions for treatment of conditions such as wounds,
CC oral or intestinal mucositis, osteoarthritis, bone disease and repair,
CC generally wherever TGF-beta3 is normally used. The crystalline form is
CC also used for structure determination in rational drug design.
CC Crystalline TGF-beta3 shows lower tendency than the dissolved protein to
CC adsorb on the walls of vials and is more stable against oxidation.
CC Variation of the properties, e.g. size, of the crystals allows control
CC over the rate at which active TGF is released in vivo.
XX
XX Sequence 339 BP; 74 A; 104 C; 86 G; 75 T; 0 other;
SQ
Query Match 100.0%; Score 339; DB 18; Length 339;
Best Local Similarity 100.0%; Pred. No. 3.3e-87;
Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 gctttggacacaaattactgttcgcgaacttgaggagaactgctgtgccccctc 60
DB 1 gctttggacacaaattactgttcgcgaacttgaggagaactgctgtgccccctc 60
QY 61 tacattgacttcgcagagatctggctggaagtgggtccatgaacctaaagggtactat 120
DB 61 tacattgacttcgcagagatctggctggaagtgggtccatgaacctaaagggtactat 120
QY 121 gccaaactctgctcaggcccttgcccatccctcgcagtcagacacacacacagcag 180
DB 121 gccaaactctgctcaggcccttgcccatccctcgcagtcagacacacacacagcag 180
QY 181 gtgctgggagactgtacacactctgaacctctgaagcatctgctcgccttgctgctgcc 240
DB 181 gtgctgggagactgtacacactctgaacctctgaagcatctgctcgccttgctgctgcc 240
QY 241 caggaacctggagccctcgaccatctgtactatgttggaggagaccccccaagtgagcag 300
DB 241 caggaacctggagccctcgaccatctgtactatgttggaggagaccccccaagtgagcag 300
QY 301 ctctccaaacatggtggaagtcttggtaaatgtagctga 339
DB 301 ctctccaaacatggtggaagtcttggtaaatgtagctga 339

```

Db 301 ctctccaacatggtggaagtgtttaaagttagctga 339

RESULT 6

AAT42773

ID AAT42773 standard; cDNA; 339 BP.

XX

AC AAT42773;

DT

XX 26-AUG-1997 (first entry)

XX

DE TGF active fragment of a TGF-beta fusion protein encoding cDNA.

XX

KW Transforming growth factor-beta fusion protein; wound healing;

KW artificial skin; surgery recovery time; ss.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT 1..339

FT /*tag= a

FT /function= TGF active fragment

XX

PN W09639430-A1.

XX

PD 12-DEC-1996.

XX

XX 05-JUN-1996; 96WO-US08973.

XX

PR 06-JUN-1995; 95US-0470837.

XX

(CHEU/) CHEUNG D T.

PA

(HALL/) HALL F L.

PA

(NIMN/) NIMNI M E.

PA

(TUAN/) TUAN T.

PA

(WULL/) WU L.

XX

Cheung DT, Hall FL, Nimni ME, Tuan T, Wu L;

PI

WPI: 1997-043065/04.

DR

P-PSDB; AAW08175.

XX

Prepn. of transforming growth factor-beta fusion protein - useful to

PT

reduce surgery recovery time and to prepare artificial skin

PT

Disclosure; Page 48; 59pp; English.

XX

A novel transforming growth factor-beta (TGF-beta) fusion protein comprises a purification tag and a TGF active fragment. The present sequence encodes a specifically claimed TGF active fragment. Additionally, the fusion protein may comprise proteinase-sensitive linker sites and binding domain so the protein sequence may contain some or all of the following elements: purification tag:proteinase site:ECM binding site:proteinase site:TGF-beta. TGF-beta promotes wound healing, and the fusion protein can be used to reduce surgery recovery time and in the preparation of artificial skin. The inclusion of a purification tag facilitates purification of the fusion protein. The proteinase site is included to permit cleavage and release of the purification tag after purification if desired. The extracellular matrix binding site facilitates delivery of the fusion protein to the desired site of action. Delivery of the TGF-beta to the site to be treated reduces the amount of TGF-beta required to be administered to be effective and reduces the concentration of circulating TGF-beta which may result in undesirable effects.

XX

SQ Sequence 339 BP; 74 A; 104 C; 86 G; 75 T; 0 other;

Query Match

Best Local Similarity 100.0%; Score 339; DB 18; Length 339;

Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gctttgacacaaattactgtccgcaacttgaggagaaactgctgtgtgccccctc 60

Db 1 gctttgacacaaattactgtccgcaacttgaggagaaactgctgtgtgccccctc 60
 QY 61 tacattgacttccacagatctggctgggaagtgggtccatgaacctaaaggctactat 120
 Db 61 tacattgacttccgacagatctggctgggaagtgggtccatgaacctaaaggctactat 120
 QY 121 gccaaacttctgtcagggcccttggccatactccgcagtcagagacacacacacagcag 180
 Db 121 gccaaacttctgtcagggcccttggccatactccgcagtcagagacacacacacagcag 180
 QY 181 gtctgggactgtacaacactctgaacctgaagcctgaagcctgtcctgcctgtcgtgcgcc 240
 Db 181 gtctgggactgtacaacactctgaacctgaagcctgtcctgcctgtcgtgcgcc 240
 QY 241 caggacctggagcccttgaccatcctgtactatgttgggagagaccccaagtggagcag 300
 Db 241 caggacctggagcccttgaccatcctgtactatgttgggagagaccccaagtggagcag 300
 QY 301 ctctccaacatggtgtgaagtctttaaatagtactga 339
 Db 301 ctctccaacatggtgtgaagtctttaaatagtactga 339

RESULT 7

AAX15247

ID AAX15247 standard; cDNA; 339 BP.

XX

AC AAX15247;

XX

DT 28-APR-1999 (first entry)

XX

DE cDNA encoding the mature form of transforming growth factor-beta-3.

XX

KW Transforming growth factor-beta-3; TGF-beta-like protein;

KW S-sulphonated TGF-beta-like protein; wound treatment; cancer;

KW bone repair; tissue repair; bone marrow protective agent;

KW cardioprotection; anti-inflammatory; immunosuppressive;

KW ulcer; bed sore; ds.

XX

OS Homo sapiens.

XX

PN EP891985-A1.

XX

PD 20-JAN-1999.

XX

PF 27-NOV-1990; 90EP-0810922.

XX

PR 06-DEC-1989; 89GB-0027546.

XX

PA (NOVS) NOVARTIS AG.

XX

PI Cerletti N, Cox D, McMaster GK, Meyhack B, Schmitz A;

XX

XX WPI: 1999-083520/08.

XX

DR P-PSDB; AAW97093.

XX

PT Producing biologically active dimeric Transforming Growth

PT Factor-beta - by refolding new monomeric Transforming Growth

PT Factor-beta, useful for treatment of wounds and cancer

XX

PS Example 1; Page 30; 32pp; English.

XX

The present sequence encodes the mature form of transforming growth factor-beta-3. Dimeric, biologically active TGF-beta-like protein can be produced by subjecting the denatured monomeric form to refolding conditions. The new monomeric S-sulphonated TGF-beta-like protein is useful for the production of the dimeric, biologically active TGF-beta-like protein, which is useful for the treatment of wounds (surface or internal) and cancer in a mammal, in bone and tissue repair, as a bone marrow protective agent, a mediator of cardioprotection, for the production of an anti-inflammatory or immunosuppressive preparation. Treatment is useful for animals,

CC especially humans, and wound treatment (e.g. ulcers, bed sores etc.) is
 CC particularly useful for the elderly.

XX Sequence 339 BP; 74 A; 104 C; 86 G; 75 T; 0 other;

Query Match 100.0%; Score 339; DB 20; Length 339;
 Best Local Similarity 100.0%; Pred. No. 3.3e-87;
 Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gcttggacacaaattactgcttcgcgaacttggagagaactgctgtgtgcgccccctc 60
 DB 1 gcttggacacaaattactgcttcgcgaacttggagagaactgctgtgtgcgccccctc 60

QY 61 tacattgacttcgcagagatctgggtggaagtgggtccatgaacctaaagggtactat 120
 DB 61 tacattgacttcgcagagatctgggtggaagtgggtccatgaacctaaagggtactat 120

QY 121 gcaacttctgtaggccttgccatcctccagctgcagtgagacacacccacagcag 180
 DB 121 gcaacttctgtaggccttgccatcctccagctgcagtgagacacacccacagcag 180

QY 181 gtgctggagactgtacacactctgaacctgaagcatctgcctcgctgtgctgccc 240
 DB 181 gtgctggagactgtacacactctgaacctgaagcatctgcctcgctgtgctgccc 240

QY 241 caggacctggagccctgacctctgtactatgttggagagaccccaagtgagagcag 300
 DB 241 caggacctggagccctgacctctgtactatgttggagagaccccaagtgagagcag 300

QY 301 ctctccacatggtggaagtctgttaaatgtagtga 339
 DB 301 ctctccacatggtggaagtctgttaaatgtagtga 339

RESULT 8

AAV99377
 ID AAV99377 standard; cDNA; 339 BP.

AC AAV99377;

XX 25-MAR-1999 (first entry)

DT cDNA encoding a transforming growth factor beta active fragment.

DE Proteinase site; bone morphogenetic fusion protein; bone binding site;
 KW bone morphogenetic protein; transforming growth factor beta;
 KW active fragment; wound healing; bone growth; purification tag; ds.

XX Homo sapiens.

XX WO9855137-A1.

XX 10-DEC-1998.

XX 02-JUN-1998; 98WO-US11189.

XX 03-JUN-1997; 97US-0868452.

XX (HALL/) HALL F L.

XX (HAMB/) HAN B.

XX (NIMN/) NIMNI M E.

XX (SHOR/) SHORS E C.

XX (WULL/) WU L.

XX Hall FL, Han B, Nimni ME, Shors EC, Wu L;

XX WPI; 1999-059875/05.

XX P-PSDB; AAW84209.

XX New bone morphogenetic fusion proteins - comprising a purification
 PT tag and a bone morphogenetic active fragment, used for enhancing
 PT wound healing or bone growth

XX
 PS

XX Disclosure; Page 43; 64pp; English.

CC The present sequence encodes a transforming growth factor beta active
 CC fragment. The protein can be used in place of a bone morphogenetic
 CC active fragment to create the fusion proteins of the invention. When a
 CC bone morphogenetic active fragment is used, the fusion proteins are
 CC designated bone morphogenetic fusion proteins. The bone morphogenetic
 CC fusion protein may contain some or all of the following elements: a
 CC purification tag, a proteinase site, an ECM/bone binding site, a second
 CC proteinase site, and a bone morphogenetic protein active fragment.
 CC The bone morphogenetic fusion proteins can be used for enhancing wound
 CC healing or bone growth.

XX Sequence 339 BP; 74 A; 104 C; 86 G; 75 T; 0 other;

Query Match 100.0%; Score 339; DB 20; Length 339;
 Best Local Similarity 100.0%; Pred. No. 3.3e-87;
 Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gcttggacacaaattactgcttcgcgaacttggagagaactgctgtgtgcgccccctc 60
 DB 1 gcttggacacaaattactgcttcgcgaacttggagagaactgctgtgtgcgccccctc 60

QY 61 tacattgacttcgcagagatctgggtggaagtgggtccatgaacctaaagggtactat 120
 DB 61 tacattgacttcgcagagatctgggtggaagtgggtccatgaacctaaagggtactat 120

QY 121 gcaacttctgtaggccttgccatcctccagctgcagtgagacacacccacagcag 180
 DB 121 gcaacttctgtaggccttgccatcctccagctgcagtgagacacacccacagcag 180

QY 181 gtgctggagactgtacacactctgaacctgaagcatctgcctcgctgtgctgccc 240
 DB 181 gtgctggagactgtacacactctgaacctgaagcatctgcctcgctgtgctgccc 240

QY 241 caggacctggagccctgacctctgtactatgttggagagaccccaagtgagagcag 300
 DB 241 caggacctggagccctgacctctgtactatgttggagagaccccaagtgagagcag 300

QY 301 ctctccacatggtggaagtctgttaaatgtagtga 339
 DB 301 ctctccacatggtggaagtctgttaaatgtagtga 339

RESULT 9

AAQ05774

ID AAQ05774 standard; cDNA; 609 BP.

XX AAQ05774;

XX 03-JAN-1991 (first entry)

DT Sequence encoding protein with tumour growth inhibitory activity.

DE Cancer; carcinoma; melanoma; leukaemia; arteriosclerosis; psoriasis;
 KW TGF-alpha; ds;

XX Homo sapiens.

XX EP384494-A.

XX 29-AUG-1990.

XX 20-OCT-1987; 87EP-0106772.

XX 01-JAN-1990; 90EP-0106772.

XX 20-OCT-1986; 86US-0922121.

XX (ONCO-) ONCOGENE SCI INC.

XX Iwata KK, Stephenson JR, Gold LI;

```

XX WPI; 1990-262507/35.
DR P-PSDB; AAR06548.
XX
XX Tissue-derived tumour growth inhibitors - used in diagnosis and
PT treatment of tumours and treatment of proliferative type
PT disorders, burns and wounds
XX
XX Disclosure; Fig 29; 81pp; English.
XX
XX Gene product may be used to inhibit growth of tumour cells, to
CC treat proliferative type disorders, burns and other wounds, and may
CC also be used as an immune modulator. Detection of proteins and of
CC TGF-alpha can indicate presence of a tumour.
CC Proteins may be produced from a bacterial or eukaryotic expression
CC system.
XX
XX Sequence 609 BP; 154 A; 172 C; 158 G; 125 T; 0 other;
SQ

```

Query Match 100.0%; Score 339; DB 11; Length 609;
Best Local Similarity 100.0%; Pred. No. 3.8e-87;
Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy 1 gctttgacacccaattactcttcgcgaacttgagagagaactgtgtgccccctc 60
Db 271 gctttgacacccaattactcttcgcgaacttgagagagaactgtgtgccccctc 330
Qy 61 tacattgacttcgcagagatcggctggaagtgggtccatgaacctaaaggtactat 120
Db 331 tacattgacttcgcagagatcggctggaagtgggtccatgaacctaaaggtactat 390
Qy 121 gccaaactctgtcagggcccttgccatactccgaactcgcagtcagacacacccagcacg 180
Db 391 gccaaactctgtcagggcccttgccatactccgaactcgcagtcagacacacccagcacg 450
Qy 181 gtctgggactgtacaacactctgaacctgaacctgaagcatctgcctgcctgtgctgccc 240
Db 451 gtctgggactgtacaacactctgaacctgaacctgaagcatctgcctgcctgtgctgccc 510
Qy 241 caggacctggagccctgacactcctgtactatgttggaggagaccccccaagtggagcag 300
Db 511 caggacctggagccctgacactcctgtactatgttggaggagaccccccaagtggagcag 570
Qy 301 ctctcaacatgtgtggaagtcttgaatgtagctga 339
Db 571 ctctcaacatgtgtggaagtcttgaatgtagctga 609

```

RESULT 10
AAQ20576
ID AAQ20576 standard; cDNA; 2529 BP.
XX AC AAQ20576;
XX
XX 05-MAY-1992 (first entry)
XX
XX Transforming Growth Factor beta 3 coding sequence.
DE
XX TGF-beta 3; homodimer; ss.
XX
XX Synthetic.
XX
XX W09200318-A.
XX
XX 09-JAN-1992.
XX
XX 25-JUN-1991; 91WO-US04541.
XX
XX 25-JUN-1990; 90US-0543348.
XX
XX (ONCO-) ONCOGENE SCI INC.
XX

```

PI Iwata KK, Foulkes JG, Tendijke P, Haley JD;
XX WPI; 1992-041510/05.
DR P-PSDB; AAR20621.
XX
XX Transforming growth factor beta 3 proteins, precursors and
PT mutants - obt'd. from polypeptide and antibodies, with optimal
PT therapeutic use due to genetic manipulation of coding sequence
XX
XX Example 2; Fig 1; 107pp; English.
XX
XX This 2529bp full-length TGF-beta3 gene sequence was obtained from
CC three shorter overlapping clones derived from human placental, human
CC umbilical cord and A673 cells cDNA libraries, respectively. The
CC predicted amino acid sequence of the gene encoding TGF-beta3 shows
CC extensive homology to TGF-beta 1 and beta 2.
CC See also AAQ22229 and AAR20622.
XX
XX Sequence 2529 BP; 617 A; 670 C; 661 G; 581 T; 0 other;
SQ

```

Query Match 100.0%; Score 339; DB 13; Length 2529;
Best Local Similarity 100.0%; Pred. No. 5.5e-87;
Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy 1 gctttgacacccaattactcttcgcgaacttgagagagaactgtgtgccccctc 60
Db 1163 gctttgacacccaattactcttcgcgaacttgagagagaactgtgtgccccctc 1222
Qy 61 tacattgacttcgcagagatcgtggctggaagtgggtccatgaacctaaaggtactat 120
Db 1223 tacattgacttcgcagagatcgtggctggaagtgggtccatgaacctaaaggtactat 1282
Qy 121 gccaaactctcagggcccttgccatactccgaactcgcagtcagacacacccagcacg 180
Db 1283 gccaaactctcagggcccttgccatactccgaactcgcagtcagacacacccagcacg 1342
Qy 181 gtctgggactgtacaacactctgaacctgaacctgaagcatctgcctgcctgtgctgccc 240
Db 1343 gtctgggactgtacaacactctgaacctgaacctgaagcatctgcctgcctgtgctgccc 1402
Qy 241 caggacctggagccctgacactcctgtactatgttggaggagaccccccaagtggagcag 300
Db 1403 caggacctggagccctgacactcctgtactatgttggaggagaccccccaagtggagcag 1462
Qy 301 ctctcaacatgtgtggaagtcttgaatgttagctga 339
Db 1463 ctctcaacatgtgtggaagtcttgaatgttagctga 1501

```

RESULT 11
AAV63209
ID AAV63209 standard; DNA; 2574 BP.
XX AC AAV63209;
XX
XX 14-JAN-1999 (first entry)
XX
XX Nucleic acid sequence of human transforming growth factor-beta 3.
DE
XX Human transforming growth factor-beta 3; TGF-beta3; oxygen tension;
KW trophoblast invasion regulation; inhibitor; HIF-1 alpha;
KW TGF-beta family cytokine receptor; hypoxia inducible factor 1 alpha;
KW preeclampsia; pregnancy; choriocarcinoma; ss.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH CDS 254..1492
FT /*tag= a
FT /product= TGF-beta3
XX
XX W09840747-A1.
XX

```

XX PD 17-SEP-1998.
XX PF 05-MAR-1998; 98WO-CA00180.
XX PR 07-MAR-1997; 97US-0039919.
XX PA (HOSP-) HOSPITAL FOR SICK CHILDREN.
XX PA (MOUN ) MOUNT SINAI HOSPITAL CORP.
XX PI Caniggia I, Lye S, Post M;
XX PR WPI; 1998-520837/44.
XX DR P-PSDB; AAW80417.
XX PT Regulation of trophoblast invasion - by, e.g. transforming growth
XX PT factor-beta3 inhibitor, useful for detecting or treating
XX PT preeclampsia in pregnant women
XX PS Disclosure; Fig 1; 59pp; English.
XX CC The present sequence encodes human transforming growth factor-beta 3
XX CC (TGF-beta3). The specification describes a composition for regulating
XX CC trophoblast invasion which comprises an inhibitor of TGF-beta3,
XX CC TGF-beta family cytokine receptors, hypoxia inducible factor 1 alpha
XX CC (HIF-1 alpha) or oxygen tension. The composition is used in methods of
XX CC diagnosing, monitoring, preventing or treating conditions requiring
XX CC regulation of trophoblast invasion, especially preeclampsia in pregnant
XX CC women or choriocarcinomas.
XX SQ Sequence 2574 BP; 629 A; 680 C; 666 G; 599 T; 0 other;

Query Match 100.0%; Score 339; DB 19; Length 2574;
Best Local Similarity 100.0%; Pred. No. 5.5e-87;
Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gctttggacacaaattactgtctccgcaacttgaggagaaactgtgtgccccctc 60
DB 1154 gctttggacacaaattactgtctccgcaacttgaggagaaactgtgtgccccctc 1213
QY 61 tacattgacttcgacagagatctgggtggaagtgggtccatgaacctaaagggtactat 120
DB 1214 tacattgacttcgacagagatctgggtggaagtgggtccatgaacctaaagggtactat 1273
QY 121 gccaaactctcagcccttgccatacctccagcagtcagacacacacacagcagc 180
DB 1274 gccaaactctcagcccttgccatacctccagcagtcagacacacacacagcagc 1333
QY 181 gtgctgggactgtacaacactctgaacctgaagcatctgctccttgcgtgccc 240
DB 1334 gtgctgggactgtacaacactctgaacctgaagcatctgctccttgcgtgccc 1393
QY 241 caggacctggagccctgacctatctgtactatgtttggaggaccccccaagtggagcag 300
DB 1394 caggacctggagccctgacctatctgtactatgtttggaggaccccccaagtggagcag 1453
QY 301 ctctccacatggtggtgaagtcttgaatgtactga 339
DB 1454 ctctccacatggtggtgaagtcttgaatgtactga 1492

RESULT 12
AAQ56926
ID AAQ56926 standard; cDNA; 2157 BP.
XX AC AAQ56926;
XX AC
XX DT 09-JUL-1994 (first entry)
XX DE Human TGF-beta-3.
XX KW TGF-beta-1; TGF-beta-2; transforming growth factor beta-1;

```

```

KW transforming growth factor beta-3; recombinant; wound healing;
XX vulnerable; ss.
XX OS Homo sapiens.
XX PN US5284763-A.
XX PD 08-FEB-1994.
XX PF 22-MAR-1985; 85US-0715142.
XX PR 22-MAR-1985; 85US-0715142.
XX PR 13-MAR-1987; 87US-0025423.
XX PR 04-AUG-1989; 89US-0389929.
XX PR 04-MAR-1992; 92US-0845893.
XX PA (GETH ) GENENTECH INC.
XX PI Derynk RMA, Goeddel DV;
XX DR WPI; 1994-056343/07.
XX DR P-PSDB; AAR46229.
XX PT Nucleic acid sequences encoding transforming growth factor-beta -
XX PT diagnostic probes, and for use in therapeutics
XX PS Disclosure; Fig 4a-c; 25pp; English.
XX CC cDNA sequences were determined for human pre-TGF-beta-1 (AAQ56923),
XX CC pig TGF-beta-3 (AAQ56925) and human TGF-beta-3 (AAQ56926), and the
XX CC corresponding amino acid sequences were determined (AAR46227-29,
XX CC respectively). A genomic fragment corresponding to a human TGF-
XX CC beta-1 exon (AAQ56924) was also isolated and its amino acid sequence
XX CC determined (AAR46230). The sequences have been used in the
XX CC construction of vectors for the expression of recombinant TGF-
XX CC beta.
XX SQ Sequence 2157 BP; 621 A; 462 C; 492 G; 582 T; 0 other;

Query Match 99.5%; Score 337.4; DB 15; Length 2157;
Best Local Similarity 99.7%; Pred. No. 1.5e-86;
Matches 338; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 gctttggacacaaattactgtctccgcaacttgaggagaaactgtgtgccccctc 60
DB 278 gctttggacacaaattactgtctccgcaacttgaggagaaactgtgtgccccctc 337
QY 61 tacattgacttcgacagagatctgggtggaagtgggtccatgaacctaaagggtactat 120
DB 338 tacattgacttcgacagagatctgggtggaagtgggtccatgaacctaaagggtactat 397
QY 121 gccaaactctcagcccttgccatacctccagtcagacacacacacagcagc 180
DB 398 gccaaactctcagcccttgccatacctccagtcagacacacacacagcagc 457
QY 181 gtgctgggactgtacaacactctgaacctgaagcatctgctcctgctgctgccc 240
DB 458 gtgctgggactgtacaacactctgaacctgaagcatctgctcctgctgctgccc 517
QY 241 caggacctggagccctgacctatctgtactatgtttggaggaccccccaagtggagcag 300
DB 518 caggacctggagccctgacctatctgtactatgtttggaggaccccccaagtggagcag 577
QY 301 ctctccacatggtggtgaagtcttgaatgtactga 339
DB 578 ctctccacatggtggtgaagtcttgaatgtactga 616

RESULT 13
AAV52935
ID AAV52935 standard; cDNA; 2157 BP.
XX

```

AC AAV52935;
 XX 21-DEC-1998 (first entry)
 XX Human transforming growth factor-beta 3 cDNA.
 XX Transforming growth factor-beta 3; TGF-beta 3; human; ss.
 XX Homo sapiens.
 OS
 XX
 FH Key Location/Qualifiers
 FT CDS 2..616
 FT /*tag= a
 FT /transl_except= (pos:50..52, aa:Thr)
 XX
 XX
 PN US5801231-A.
 XX
 PD 01-SEP-1998.
 XX
 PF 22-MAR-1985; 85US-0715142.
 XX
 PR 13-MAR-1987; 87US-0025423.
 PR 22-MAR-1985; 85US-0715142.
 PR 04-AUG-1989; 89US-0389929.
 PR 04-MAR-1992; 92US-0845893.
 PR 05-NOV-1993; 93US-0147364.
 PR 30-MAY-1995; 95US-0454468.
 XX
 XX (GETH) GENENTECH INC.
 XX
 XX Derynck RMA, Goeddel DV;
 PI
 DR WPI; 1998-494840/42.
 DR P-PSDB; AAW78787.
 XX
 XX DNA encoding transforming growth factor-beta precursor sequence -
 PT useful for analysis to perform manipulations to increase yield of
 PT recombinant production of the protein
 XX
 PS Example 6; Fig 4a-c; 26pp; English.
 XX
 CC This nucleotide sequence, hu4, codes for a human partial
 CC transforming growth factor-beta 3 (TGF-beta 3) sequence including
 CC all of the mature sequence. Clone hu4 was isolated from a human
 CC ovarian cDNA library using porcine TGF-beta 3 cDNA (see AAV52934)
 CC as probe. The invention relates to the recombinant production of
 CC TGF-beta. Biologically active TGF-beta is defined as being capable
 CC of inducing EGF-potential anchorage independent growth of target
 CC cell lines and/or growth inhibition of neoplastic cell lines.
 CC Nucleic acids encoding TGF-beta have been isolated and cloned into
 CC vectors which are replicated in bacteria and expressed in
 CC eukaryotic cells. TGF-beta recovered from transformed cells is
 CC used in known therapeutic applications. TGF-beta nucleic acids are
 CC also useful in diagnosis and identification of TGF-beta clones.
 XX
 SQ Sequence 2157 BP; 621 A; 462 C; 492 G; 582 T; 0 other;

Query Match 99.5%; Score 337.4; DB 19; Length 2157;
 Best Local Similarity 99.7%; Pred. No. 1.5e-86;
 Matches 338; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 gctttggacacaaattactgcttcgcgaacttggaggagaactgctgtgccccctc 60
 DB 278 gctttggacacaaattactgcttcgcgaacttggaggagaactgctgtgccccctc 337
 QY 61 tacattgacttcgcacaggaatcggctggaagtgggtccatgaacctaaagggtactat 120
 DB 338 tacattgacttcgcacaggaatcggctggaagtgggtccatgaacctaaagggtactat 397
 QY 121 gccaaacttctgctcaggcccttgcccatacctccgcagtcagtcagacacacccacagcag 180
 DB 398 gccaaacttctgctcaggcccttgcccatacctccgcagtcagtcagacacacccacagcag 457

QY 181 gtctgggactgtacaaactctgaacctgaagcatctgctgcctgctgtgctgccc 240
 DB 458 gtctgggactgtacaaactctgaacctgaagcatctgctgcctgctgtgctgccc 517
 QY 241 caggacctggagccctgacacatcctgtactatctgtgggagagaccccaagtggagcag 300
 DB 518 caggacctggagccctgacacatcctgtactatctgtgggagagaccccaagtggagcag 577
 QY 301 ctctcaacatggtgggaagtctttaaattgaactga 339
 DB 578 ctctcaacatggtgggaagtctttaaattgaactga 616
 RESULT 14
 AAQ02820
 ID AAQ02820 standard; DNA; 2158 BP.
 XX
 AC AAQ02820;
 XX
 DT 31-MAY-1989 (first entry)
 XX
 DE cDNA sequence encoding human TGF-beta 3.
 XX
 KW Transforming growth factor beta-3 (TGF beta 3); tumour cells; growth
 KW inhibition.
 XX
 PN W08912101-A.
 XX
 PD 14-DEC-1989.
 XX
 PF 08-JUN-1988; 88WO-US01945.
 XX
 PR 08-JUN-1988; 88WO-U001945.
 XX
 XX (GETH) GENENTECH INC.
 PA
 PI Derynck RM, Goeddel DV;
 XX
 DR WPI; 1990-007474/01.
 XX
 PT Nucleotide sequence encoding transforming growth factor beta-3 -used as a
 PT probe, or to produce TGF beta 3, for inhibition of growth of normal
 PT and neoplastic cells, eg A549.
 XX
 PS Disclosure; Fig. 4; 61pp; English.
 XX
 CC This sequence encodes human transforming growth factor-beta 3 (TGF-
 CC beta 3) polypeptide. The nucleic acid sequence encoding this subtype is
 CC useful as a probe or to produce TGF-beta 3 for both normal and neoplastic
 CC cell growth inhibition.
 XX
 SQ Sequence 2158 BP; 621 A; 462 C; 493 G; 582 T; 0 other;

Query Match 99.5%; Score 337.4; DB 11; Length 2158;
 Best Local Similarity 99.7%; Pred. No. 1.5e-86;
 Matches 338; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 gctttggacacaaattactgcttcgcgaacttggaggagaactgctgtgccccctc 60
 DB 278 gctttggacacaaattactgcttcgcgaacttggaggagaactgctgtgccccctc 337
 QY 61 tacattgacttcgcacaggaatcggctggaagtgggtccatgaacctaaagggtactat 120
 DB 338 tacattgacttcgcacaggaatcggctggaagtgggtccatgaacctaaagggtactat 397
 QY 121 gccaaacttctgctcaggcccttgcccatacctccgcagtcagtcagacacacccacagcag 180
 DB 398 gccaaacttctgctcaggcccttgcccatacctccgcagtcagtcagacacacccacagcag 457
 QY 181 gtctgggactgtacaaactctgaacctgaagcatctgctgcctgctgtgctgccc 240
 DB 458 gtctgggactgtacaaactctgaacctgaagcatctgctgcctgctgtgctgccc 517

Db 458 gtgtgggactgtacaacactctgaacctgaagcatctgctcgcttgcctgcatgcc 517
 Qy 241 cagacactggagccctgacctctgactatgtgtggagagaccocccaaaagtggagcag 300
 Db 518 caggacctggagccctgacctctgactatgtgtggagagaccocccaaaagtggagcag 577
 Qy 301 ctctccaacatgggtgaagtcttctgtaaatgtagctga 339
 Db 578 ctctccaacatgggtgaagtcttctgtaaatgtagctga 616

RESULT 15
 ID AAQ22229 standard; cDNA; 1239 BP.
 XX AC AAQ22229;
 XX DT 05-MAY-1992 (first entry)
 XX DE Mutant transforming growth factor beta 3 coding sequence.
 XX KW TGF-beta 3; homodimer; ss.
 XX OS Synthetic.
 FH Key Location/Qualifiers
 FT misc_feature 1..888
 FT FT /*tag= a
 FT /*note= "nucleotides 263-1150 of TGF-beta3"
 FT misc_feature 889..903
 FT FT /*tag= b
 FT /*note= "encodes Factor Xa cleavage site
 FT followed by a methionine residue"
 FT misc_feature 904..1212
 FT FT /*tag= c
 FT /*note= "nucleotides 1163-1471 of TGF-beta3"
 FT misc_difference 1213..1215
 FT FT /*tag= d
 FT /*note= "wild-type codon = ATG. May be replaced by
 FT any other codon to give mutant sequence"
 FT misc_feature 1216..1239
 FT FT /*tag= e
 FT /*note= "nucleotides 1475-1498 of TGF-beta3"
 XX WO9200318-A.
 XX 09-JAN-1992.
 XX 25-JUN-1991; 91WO-US04541.
 XX 25-JUN-1990; 90US-0543348.
 XX (ONCO-) ONCOGENE SCI INC.
 PI Iwata KK, Foulkes JG, Tendijke P, Haley JD;
 XX WPI; 1992-041510/05.
 DR P-PSDB; AAR22038.
 XX Transforming growth factor beta 3 proteins, precursors and
 PT mutants - obt'd. from polypeptide and antibodies, with optimal
 PT therapeutic use due to genetic manipulation of coding sequence
 XX Claim 12; Page 66; 107pp; English.
 XX This sequence has been compiled from the description of a mutant TGF-
 CC beta3 contained in the claims. The sequence coding for the Factor Xa
 CC cleavage site may be replaced by one encoding a similar protease
 CC recognition site, e.g. for collagenase. The coding sequence may
 CC also include a region encoding a hydrophobic transmembrane amino
 CC acid sequence, e.g. from c-erbB2 cDNA and a "stop transfer"
 CC sequence. The protease recognition site is located between the
 CC C-terminal of the transmembrane region and the N-terminal of the

CC TGF-beta 3 precursor. Mature TGF-beta 3 can then be efficiently
 CC cleaved from the membrane. See also AAQ20576 and AAR20622.
 XX Sequence 1239 BP; 308 A; 348 C; 328 G; 248 T; 7 other;
 SQ

Query Match 98.2%; Score 333; DB 13; Length 1239;
 Best Local Similarity 99.1%; Pred. No. 2.3e-85;
 Matches 333; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 gcttggacaccaaattactgtctccgaacttggagagaaactgtgtgccccctc 60
 Db 904 gcttggacaccaaattactgtctccgaacttggagagaaactgtgtgccccctc 963
 Qy 61 tacattgacttccgacagatctcggctggaagtgggtccatgaacctaaagggtactat 120
 Db 964 tacattgacttccgacagatctcggctggaagtgggtccatgaacctaaagggtactat 1023
 Qy 121 gcaacttctgcagggcccttgcccatcctccgcagtcgacagacacacccagcacg 180
 Db 1024 gcaacttctgcagggcccttgcccatcctccgcagtcgacagacacacccagcacg 1083
 Qy 181 gtgctggagactgtacaacactctgaacctgaagcatctgcctcgcttgcgtgcgcc 240
 Db 1084 gtgctggagactgtacaacactctgaacctgaagcatctgcctcgcttgcgtgcgcc 1143
 Qy 241 caggacctggagccctgacctctgtactatgttgggagagaccccaagtgagagcag 300
 Db 1144 caggacctggagccctgacctctgtactatgttgggagagaccccaagtgagagcag 1203
 Qy 301 ctctccaacatgggtggaagtcttctgtaaatgtagc 336
 Db 1204 ctctccaacnnngtggtagcttctgtaaatgtagc 1239

RESULT 16
 AAQ06496
 ID AAQ06496 standard; cDNA; 498 BP.
 XX AC AAQ06496;
 XX DT 12-JUN-1996 (first entry)
 XX DE Tissue-derived tumour growth inhibitor-1 coding sequence.
 KW Tumour growth inhibitor; carcinoma; melanoma; leukaemia;
 KW arteriosclerosis; inflammation; psoriasis; therapy; vulneryary;
 KW immunomodulator; ss.
 XX OS Homo sapiens.
 FH Key Location/Qualifiers
 FT CDS 1..498
 FT FT /*tag= a
 FT /*product= tumour_growth_inhibitor_precursor
 FT /*note= "see AAR86771"
 FT misc_feature 159..160
 FT FT /*tag= b
 FT /*note= "the codons at positions -40 to -1 (i.e. 117
 FT nucleotides) are not given in the
 FT specification"
 FT mat_peptide 160..495
 FT FT /*tag= c
 FT /*product= mature_tumour_growth_inhibitor
 FT /*note= "see AAR86770"
 XX EP684260-A2.
 XX PN 29-NOV-1995.
 XX PD 20-OCT-1987; 87EP-0109866.
 XX PF 20-OCT-1986; 86US-0922121.
 XX PR

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XX PA (ONCO-) ONCOGENE SCI INC.
XX PI Gold LI, Iwata KK, Stephenson JR;
XX DR WPI; 1996-000991/01.
XX DR P-PSDB; AAR86770, AAR86771.
XX XX
XX PT Tissue-derived growth inhibitor and corresponding genes - useful for
XX PT detection of tumours, inhibition of tumour growth, treatment of
XX PT proliferative disorders and healing of burns and wounds.
XX PS Claim 6; Fig 29; 83pp; English.
XX CC The sequence encodes a 112 amino acid tumor growth inhibitor (TGI)
XX CC (AAR86770) or a 205 precursor TGI (AAR86771) comprising TGI with an
XX CC additional 93 amino acid residues at the N-terminus. However, the
XX CC nucleotides representing codons -40 to -1 of the precursor TGI are
XX CC not specified in Figure 29, i.e. the cDNA is 498 nucleotides in
XX CC length, but should be 615 nucleotides long. The DNA is used to
XX CC produce the inhibitors by recombinant methods i.e. vector
XX CC expression in bacterium or eukaryotic host cells. The proteins can
XX CC be used to inhibit the growth of human tumour cells, e.g.
XX CC carcinoma, melanoma or leukaemia cells, in the treatment of
XX CC proliferative disorders e.g. arteriosclerosis, inflammation and
XX CC psoriasis, or for the treatment of burns to facilitate wound
XX CC healing. They can also be used as immunomodulators. Although the
XX CC proteins have tumour growth inhibitory activity, they are not
XX CC transforming growth factor-beta-1 or -beta-2.
XX SQ Sequence 498 BP; 122 A; 136 C; 129 G; 111 T; 0 other;

Query Match          98.1%; Score 332.6; DB 17; Length 498;
Best Local Similarity 98.8%; Pred. No. 2.4e-85;
Matches 335; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 gcttggacaccaattactgtctccgcaacttgaggaggaactgtgtgccccctc 60
   |||||||
Db 160 gcttggacaccaattactgtctccgcaacttgaggaggaactgtgtgccccctc 219

QY 61 tacattgacttcgcagagatctgggtggaagtgggtcccatgaacctaaagggtactat 120
   |||||||
Db 220 tacattgacttcgcagagatctgggtggaagtgggtcccatgaacctaaagggtactat 279

QY 121 gcaacttctgtcaggcccttgccatacctcgcgaagtgcagacacacacacagcag 180
   |||||||
Db 280 gcaacttctgtcaggcccttgccatacctcgcgaagtgcagacacacacacagcag 339

QY 181 gtgtgggactgtacaacactctgaaccttgagcatctgctcgtcgtgccc 240
   |||||||
Db 340 gtgtgggactgtacaacactctgaaccttgagcatctgctcgtcgtgccc 399

QY 241 caggacctgagccctgacctctgtactatgttggaggagaccccaagtggagcag 300
   |||||||
Db 400 caggacctgagccctgacctctgtactatgttggaggagaccccaagtggagcag 459

QY 301 ctctcaacatgggtgagttgttaattgtactga 339
   |||||||
Db 460 ctctcaacatgggtgagttgttaattgtactga 498

RESULT 17
AAQ06845
ID AAQ06845 standard; cDNA; 2530 BP.
XX AC
XX AC AAQ06845;
XX DT 05-MAR-1991 (first entry)
XX XX
XX DE Sequence encoding tumour growth inhibitor.
XX XX
XX KW TGI; carcinoma; melanoma; leukaemia; arteriosclerosis; inflammation;

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KW XX psoriasis; ss.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT CDS 263..1501
XX FT /tag= a
XX FT polyA_signal 2506..2511
XX FT /tag= b
XX FT polyA_site 2529
XX FT /tag= c
XX PN W09014360-A.
XX PD 29-NOV-1990.
XX PF 17-MAY-1990; 90WO-US02753.
XX PR 17-MAY-1989; 89US-0353410.
XX PR 19-APR-1985; 85US-0725003.
XX PR 07-APR-1986; 86US-0847931.
XX PR 20-OCT-1986; 86US-0992121.
XX PR 20-OCT-1987; 87US-0111022.
XX PR 20-APR-1988; 88US-0183224.
XX PA (ONCO-) ONCOGENE SCI INC.
XX XX Iwata KK, Stephenson JR, Tendijke P, Franco R, Gold LI, Foulkes JG;
XX DR WPI; 1990-375949/50.
XX DR P-PSDB; AAR08264.
XX PT Tissue-derived tumour growth inhibitors - comprise specified
XX PT protein sequences used to detect, and treat tumours, burns and
XX PT wounds.
XX PS Claim 10; Fig 41; 190pp; English.
XX XX The plasmid was isolated from a human cDNA library prepd. from the
XX CC DNA of a chronic myelocytic leukaemia cell line (K562). The
XX CC sequence can be used to produce the tumour growth inhibitor (TGI)
XX CC by recombinant techniques. The protein may also be isolated from
XX CC human umbilical cord and placental tissues. It can be used to
XX CC inhibit tumour cell growth, to treat burns, to facilitate the
XX CC healing of wounds or to treat proliferative disorders. The
XX CC protein and Abs raised to it can be used for detection and typing
XX CC of tumours. The Abs can also be used to inhibit the activity of
XX CC the TGI.
XX SQ Sequence 2530 BP; 619 A; 671 C; 659 G; 581 T; 0 other;

Query Match          96.2%; Score 326.2; DB 11; Length 2530;
Best Local Similarity 97.6%; Pred. No. 2.4e-83;
Matches 331; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 gcttggacaccaattactgtctccgcaacttgaggaggaactgtgtgccccctc 60
   |||||||
Db 1163 gcttggacaccaattactgtctccgcaacttgaggaggaactgtgtgccccctc 1222

QY 61 tacattgacttcgcagagatctgggtggaagtgggtccatgaacctaaagggtactat 120
   |||||||
Db 1223 tacattgacttcgcagagatctgggtggaagtgggtccatgaacctaaagggtactat 1282

QY 121 gccaaacttctgtcaggcccttgccatacctcccgagtgccagacacacacacagcag 180
   |||||||
Db 1283 gccaaacttctgtcaggcccttgccatacctcccgagtgccagacacacacacagcag 1342

QY 181 gtgtgggactgtacaacactctgaaccttgaaacctgaagcatctgcctgtgctgccc 240
   |||||||
Db 1343 gtgtgggactgtacaacactctgaaccttgaaacctgaagcatctgcctgtgctgccc 1402

QY 241 caggacctgagccctgacctctgtactatgttggaggagaccccaagtggagcag 300

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Db 1403 caggacctggagcccttgaccatctgtactatgttggaggagccccaagaaggagcaag 1462
|||||
Qy 301 ctctccacatggtggaagctcttgtaaatgtagctga 339
|||||
Db 1463 ctctccacatggtggaagctcttgtaaatgtagctga 1501
|||||

RESULT 18
AAQ02819
ID AAQ02819 standard; DNA; 2676 BP.
XX
AC AAQ02819;
XX
DT 31-MAY-1989 (first entry)
XX
DE cDNA sequence encoding porcine TGF-beta 3.
XX
KW Transforming growth factor beta-3 (TGF beta 3); tumour cells; growth
inhibition.
XX
PN W08912101-A.
XX
PD 14-DEC-1989.
XX
PF 08-JUN-1988; 88WO-US01945.
XX
PR 08-JUN-1988; 88WO-UO01945.
XX
PA (GETH ) GENENTECH INC.
XX
PI Derynck RM, Goeddel DV;
XX
CC WPI; 1990-007474/01.
DR P-PSDB; AAR04080.
XX
PT Nucleotide sequence encoding transforming growth factor beta-3 -used as a
PT probe, or to produce TGF beta 3, for inhibition of growth of normal
PT and neoplastic cells, eg A549.
XX
PS Disclosure; Fig. 4; 6lpp; English.
XX
CC This sequence encodes porcine transforming growth factor-beta 3 (TGF-
CC beta 3) polypeptide. The nucleic acid sequence encoding this subtype is
CC useful as a probe or to produce TGF-beta 3 for both normal and neoplastic
CC cell growth inhibition.
XX
SQ Sequence 2676 BP; 704 A; 705 C; 699 G; 568 T; 0 other;

Query Match 92.9%; Score 315; DB 11; Length 2676;
Best Local Similarity 95.6%; Pred. No. 3.6e-80;
Matches 324; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Qy 1 gttttggacacaaattactgtctccgcaacttgaggagaaactgtgtgccccctc 60
|||||
Db 1175 gccctggacacaaactactctctccgcaatttggagggaactgtgtgccccctc 1234
|||||

Qy 61 tacattgacttcgacaggaatggtggaagtgggtccatgaacctaaagggtactat 120
|||||
Db 1235 tacattgacttcgacaggaatggtggaagtgggtccatgaacctaaagggtactat 1294
|||||

Qy 121 gccaaacttgctcagggcccttgcccatcctccagtcagtcgagacaaacccacagcag 180
|||||
Db 1295 gccaaacttgctcagggcccttgcccatcctccagtcagtcgagacaaacccacagcag 1354
|||||

Qy 181 gtgctgggaactgtacaacactctgaacctgaacctgaacctgacctgacctgacctgccc 240
|||||
Db 1355 gtgctgggaactgtacaacactctgaacctgaacctgaacctgacctgacctgacctgccc 1414
|||||

Qy 241 caggacctggagcccttgacacatctgtactatgtttggaggagcccccacaaagtggagcag 300
|||||
Db 1415 caggacctggagcccttgacacatctgtactatgtctcgaggagaccgccaagtggagcag 1474
|||||
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Qy 301 ctctccacatggtggaagctcttgtaaatgtagctga 339
|||||
Db 1475 ctctccacatggtggaagctcttgtaaatgtagctga 1513
|||||

RESULT 19
AAV52934
ID AAV52934 standard; cDNA; 2639 BP.
XX
AC AAV52934;
XX
DT 21-DEC-1998 (first entry)
XX
DE Pig transforming growth factor-beta 3 cDNA.
XX
KW Transforming growth factor-beta 3; TGF-beta 3; pig; ss.
XX
OS Sus scrofa.
XX
FH Key Location/Qualifiers
FT CDS 127..1497
FT /*tag= a
FT /transl_except= (pos:481..483, aa:Met)
XX
PN US5801231-A.
XX
PD 01-SEP-1998.
XX
PF 22-MAR-1985; 85US-0715142.
XX
PR 13-MAR-1987; 87US-0025423.
PR 22-MAR-1985; 85US-0715142.
PR 04-AUG-1989; 89US-0389929.
PR 04-MAR-1992; 92US-0845893.
PR 05-NOV-1993; 93US-0147364.
PR 30-MAY-1995; 95US-0454468.
XX
PA (GETH ) GENENTECH INC.
XX
PI Derynck RMA, Goeddel DV;
XX
CC WPI; 1998-494840/42.
DR P-PSDB; AAW78786.
XX
PT DNA encoding transforming growth factor-beta precursor sequence -
PT useful for analysis to perform manipulations to increase yield of
PT recombinant production of the protein
XX
PS Example 6; Fig 4a-c; 26pp; English.
XX
CC This nucleotide sequence, termed 10+11.3, codes for the porcine
CC transforming growth factor-beta 3 precursor (prefTGF-beta 3, see
CC AAW78786). A porcine ovarian cDNA library was screened using human
CC TGF-beta 1 cDNA (see AAV52933) as probe. A hybridising clone,
CC designated lambda 11.3, was used to rescreen the library to
CC identify clone lambda 10. The was combined with clone lambda 11.3
CC to provide the 10+11.3 sequence. The invention relates to the
CC recombinant production of TGF-beta. Biologically active TGF-beta
CC is defined as being capable of inducing EGF-potentiated anchorage
CC independent growth of target cell lines and/or growth inhibition of
CC neoplastic cell lines. Nucleic acids encoding TGF-beta have been
CC isolated and cloned into vectors which are replicated in bacteria
CC and expressed in eukaryotic cells. TGF-beta recovered from
CC transformed cells is used in known therapeutic applications.
CC TGF-beta nucleic acids are also useful in diagnosis and
CC identification of TGF-beta clones.
XX
SQ Sequence 2639 BP; 677 A; 702 C; 697 G; 563 T; 0 other;

Query Match 89.1%; Score 302.2; DB 19; Length 2639;
Best Local Similarity 93.2%; Pred. No. 1.6e-76;
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Query Match      89.1%; Score 302.2; DB 11; Length 2671;
Best Local Similarity 93.2%; Pred. No. 1.6e-76;
Matches 316; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 1 gctttggacacaaataactgcttcgcgaacttggaggaactgctgtgtgcgccctc 60
DB 1159 gccctggacacaaataactgcttcgcgaatttggaggaactgctgtgtgcgccctc 1218
QY 61 tacattgacttcgcagagatcggtggagtggtggtccatgaacctaaagggtactat 120
DB 1219 tacattgacttcgcagagatcggtggagtggtggtccatgaacctaaagggtactat 1278
QY 121 gccaaacttctgctcaggcccttgcacatactcccgagtcagacacaaacccacagcag 180
DB 1279 gccaaacttctgctcaggcccttgcacatactcccgagtcagacacaaacccacagcag 1338
QY 181 gtctgggactgtacaaactctgaacctgaacctgaagcatctgctcgcctgtgctgccc 240
DB 1339 gtctgggactgtacaaactctgaacctgaacctgaagcatctgctcgcctgtgctgccc 1398
QY 241 caggacctggagcccttgcacatactctgactatgttggaggaaccccaaaagtggagcag 300
DB 1399 caggacctggagcccttgcacatactctgactatgttggaggaaccccaaaagtggagcag 1458
QY 301 ctctccacatggtgtgaagtctgttaaatgtactga 339
DB 1459 ctctccacatggtgtgaagtctgttaaatgtactga 1497

RESULT 22
AAQ41603
ID AAQ41603 standard; cDNA; 336 BP.
XX AC AAQ41603;
XX DT 26-AUG-1993 (first entry)
XX DE Transforming Growth Factor-beta1(44/45)beta3 hybrid.
XX KW hTGF-beta1; hTGF-beta3; hybrid protein; wound healing;
XX KW cancer treatment; bone repair; growth regulation; ss.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT mat_peptide 1..336
XX FT /*tag= a
XX FT /note= "TGF-beta1=1-132, TGF-beta3=133-336"
XX DN EP542679-A.
XX XX
XX PD 19-MAY-1993.
XX XX
XX PF 03-NOV-1992; 92EP-0810845.
XX XX
XX PR 11-NOV-1991; 91EP-0810870.
XX XX
XX PA (CIBA ) CIBA GEIGY AG.
XX XX
XX PI McMaster GK, Cox D, Cerletti N, Kuhla J;
XX XX
XX DR WPI; 1993-161126/20.
XX DR P-PSDB; AAR39642.
XX XX
XX PT New hybrid transforming growth factor-beta molecules - comprise
XX PT portions of mature TGF-beta isoforms; useful as wound healants,
XX PT cardioprotective, antiinflammatory and immunosuppressive agents etc.
XX XX
XX PS Claim 8; Page 26-27; 48pp; English.
XX XX
XX DR The invention covers hybrid TGF-beta molecules consisting of parts
XX CC

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CC of the human isoforms TGF-beta1, TGF-beta2 and TGF-beta3 (see AAQ41599,
CC AAQ41600 and AAQ41601, respectively). The hinge points between parts
CC derived from different parent isoforms are pref. between amino acids
CC 44 and 45, 56 and 57, 79 and 80, 90 and 91, or 22 and 23. Of the 30
CC possible hybrids using these hinge points and one part each
CC from two of the isoforms, 6 are preferred including the hybrid
CC TGF-beta1(44/45)beta3. The hybrid molecules promote cell migration,
CC inhibit the growth of A375 melanoma cells, accelerate the healing of
CC partial-thickness burn wounds and full-thickness incisional wounds and
CC increase formation of fibrous granular tissue.
CC See AAQ41602-Q41607 for the most pref. hybrids.
XX XX
XX SQ Sequence 336 BP; 75 A; 109 C; 86 G; 66 T; 0 other;

Query Match      87.8%; Score 297.6; DB 14; Length 336;
Best Local Similarity 92.9%; Pred. No. 1.9e-75;
Matches 312; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 1 gctttggacacaaataactgcttcgcgaacttggaggaactgctgtgtgcgccctc 60
DB 1159 gccctggacacaaataactgcttcgcgaatttggaggaactgctgtgtgcgccctc 60
QY 61 tacattgacttcgcagagatcggtggagtggtggtccatgaacctaaagggtactat 120
DB 61 tacattgacttcgcagagatcggtggagtggtggtccatgaacctaaagggtactat 120
QY 121 gccaaacttctgctcaggcccttgcacatactcccgagtcagacacaaacccacagcag 180
DB 121 gccaaacttctgctcaggcccttgcacatactcccgagtcagacacaaacccacagcag 180
QY 181 gtctgggactgtacaaactctgaaccttgaaccttgaaccttgcctgtgctgccc 240
DB 181 gtctgggactgtacaaactctgaaccttgaaccttgaaccttgcctgtgctgccc 240
QY 241 caggacctggagcccttgcacatactctgactatgttggaggaaccccaaaagtggagcag 300
DB 241 caggacctggagcccttgcacatactctgactatgttggaggaaccccaaaagtggagcag 300
QY 301 ctctccacatggtgtgaagtctgttaaatgtactga 336
DB 301 ctctccacatggtgtgaagtctgttaaatgtactga 336

RESULT 23
AAQ417237
ID AAQ417237 standard; DNA; 336 BP.
XX AC AAQ417237;
XX DT 17-JUL-1996 (first entry);
XX DE Hybrid TGF-beta 1-3 DNA.
XX KW Transforming growth factor type beta; TGF-beta 1; TGF-beta 3;
XX KW protein renaturation; protein folding; ds.
XX OS Synthetic.
XX XX
XX PN WO9603433-A1.
XX XX
XX PD 08-FEB-1996.
XX XX
XX PF 12-JUL-1995; 95WO-EP02719.
XX XX
XX PR 25-JUL-1994; 94EP-0810439.
XX XX
XX PA (CIBA ) CIBA GEIGY AG.
XX XX
XX PI Cerletti N;
XX XX
XX DR WPI; 1996-117000/12.
XX DR P-PSDB; AAR92775.

```

```

XX      prodn. of dimeric biologically active transforming growth factor
PT      by refolding denatured monomer in detergent-free folding buffer
PT      contg. specific organic solvent to improve yield
XX
XX      Example 10; Page 36-37; 54pp; English.
XX
CC      A DNA sequence (AAT17237) codes for a recombinant hybrid of human
CC      transforming growth factor-beta, TGF-beta 1-3 (AAR92775), in which
CC      the N-terminal 44 amino acids are from TGF-beta 1 (see also AAR92773)
CC      and the C-terminal 68 amino acids from TGF-beta 3 (see also AAR92772).
CC      The DNA was subcloned in pPLMu, yielding plasmid pPLMu.htGF-beta
CC      1(44/45)beta3. Non-soluble, monomeric hybrid TGF-beta 1-3 was
CC      recovered from E. coli transformants. A biologically active,
CC      dimeric form of the hybrid was obtd. by refolding the monomer in
CC      detergent-free buffer contg. DMSO and/or DMF. Hybrid dimers
CC      TGF-beta 2-3 (AAR92776) and TGF-beta 3-2 (AAR92777) were similarly
CC      produced.
XX
XX      Sequence 336 BP; 75 A; 109 C; 86 G; 66 T; 0 other;
XX
XX      Query Match      87.8%; Score 297.6; DB 17; Length 336;
XX      Best Local Similarity 92.9%; Pred. No. 1.9e-75;
XX      Matches 312; Conservative 0; Mismatches 24; Indels 0; Gaps 0;
XX
QY      1 gcttggacacaaattactgcttcgcgaacttggaggagaactgctgtgccccttc 60
Db      || ||||| || ||||| || ||||| || ||||| || ||||| || ||||| ||
Db      1 gccctggacacaaactattgctcagctccacggagagaactgctgctgcccagctg 60
QY      61 tacattgacttcgcacagatctgggctggaagtgggtccatgaacctaaaggctactat 120
Db      || ||||| || ||||| || ||||| || ||||| || ||||| || ||||| ||
Db      61 tacattgacttcgcgaagacctcgctggaagtggatccacgagcccgaaggctaccat 120
QY      121 gccaaacttctcagggcccttgccataacctcccgagtcagagacacacccacagcag 180
Db      || ||||| || ||||| || ||||| || ||||| || ||||| || ||||| ||
Db      121 gccaaacttctcagggcccttgccataacctcccgagtcagagacacacccacagcag 180
QY      181 gtgctgggactgtacaacactctgaacctgaagcatctgcctgccttgcctgctgccc 240
Db      || ||||| || ||||| || ||||| || ||||| || ||||| || ||||| ||
Db      181 gtgctgggactgtacaacactctgaacctgaagcatctgcctgccttgcctgctgccc 240
QY      241 caggacctggagcccttgaccatctctgtactatgttggaggaccacccaaagtggagcag 300
Db      || ||||| || ||||| || ||||| || ||||| || ||||| || ||||| ||
Db      241 caggacctggagcccttgaccatctctgtactatgttggaggaccacccaaagtggagcag 300
QY      301 ctctccacatggtggtgaagtcttgaatgtagc 336
Db      || ||||| || ||||| || ||||| || ||||| || ||||| || ||||| ||
Db      301 ctctccacatggtggtgaagtcttgaatgtagc 336
XX
RESULT 24
AAT15465
ID      AAT15465 standard; cDNA to mRNA; 336 BP.
XX
AC      AAT15465;
XX
DT      10-JUN-1996 (first entry)
XX
DE      cDNA encoding human TGF-beta-like protein, TGF-beta-1-3.
XX
KW      Transforming growth factor beta; TGF; regulator; method;
KW      proliferation; differentiation; wound healing; solvent; ds.
XX
OS      Homo sapiens.
XX
XX      Key      Location/Qualifiers
XX      CDS      1..336 a
XX      /tag= a
XX      /product= hybrid_TGF-beta-1-3
XX      mat_peptide 1..132
XX      /tag= b
XX      /note= "encodes N-terminal 44 amino acids of

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```

FT      mat_peptide 133..336 TGF-beta-1"
FT      /*tag= c
FT      /note= "encodes C-terminal 68 amino acids of
FT      TGF-beta-3"
XX
XX      WO9603432-A1.
XX
XX      08-FEB-1996.
XX
XX      12-JUL-1995; 95WO-EP027118.
XX
XX      25-JUL-1994; 94EP-0810438.
XX
XX      (CIBA ) CIBA GEIGY AG.
XX
XX      Cerletti N;
XX
XX      WPI; 1996-1116999/12.
XX      P-PSDB; AAR91959.
XX
XX      Prodn. of dimeric, biologically active transforming growth factor
XX      beta - by refolding denatured monomer in buffer contg. mild
XX      detergent and specific organic solvents to improve yields
XX
XX      Claim 17; Page 39-40; 59pp; English.
XX
XX      AAT15465 encodes transforming growth factor (TGF) beta-like protein,
XX      TGF-beta-1-3. TGF-beta-1-3 is a hybrid of TGF-1 and TGF-3. TGF beta
XX      hybrids were made using a new process of producing dimeric,
XX      biologically active TGF beta-like proteins. The new process involves
XX      treating denatured TGF beta monomers with folding buffer contg. a
XX      mild detergent (CHAPS, CHAPSO or digitonin) and at least one of the
XX      solvents DMSO (dimethyl sulphoxide), DMSO2 (dimethylsulphone) and
XX      DMF (dimethyl formamide). The detergent allows folding of the monomer
XX      such that, after dimerisation, the TGF beta-like protein retains
XX      biological activity and remains in soluble form. The method allows
XX      relatively high yields of biologically active TGF beta-like proteins
XX      in their native dimeric form. TGF-beta like proteins are multifunctional
XX      regulators of cellular activity and a typical use is to stimulate wound
XX      healing.
XX
XX      Sequence 336 BP; 75 A; 109 C; 86 G; 66 T; 0 other;
XX
XX      Query Match      87.8%; Score 297.6; DB 17; Length 336;
XX      Best Local Similarity 92.9%; Pred. No. 1.9e-75;
XX      Matches 312; Conservative 0; Mismatches 24; Indels 0; Gaps 0;
XX
QY      1 gcttggacacaaattactgcttcgcgaacttggaggagaactgctgtgccccttc 60
Db      || ||||| || ||||| || ||||| || ||||| || ||||| || ||||| ||
Db      1 gccctggacacaaactattgctcagctccacggagagaactgctgctgcccagctg 60
QY      61 tacattgacttcgcacagatctgggctggaagtgggtccatgaacctaaaggctactat 120
Db      || ||||| || ||||| || ||||| || ||||| || ||||| || ||||| ||
Db      61 tacattgacttcgcgaagacctcgctggaagtggatccacgagcccgaaggctaccat 120
QY      121 gccaaacttctcagggcccttgccataacctcccgagtcagagacacacccacagcag 180
Db      || ||||| || ||||| || ||||| || ||||| || ||||| || ||||| ||
Db      121 gccaaacttctcagggcccttgccataacctcccgagtcagagacacacccacagcag 180
QY      181 gtgctgggactgtacaacactctgaacctgaagcatctgcctgccttgcctgctgccc 240
Db      || ||||| || ||||| || ||||| || ||||| || ||||| || ||||| ||
Db      181 gtgctgggactgtacaacactctgaacctgaagcatctgcctgccttgcctgctgccc 240
QY      241 caggacctggagcccttgaccatctctgtactatgttggaggaccacccaaagtggagcag 300
Db      || ||||| || ||||| || ||||| || ||||| || ||||| || ||||| ||
Db      241 caggacctggagcccttgaccatctctgtactatgttggaggaccacccaaagtggagcag 300
QY      301 ctctccacatggtggtgaagtcttgaatgtagc 336
Db      || ||||| || ||||| || ||||| || ||||| || ||||| || ||||| ||
Db      301 ctctccacatggtggtgaagtcttgaatgtagc 336

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```
RESULT 25
AAF55131
ID AAF55131 standard; DNA; 4382 BP.
XX
AC AAF55131;
XX
29-MAY-2001 (first entry)
XX
DE Nucleotide sequence of the vector puhd10-3-tgf.
XX
KW Stem cell; gene therapy; cell therapy; stem cell disorder; ss.
XX
OS Synthetic.
XX
PN WO200114530-A2.
XX
PD 01-MAR-2001.
XX
PF 24-AUG-2000; 2000WO-EP08247.
XX
PR 24-AUG-1999; 99EP-0116533.
XX
PA (CHEN/) CHEN U.
XX
PI Chen U;
XX
DR WPI; 2001-218440/22.
XX
CC Growing stem cells useful as therapeutic, involves providing stem cells
CC with supporters which are genetically modified to provide externally
CC regulatable interactions, and applying an external signal
CC
PS Disclosure; Fig 26; 92pp; English.
XX
CC The specification describes a method for growing stem cells. The method
CC involves providing stem cells with supporters which are genetically
CC modified in order to provide externally regulatable interactions between
CC the supporters and the stem cells, and applying an external signal for
CC starting or stopping the interactions. The cells are useful for curing
CC diseases by gene therapy and/or cell therapy in combination with tissue
CC engineering, when the functional expression of stem cells is helped
CC with engineered architecture of the tissue, which diseases are related
CC to insufficient and/or lack and/or disorders of stem cells. The present
CC sequence represents a vector, which is used in the method of the
CC invention.
XX
SQ Sequence 4382 BP; 1153 A; 1120 C; 1091 G; 1018 T; 0 other;

Query Match 85.8%; Score 291; DB 22; Length 4382;
Best Local Similarity 91.2%; Pred. No. 2.7e-73;
Matches 309; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

QY 1 gcttgacacaaattactgttcgcaacttgaggagagaactgctgtgtgcgccctc 60
   || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1358 gccctggacacaaattactgttcgcaacttgaggagagaactgctgtgtgcgccctc 1417
   || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 61 tacattgacttcgacagagatctggctggagtggtggtccatgaacctaaaggctactat 120
   || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1418 tatattgacttcgagagatcaggctggagaaatgggtccacgaacctaaagggttactat 1477
   || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 121 gccaaattctgctcaggcccttgccataacctccgcagtcgacacacacccacagcacg 180
   || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1478 gccaaattctgctcaggcccttgccataacctccgcagtcgacacacacccatagcacg 1537
   || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 181 gtgctggagactgtacacactctgaacctgaagcctgctgctgctgctgtgtgtgccc 240
   || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1538 gtgcttgactatatacacacctgaacctgaagcctgctgctgctgctgtgtgtgtccc 1597
   || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 241 caggaacctggagcccttgacctctgtactatgttggtggagaccacccaaagtggagcacg 300
   || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1598 caggaacctggagcccttgacctctgtactatgttggtggagaccacccaaagtggagcacg 1657
   || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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```
QY 301 ctctcaacatggtggtgaagtgttttaaatgtagtga 339
   || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1658 ctgtccaacatggtggtgaagtgtgttaagtgcagctga 1696
   || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 26
AAQ41605
ID AAQ41605 standard; cDNA; 336 BP.
XX
AC AAQ41605;
XX
26-AUG-1993 (first entry)
XX
DE Transforming Growth Factor-beta2(44/45)beta3 hybrid.
XX
KW hTGF-beta2; hTGF-beta3; hybrid protein; wound healing;
KW cancer treatment; bone repair; growth regulation; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT mat_peptide 1..336
FT /tag= a
FT /note= "TGF-beta2-1-132, TGF-beta3-133-336"
XX
PN EP542679-A.
XX
PD 19-MAY-1993.
XX
PF 03-NOV-1992; 92EP-0810845.
XX
PR 11-NOV-1991; 91EP-0810870.
XX
PA (CIBA ) CIBA GEIGY AG.
XX
PI McMaster GK, Cox D, Cerletti N, Kuhla J;
XX
DR WPI; 1993-161126/20.
XX
P-PSDB; AAR39644.
XX
PT New hybrid transforming growth factor-beta molecules - comprise
PT portions of mature TGF-beta isoforms; useful as wound healants,
PT cardioprotective, antiinflammatory and immunosuppressive agents etc.
XX
PS Claim 8; Page 29-30; 48pp; English.
XX
CC The invention covers hybrid TGF-beta molecules consisting of parts
CC of the human isoforms TGF-beta1, TGF-beta2 and TGF-beta3 (see AAQ41599,
CC AAQ41600 and AAQ41601, respectively). The hinge points between parts
CC derived from different parent isoforms are pref. between amino acids
CC 44 and 45, 56 and 57, 79 and 80, 90 and 91, or 22 and 23. Of the 30
CC possible hybrids using these hinge points and one part each
CC from two of the isoforms, 6 are preferred including the hybrid
CC TGF-beta2(44/45)beta3. The hybrid molecules promote cell migration,
CC inhibit the growth of A375 melanoma cells, accelerate the healing of
CC partial-thickness burn wounds and full-thickness incisional wounds and
CC increase formation of fibrous granular tissue.
CC See AAQ41602-Q41607 for the most pref. hybrids.
XX
SQ Sequence 336 BP; 81 A; 94 C; 84 G; 77 T; 0 other;
```

```
Query Match 81.7%; Score 276.8; DB 14; Length 336;
Best Local Similarity 89.0%; Pred. No. 1.5e-69;
Matches 299; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

QY 1 gctttggacacaaattactgttcgcaacttgaggagagaactgctgtgtgcgccctc 60
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1 gctttggatggcgccattgcttttagaaatgctgaggaataatgctgcttaagctcact 60
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 61 tacattgacttcgacagagatctggctggagagtggtccatgaacctaaagggtactat 120
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
```


PS Claim 17; Page 42; 59pp; English.

XX AAL15466 encodes transforming growth factor (TGF) beta-like protein, TGF-beta-2-3. TGF beta-2-3 is a hybrid of TGF-2 and TGF-3. TGF beta hybrids were made using a new process of producing dimeric, biologically active TGF beta-like proteins. The new process involves treating denatured TGF beta monomers with folding buffer contg. a mild detergent (CHAPS, CHAPSO or digitonin) and at least one of the solvents DMSO (dimethyl sulphoxide), DMSO2 (dimethylsulphone) and DMF (dimethyl formamide). The detergent allows folding of the monomer such that, after dimerisation, the TGF beta-like protein retains biological activity and remains in soluble form. The method allows relatively high yields of biologically active TGF beta-like proteins in their native dimeric form. TGF-beta like proteins are multifunctional regulators of cellular activity and a typical use is to stimulate wound healing.

XX Sequence 336 BP; 81 A; 94 C; 84 G; 77 T; 0 other;

Query Match 81.7%; Score 276.8; DB 17; Length 336;
Best Local Similarity 89.0%; Pred. No. 1.5e-69;
Matches 299; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

Qy 1 gcttggacacaaattactgtctccgaacttggaggagaactgtgtgtgccccctc 60
Db 1 gcttggatgcggcctattgtttgaaatgtgcaggataattgtcctacgtccactt 60

Qy 61 tacattgacttccgacagatctggctggaagtgggtccatgaacctaaaggtactat 120
Db 61 tacattgattccaaggagatctagggtggaaatggatcacgaccccaaggtacaa 120

Qy 121 gccaaacttctgcaggcccttgccatactcccgagtcgagacacacccacagcacg 180
Db 121 gccaaacttctgcaggcccttgccatactcccgagtcgagacacacccacagcacg 180

Qy 181 gtgctgggaactgtacaaactgtgaacctgaagcatctgcctgccttgcgtgcc 240
Db 181 gtgctgggaactgtacaaactgtgaacctgaagcatctgcctgccttgcgtgcc 240

Qy 241 caggacctgagccctgacctctgtactatgttggaggagacccccaaagtggagcag 300
Db 241 caggacctgagccctgacctctgtactatgttggaggagacccccaaagtggagcag 300

Qy 301 ctctccaacatggtgtgaagctctgttaaatgtagc 336
Db 301 ctctccaacatggtgtgaagctctgttaaatgtagc 336

RESULT 29
AAQ41606
ID AAQ41606 standard; cDNA; 336 BP.
XX
AC AAQ41606;
XX
XX 26-AUG-1993 (first entry)
XX
DE Transforming Growth Factor-beta3(44/45)beta1 hybrid.
XX hTGF-beta1; hTGF-beta3; hybrid protein; wound healing;
KW cancer treatment; bone repair; growth regulation; ss.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FT mat_peptide 1..336
FT /*tag= a
FT /note= "TGF-beta3=1-132, TGF-beta1=133-336"
XX
PN EP542679-A.
XX
XX PD 19-MAY-1993.
XX

PF 03-NOV-1992; 92EP-0810845.
XX
PR 11-NOV-1991; 91EP-0810870.
XX
PA (CIBA) CIBA GEIGY AG.
XX
PI McMaster GK, Cox D, Cerletti N, Kuhla J;
XX
XX WPI; 1993-161126/20.
DR P-PSDB; AAR39645.
XX
XX New hybrid transforming growth factor-beta molecules - comprise portions of mature TGF-beta isoforms; useful as wound healants, cardioprotective, antiinflammatory and immunosuppressive agents etc.
XX
PS Claim 8; Page 30-31; 48pp; English.
XX
XX The invention covers hybrid TGF-beta molecules consisting of parts of the human isoforms TGF-beta1, TGF-beta2 and TGF-beta3 (see AAQ41599, AAQ41600 and AAQ41601, respectively). The hinge points between parts derived from different parent isoforms are pref. between amino acids 44 and 45, 56 and 57, 79 and 80, 90 and 91, or 22 and 23. Of the 30 possible hybrids using these hinge points and one part each from two of the isoforms, 6 are preferred including the hybrid TGF-beta3(44/45)beta1. The hybrid molecules promote cell migration, inhibit the growth of A375 melanoma cells, accelerate the healing of partial-thickness burn wounds and full-thickness incisional wounds and increase formation of fibrous granular tissue.
XX See AAQ41602-041607 for the most pref. hybrids.
XX
SQ Sequence 336 BP; 63 A; 109 C; 98 G; 66 T; 0 other;

Query Match 70.8%; Score 240; DB 14; Length 336;
Best Local Similarity 82.1%; Pred. No. 4.2e-59;
Matches 276; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

Qy 1 gcttggacacaaattactgtctccgaacttggaggagaactgtgtgtgccccctc 60
Db 1 gcttggacacaaattactgtctccgaacttggaggagaactgtgtgtgccccctc 60

Qy 61 tacattgacttccgacagatctggctggaagtgggtccatgaacctaaaggtactat 120
Db 61 tacattgacttccgacagatctggctggaagtgggtccatgaacctaaaggtactat 120

Qy 121 gccaaacttctgcaggcccttgccatactcccgagtcgagacacacccacagcacg 180
Db 121 gccaaacttctgcaggcccttgccatactcccgagtcgagacacacccacagcacg 180

Qy 181 gtgctgggaactgtacaaactgtgaacctgaagcatctgcctgccttgcgtgcc 240
Db 181 gtgctgggaactgtacaaactgtgaacctgaagcatctgcctgccttgcgtgcc 240

Qy 241 caggacctgagccctgacctctgtactatgttggaggagacccccaaagtggagcag 300
Db 241 caggacctgagccctgacctctgtactatgttggaggagacccccaaagtggagcag 300

Qy 301 ctctccaacatggtgtgaagctctgttaaatgtagc 336
Db 301 ctctccaacatggtgtgaagctctgttaaatgtagc 336

RESULT 30
AAQ41607
ID AAQ41607 standard; cDNA; 336 BP.
XX
AC AAQ41607;
XX
XX 26-AUG-1993 (first entry)
XX
XX Transforming Growth Factor-beta3(44/45)beta2 hybrid.
XX hTGF-beta2; hTGF-beta3; hybrid protein; wound healing;
KW

KW cancer treatment; bone repair; growth regulation; ss.

OS Homo sapiens.

XX Key Location/Qualifiers
FH mat_peptide 1..336
FT /*tag= a
FT /note= "TGF-beta3=1-132, TGF-beta2=133-336"
XX

PN EP542679-A.

XX 19-MAY-1993.

XX 03-NOV-1992; 92EP-0810845.

XX 11-NOV-1991; 91EP-0810870.

XX (CIBA) CIBA GEIGY AG.

XX McMaster GK, Cox D, Cerletti N, Kuhla J;

XX WPI; 1993-161126/20.

XX P-PSDB; AAR39646.

XX New hybrid transforming growth factor-beta molecules - comprise portions of mature TGF-beta isoforms; useful as wound healants, cardioprotective, antiinflammatory and immunosuppressive agents etc.

XX Claim 9; Page 32; 48pp; English.

XX The invention covers hybrid TGF-beta molecules consisting of parts of the human isoforms TGF-beta1, TGF-beta2 and TGF-beta3 (see AAQ41599, CC AAQ41600 and AAQ41601, respectively). The hinge points between parts CC derived from different parent isoforms are pref. between amino acids CC 44 and 45, 56 and 57, 79 and 80, 90 and 91, or 22 and 23. Of the 30 CC possible hybrids using these hinge points and one part each CC from two of the isoforms, 6 are preferred, esp. the hybrid CC TGF-beta3(44/45)beta2. The hybrid molecules promote cell migration, CC inhibit the growth of A375 melanoma cells, accelerate the healing of CC partial-thickness burn wounds and full-thickness incisional wounds and CC increase formation of fibrous granular tissue.

XX See AAQ41602-Q41606 for the other pref. hybrids.

XX Sequence 336 BP; 88 A; 87 C; 71 G; 90 T; 0 other;

Query Match 70.8%; Score 240; DB 14; Length 336;
Best Local Similarity 82.1%; Pred. No. 4.2e-59;
Matches 276; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

```
QY 1 gctttggacacaaattactgtcttcgcaacttggagagaaactgtgtgccccctc 60
DB 1 gctttggacacaaattactgtcttcgcaacttggagagaaactgtgtgccccctc 60
QY 61 tacattgacttcgcagagatctggctggaagtgggtccatgaacctaaaggctactat 120
DB 61 tacattgacttcgcagagatctggctggaagtgggtccatgaacctaaaggctactat 120
QY 121 gccaaactctgtcagcccttgccatccctccagctgcagacacacacacagcag 180
DB 121 gccaaactctgtcagcccttgccatccctccagctgcagacacacacacagcag 180
QY 181 gtgctgggactgtacaacctgtgaacctgaagcatctgctcgcctgtcgtgccc 240
DB 181 gtgctgggactgtacaacctgtgaacctgaagcatctgctcgcctgtcgtgccc 240
QY 241 caggacctggagccctgaccatccctgtactatgtttggaggagcccccagtgagcag 300
DB 241 caagatttgaaccttaacctctctactacattcgttgcgaacaccccaagattgaacag 300
QY 301 ctctcaacatgtgtgtgaagtcttgaatgtagc 336
DB 301 ctctcaacatgtgtgtgaagtcttgaatgtagc 336
```

RESULT 31

AAT17239

ID AAT17239 standard; DNA; 336 BP.

XX AC AAT17239;

XX DT 17-JUL-1996 (first entry)

XX DE Hybrid TGF-beta 3-2 DNA.

XX Transforming growth factor type beta; TGF-beta 2; TGF-beta 3;
KW protein renaturation; protein folding; ds.

XX OS Synthetic.

XX PN WO9603433-A1.

XX PD 08-FEB-1996.

XX PF 12-JUL-1995; 95WO-EP02719.

XX PR 25-JUL-1994; 94EP-0810439.

XX PA (CIBA) CIBA GEIGY AG.

XX PI Cerletti N;

XX DR WPI; 1996-117000/12.

XX P-PSDB; AAR92777.

XX Prodn. of dimeric biologically active transforming growth factor -
PT by refolding denatured monomer in detergent-free folding buffer
PT contg. Specific organic solvent to improve yield

XX Example 10; Page 41-42; 54pp; English.

XX A DNA sequence (AAT17239) codes for a recombinant hybrid of human
CC transforming growth factor-beta, TGF-beta 3-2 (AAR92777), in which
CC the N-terminal 44 amino acids are from TGF-beta 3 (see also AAR92772)
CC and the C-terminal 68 amino acids from TGF-beta 2 (see also AAR92774).
CC The DNA was subcloned in pPLMu, yielding plasmid pPLMu.hTGF-beta
CC 3(44/45)beta2. Non-soluble, monomeric hybrid TGF-beta 3-2 was
CC recovered from E. coli LC137 transformants. A biologically active,
CC dimeric form of the hybrid was obtnd. by refolding the monomer in
CC detergent-free buffer contg. DMSO and/or DMF. Hybrid dimers
CC TGF-beta 1-3 (AAR92775) and TGF-beta 2-3 (AAR92776) were similarly
CC produced.

XX Sequence 336 BP; 88 A; 87 C; 71 G; 90 T; 0 other;

Query Match 70.8%; Score 240; DB 17; Length 336;
Best Local Similarity 82.1%; Pred. No. 4.2e-59;
Matches 276; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

```
QY 1 gctttggacacaaattactgtcttcgcaacttggagagaaactgtgtgccccctc 60
DB 1 gctttggacacaaattactgtcttcgcaacttggagagaaactgtgtgccccctc 60
QY 61 tacattgacttcgcagagatctggctggaagtgggtccatgaacctaaaggctactat 120
DB 61 tacattgacttcgcagagatctggctggaagtgggtccatgaacctaaaggctactat 120
QY 121 gccaaactctgtcagcccttgccatccctccagctgcagacacacacacagcag 180
DB 121 gccaaactctgtcagcccttgccatccctccagctgcagacacacacacagcag 180
QY 181 gtgctgggactgtacaacctgtgaacctgaagcatctgctcgcctgtcgtgccc 240
DB 181 gtgctgggactgtacaacctgtgaacctgaagcatctgctcgcctgtcgtgccc 240
```

```

QY 241 caggaccctggagccctgaacacatctgtactatgttggaggagaccccccaaaagtggagcag 300
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 301 ctctccaaacatggtggaagtcttgtaaatgtagc 336
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
301 cttctaatatgattgtaaaagtcttgcaaatgcagc 336

RESULT 32
AAT15467
ID AAT15467 standard; cDNA to mRNA; 336 BP.
XX
AC AAT15467;
XX
DT 10-JUN-1996 (first entry)
XX
DE cDNA encoding human TGF-beta-like protein, TGF-beta-3-2.
XX
KW Transforming growth factor beta; TGF; regulator; method;
proliferation; differentiation; wound healing; solvent; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
CDS 1..336
FT /*tag= a
FT /product= hybrid_TGF-beta-3-2
FT mat_peptide 1..132
FT /*tag= b
FT /note= "encodes N-terminal 44 amino acids of
TGF-beta-3"
FT mat_peptide 133..336
FT /*tag= c
FT /note= "encodes C-terminal 68 amino acids of
TGF-beta-2"
XX
FN WO9603432-A1.
XX
PD 08-FEB-1996.
XX
PF 12-JUL-1995; 95WO-EP02718.
XX
PR 25-JUL-1994; 94EP-0810438.
XX
PA (CIBA ) CIBA GEIGY AG.
XX
PI Cerletti N;
XX
DR WPI; 1996-116999/12.
DR P-PSDB; AAR91961.
XX
XX Prodn. of dimeric, biologically active transforming growth factor
beta - by refolding denatured monomer in buffer contg. mild
detergent and specific organic solvents to improve yields
XX
PS Claim 17; Page 44-45; 59pp; English.
XX
XX AAT15467 encodes transforming growth factor (TGF) beta-like protein,
TGF-beta-3-2. TGF beta-3-2 is a hybrid of TGF-3 and TGF-2. TGF beta
hybrids were made using a new process of producing dimeric,
biologically active TGF beta-like proteins. The new process involves
treating denatured TGF beta monomers with folding buffer contg. a
mild detergent (CHAPS, CHAPSO or digitonin) and at least one of the
solvents DMSO (dimethyl sulphoxide), DMSO2 (dimethylsulphone) and
DMF (dimethyl formamide). The detergent allows folding of the monomer
such that, after dimerisation, the TGF beta-like protein retains
biological activity and remains in soluble form. The method allows
relatively high yields of biologically active TGF beta-like proteins
in their native dimeric form. TGF-beta like proteins are multifunctional
regulators of cellular activity and a typical use is to stimulate wound
healing.
XX

```

```

SQ Sequence 336 BP; 88 A; 87 C; 71 G; 90 T; 0 other;
Query Match 70.8%; Score 240; DB 17; Length 336;
Best Local Similarity 82.1%; Pred. No. 4.2e-59;
Matches 276; Conservative 0; Mismatches 60; Indels 0; Gaps 0;
QY 1 gctttggacaccaaattactgtcttcgcgaacttgaggagaaactgtgtgccccctc 60
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 61 tacattgaacttcgcagcaggatctggcctggaagtgggtccatgaacctaaagggtactat 120
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 61 tacattgaacttcgcagcaggatctggcctggaagtgggtccatgaacctaaagggtactat 120
QY 121 gccaaattctgtccaggcccttgcacatctcgcagatcgcatgacacacacacagcag 180
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 121 gccaaattctgtgtggagcatgcccgatttatggagttcagacactcagcagcagcag 180
QY 181 gtgtgtgggactgtacaacactctgaacccctgaagcatctgcctcgccttgcgtgccc 240
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 181 gtctgtgagcttataataaccataaaatccagaagcatctgtcttctcctgtcggtgcc 240
QY 241 caggacctggagccccctgacctcctgtactatgttggaggagcccccaagtggagcag 300
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 241 caagatttagaacctctaacattctctactactatggcaaacacacccaagattgaacag 300
QY 301 ctctccaaacatggtggaagtcttgtaaatgtagc 336
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
301 cttctaatatgattgtaaaagtcttgcaaatgcagc 336

RESULT 33
AAT42771
ID AAT42771 standard; cDNA; 339 BP.
XX
AC AAT42771;
XX
DT 26-AUG-1997 (first entry)
XX
DE TGF-beta1 active fragment of a TGF-beta fusion protein encoding cDNA.
XX
KW Transforming growth factor-beta fusion protein; wound healing;
artificial skin; surgery recovery time; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
CDS 1..339
FT /*tag= a
FT /function= TGF active fragment
XX
XX WO9639430-A1.
XX
PD 12-DEC-1996.
XX
PF 05-JUN-1996; 96WO-US08973.
XX
PR 06-JUN-1995; 95US-0470837.
XX
XX (CHEU/) CHEUNG D T.
XX (HALL/) HALL F L.
XX (NIMN/) NIMNI M E.
XX (TUAN/) TUAN T.
XX (WULL/) WU L.
XX
XX Cheung DT, Hall FL, Nimni ME, Tuan T, Wu L;
XX WPI; 1997-043065/04.
XX P-PSDB; AAW08173.
XX
XX Prepn. of transforming growth factor-beta fusion protein - useful to
PT reduce surgery recovery time and to prepare artificial skin

```



```

Db 241 ||||| ||||| ||| ||||| ||||| ||| ||| ||||| ||||| |||||
Qy 301 ctctccaaatggtggtgaagctgtgtaataatgtagctga 339
Db 301 ctgtccaaatgatgctgctgctcctgcaagtgcagctga 339

RESULT 37
AAQ09317
ID AAQ09317 standard; cDNA; 1303 BP.
XX
AC AAQ09317;
XX
DT 12-AUG-1990 (first entry)
XX
DE Monkey transforming growth factor-beta cDNA.
XX
KW Transforming growth factor-beta; simian; psoriasis;
KW TGF-beta.
XX
OS Monkey.
XX
FH Key Location/Qualifiers
FT sig_peptide 22..63
FT mat_peptide 836..1170
FT /*tag= a
FT /*tag= b
FT /*product=monkey transforming growth factor-beta
PN EP353772-A.
XX
XX 07-FEB-1990.
PD
PF 04-AUG-1989; 89EP-0114458.
XX
PR 05-AUG-1988; 88US-0229133.
XX
PA (ONCO-) ONCOGEN LTD PARTNER.
XX
PI Twardzik DR, Purchio AF, Ranchalis JE, Stevens V;
XX
XX WPI; 1990-038499/06.
DR P-PSDB; AAR03743.
XX
XX Inhibition of proliferation of epidermal cells -
PT used to treat psoriasis by contacting cells with compositions
PT containing transforming growth factor-beta.
XX
PS Disclosure; fig 1; 20pp; English.
XX
XX TGF-beta may be used in the treatment of hyperplasia
CC associated with acanthosis-categorised skin diseases, and
CC in alleviating psoriatic symptoms associated with cytokine-
CC induced phenomena. See also AAQ03268 and AAR03750.
XX
XX Sequence 1303 BP; 263 A; 442 C; 378 G; 217 T; 3 other;
SQ

```

```

Query Match 60.4%; Score 204.6; DB 11; Length 1303;
Best Local Similarity 75.2%; Pred. No. 6.7e-49;
Matches 255; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

Qy 1 gctttggacacaaataactgtctccgcaacttgggggagaactgtgtgtgccccctc 60
Db 838 gctttggacacaaataactgtctccgcaacttgggggagaactgtgtgtgccccctc 60
Qy 61 tacattgacttcgacagatgctggctggaagtgggtccatgaaccttaaggctactat 120
Db 898 tatattgacttcgacagatgctggctggaagtgggtccatgaaccttaaggctactat 120
Qy 121 gcaacttctgctcaggcccttgccatctcccgagtgagacacacacacagcagcag 180

```

```

Db 958 gccaaatttgcctggggccctgtccctacatttggagcctggacacgacgtacagcaag 1017
Qy 181 gtctgtggactgtacaacactctgaacctgtgaagcatctgtcctgtgtgtgcccc 240
Db 1018 gtctgtggccctgtacaacacgataaacccggcgctcggcgccgtgtgtgtgcccc 1077
Qy 241 caggacctggagccctgacacactctgtactatgtttggagagaccccaagtgagcag 300
Db 1078 caggcgctggagccactgcccactgtgtactacgtgggcccgaagcccaagtgagcag 1137
Qy 301 ctctccaaatggtggtgaagctgtttaaattgtagctga 339
Db 1138 ctgtccaaatgatgctgctgctcctctgcaaatgcagctga 1176

RESULT 38
AAQ20289
ID AAQ20289 standard; cDNA; 1559 BP.
XX
AC AAQ20289;
XX
DT 16-APR-1992 (first entry)
XX
DE Sequence encoding simian transforming growth factor (TGF) beta-1.
XX
KW Hypertension therapy; hypotensive agent; blood pressure modulator;
KW ss.
XX
OS Monkey.
XX
FH Key Location/Qualifiers
FT CDS 262..282
FT /*tag= a
FT sig_peptide 283..324
FT /*tag= b
FT CDS 325..1098
FT /*tag= c
FT mat_peptide 1099..1436
FT /*tag= d
XX
XX W09119513-A.
XX
XX 26-DEC-1991.
XX
XX 20-JUN-1991; 91WO-US04449.
XX
XX 20-JUN-1990; 90US-0541221.
XX
XX (BRIM ) BRISTOL-MYERS SQUIB.
XX
XX Oleson FB, Comereski CR;
XX
XX WPI; 1992-024199/03.
DR P-PSDB; AAR20124.
XX
XX Use of transforming growth factor (TGF)-beta and their
PT antagonists - for modulating blood pressure, for treating
PT hypertension and hypotension
XX
XX Disclosure; Fig 1; 42pp; English.
XX
XX A new method for treating hypertension comprises administering a
CC transforming growth factor (TGF)-beta to an individual at a dose
CC effective for lowering blood pressure; the TGF-beta may be e.g.
CC mature TGF-beta, TGF-beta2, a mature TGF-beta1/beta2 hybrid, TGF-
CC beta1 precursor, a latent TGF-beta2 precursor, hybrid TGF-beta1/TGF-
CC beta2 precursor, a latent TGF-beta1 complex or a latent TGF-beta2
CC complex.
XX
SQ Sequence 1559 BP; 300 A; 546 C; 446 G; 267 T; 0 other;

Query Match 60.4%; Score 204.6; DB 13; Length 1559;

```


CC TGF-beta may be used in vivo to prevent formation of syncytia and
CC inhibit HIV infection. rGF may also be used with other HIV treatments
CC (AZT, soluble CD4 etc.).
XX
XX Disclosure; Fig 1; 20pp; English.
XX
SQ Sequence 1560 BP; 301 A; 547 C; 445 G; 267 T; 0 other:

```

PI Brankovan V, Lioubin M, Purchio A;
XX
DR WPI; 1990-068723/10.
DR P-PSDB; AAR05664.
XX
XX Compsns. contg. transforming growth factor beta -
PT used for inhibitions of HIV infection and replication in vivo.
XX
CC TGF-beta may be used in vivo to prevent formation of synctia and
CC inhibit HIV infection. TGF may also be used with other HIV treatments
CC (AZT, soluble CD4 etc.).
XX
XX PS Disclosure; Fig 1; 20pp; English.
XX
SQ Sequence 1569 BP; 295 A; 565 C; 444 G; 265 T; 0 other;
O;

Query Match          60.4%; Score 204.6; DB 11; Length 1569;
Best Local Similarity 75.2%; Pred. No. 7e-49;
Matches 255; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

QY      1 gctttggacaccaattactgtcttcgcgaacttgagagaactcgtgtgcgccccctc 60
       ||| ||||| ||| ||||| ||| ||||| ||||| ||||| ||| |||
Db     1104 gccctggacaccaactattgttcagtcccacggagagaactcgtcgctgcgagctg 1163

QY      61 tacattgacttccgcacaggatctggctggaagtgggtccatgaacctaaaggctactat 120
       ||| ||||| ||| ||||| ||| ||||| ||||| ||||| ||| |||
Db     1164 tacattgacttccgaaggacctggctgggaagtggatccacgagcccaaggctaccat 1223

QY      121 gccaaacttgtctcagcgcccttgccccatactccgcagtgcacacaacccacagcacg 180
       ||| ||||| ||| ||||| ||| ||||| ||||| ||||| ||| |||
Db     1224 gccaaacttgtcctcggcgccctgccccatacttggagcctggacacgcagtacagcaag 1283

QY      181 gtgctggagactgtacaacactctaaccctgaagcatctgcctcgcttgcgtgcgtgcc 240
       ||| ||||| ||||| ||| ||||| ||| ||||| ||||| ||| |||
Db     1284 gtccctggccctgtacaaccagcataaccggcgccctcggcgcgctgtgcgtgcgcg 1343

QY      241 caggacactggagcccttgaccatcctgtactatgttggagagacccccaaaagtggagcag 300
       ||| ||||| ||| ||||| ||| ||||| ||||| ||||| ||| |||
Db     1344 caggcgtggagcgcgtgcccatcgttactacgtgggcgcgaagcccaagtgtagcag 1403

QY      301 ctctccaacatggtggtggaagctctgttaaatgtagctga 339
       ||| ||||| ||| ||||| ||| ||||| ||||| ||||| ||| |||
Db     1404 ctgtccaacatgatcgtgcgtcctgaaagtgcagctga 1442

RESULT 43
AAQ03269
ID AAQ03269 standard; DNA; 1571 BP.
AC XX
AC AAQ03269;
CT XX
DT 12-AUG-1990 (first entry)
XX
XX Human transforming growth factor-beta cDNA.
DE XX
KW Transforming growth factor-beta; psoriasis;
KW TGF-beta.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH FH sig_peptide 22..63
FT FT /*tag= a
FT FT mat_peptide 836..1170
FT FT /*tag= b
XX XX /product=human transforming growth factor-beta
XX
XX EP353772.A.
XX
XX PD 07-FEB-1990.
XX
XX PF 04-AUG-1989; 89EP-0114458.

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XX 05-AUG-1990 (first entry)
 XX cDNA encoding human pre-transforming growth factor-beta-1 (pre-TGF-beta-1).
 DE
 DE
 XX Transforming growth factor-beta-1 (TGF-beta-1);
 XX neoplastic cell line inhibition;
 KW EGF-potentiated anchorage-independent growth;
 XX
 XX Homo sapiens.
 OS
 XX
 XX
 FH Key Location/Qualifiers
 FT CDS 842..2014
 FT /tag= a
 FT mat_peptide 1676..2011
 FT /tag= b
 FT misc_difference 37..113
 FT /tag= c
 FT /note="stable hairpin loops"
 FT misc_feature 2015..2100
 FT /tag= d
 FT /note="G-C rich sequence
 FT and a downstream TATA-like sequence"
 FT
 XX US4886747-A.
 XX
 XX 12-DEC-1989.
 XX
 XX 13-MAR-1987; 87US-0025423.
 XX
 XX 13-MAR-1987; 87US-0025423.
 PR
 XX (GETH) GENENTECH INC.
 XX
 XX Derynck RMA, Goeddel DV;
 XX WPI; 1990-051338/07.
 DR P-PSDB; AAR05258.
 XX
 XX Nucleic acid encoding transforming growth factor-beta -
 PT cloned into expression vectors for expression in eukaryotic host
 PT cells for therapeutic use
 XX
 XX Disclosure; Fig 1b; 28pp; English.
 XX
 XX It was obtained by an analysis of several overlapping cDNAs and gene
 CC fragments, leading to the detn. of a continuous sequence corresp. to the
 CC TGF-beta-1 precursor mRNA. It is useful in constructing vectors that
 CC encode biologically active transforming growth factor (TGF-beta),
 CC operably linked to DNA that encodes a secretory leader (SL). It, or a
 CC nucleic acid capable of hybridising with it, can also be labelled and
 CC used in diagnostic assays for DNA or mRNA encoding TGF-beta or related
 CC proteins.
 XX
 XX Sequence 2537 BP; 473 A; 893 C; 739 G; 432 T; 0 other;

Query Match 60.4%; Score 204.6; DB 11; Length 2537;
 Best Local Similarity 75.2%; Pred. NO. 7.9e-49;
 Matches 255; Conservative 0; Mismatches 84; Indels 0; Gaps 0;
 Qy 1 gctttggacacaaataactgtctcgcgaacttggaggagaactgtgtgtgcgccccctc 60
 || ||||| ||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
 Db 1676 gccctggacacaaataactgtctcgcgaacttggaggagaactgtgtgtgcgagctg 1735
 Qy 61 tacattgactccgacagatctggctgggaagtggccatgaacctaaaggtactat 120
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
 Db 1736 tacattgactccgacagacactcggctgggaagtggatccacagagcccaagggctacat 1795
 Qy 121 gccaaactctgtcagggcccttgccataacctcccgagcagtgacagacacacacagcag 180
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
 Db 1796 gccaaactctgtcagggcccttgccataacctcatttgagcctggacagcagtacagcaag 1855

QY 181 gtctgggagctgtacaacactctgaacccctgaagcatctgcctcgtcctgtcgtgctgcc 240
 || |||| ||||| || ||||| || ||||| || ||||| ||||| ||||| ||||| ||||| ||
 Db 1856 gtctggcctgtacaacagataaacccggcgctcgcggcgcgctgtcgtgctgccg 1915
 QY 241 caggacactggagcccttgaccatcctgtactatgtgtggaggagcccccacaaagtggagcag 300
 |||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
 Db 1916 caggcgctggagcgtgccatcgtgtactacgtggcgccgaagcccaaggtggagcag 1975
 QY 301 ctctccaacatgtgtggaagtcttgaatgtagctga 339
 || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
 Db 1976 ctgtccaacatgatcgtgcgtcctcctcaagtgcagctga 2014
 RESULT 47
 AAQ02814
 ID AAQ02814 standard; cDNA; 2537 BP.
 XX
 AC AAQ02814;
 XX
 DT 31-MAY-1989 (first entry)
 XX
 XX Sequence of pre-TGF-beta1 cDNA.
 DE
 XX Transforming growth factor beta-3 (TGF beta 3); tumour cells; growth
 KW inhibition.
 KW
 FH Key Location/Qualifiers
 FT CDS 842..2011
 FT /tag= a
 FT /label=pre-TGF beta 1
 FT 1677..2011
 FT /tag= b
 FT /label=mature TGF-beta 1
 FT 2015..2092
 FT /tag= c
 FT misc_feature 2093..2099
 FT /tag= d
 FT /label=TATA-like sequence
 FT 37..113
 FT /tag= e
 FT misc_feature 863..911
 FT /tag= f
 FT /label=hydrophobic domain
 XX
 XX WO8912101-A.
 XX
 XX 14-DEC-1989.
 XX
 XX 08-JUN-1988; 88WO-US01945.
 XX
 XX 08-JUN-1988; 88WO-UO01945.
 XX
 XX (GETH) GENENTECH INC.
 XX
 XX Derynck RM, Goeddel DV;
 XX
 XX WPI; 1990-007474/01.
 DR P-PSDB; AAR04034.
 XX
 XX Nucleotide sequence encoding transforming growth factor beta-3 -used as a
 PT probe, or to produce TGF beta 3, for growth inhibition of certain normal
 PT and neoplastic cells, eg A549.
 XX
 PS Disclosure; Fig. 1b; 61pp; English.
 XX
 CC Sequence encodes the 390 amino acid (AA) precursor transforming growth
 CC factor-beta 1 (pre-TGF-beta 1) polypeptide. The 5' untranslated region of
 CC the TGF-beta 1 mRNA is 841 bases long, is purine rich and has a region of
 CC potential secondary structure. The TATA-like sequence in the 3' untrans-
 CC lated region of the gene is presumably a polyadenylation signal. Mature
 CC TGF-beta 1 comprises the C-terminal 112 AA's of pre-TGF-beta 1 and is
 CC cleaved at the Arg-Arg dipeptide preceding its NH2 terminus. The nucleic


```

FT misc_feature 37..113
FT /*tag= b
FT /note= "GC-rich region forms stable hairpin loops;
FT similar to structural organisation of c-myc RNA,
FT could play role in mRNA stability or in
FT regulation of transcription"
FT
FT CDS
FT 842..2014
FT /*tag= c
FT /product= pre-TGF_beta_1
FT 1676..2011
FT /*tag= d
FT /product= mature_TGF_beta_1
FT 2015..2100
FT /*tag= e
FT /note= "GC-rich region; possibly responsible for the
FT fact 3'UTR of mRNA could not be cloned as cDNA;
FT may be important for transcription efficiency"
FT
FT repeat_unit 2019..2023
FT /*tag= f
FT TATA_signal 2094..2100
FT /*tag= g
FT /note= "TATA-like sequence; no evidence that this
FT functions a promoter"
FT
FT polyA_signal 2514..2520
FT /*tag= h
FT misc_signal 2529..2536
FT /*tag= i
FT /note= "consensus sequence immediately precedes
FT polyA-tail (Benoist et al)"
FT
XX US5482851-A.
XX
XX 09-JAN-1996.
XX
XX 22-MAR-1985; 85US-0715142.
XX
XX 13-MAR-1987; 87US-0025423.
XX 22-MAR-1985; 85US-0715142.
XX 04-AUG-1989; 89US-0389929.
XX 04-MAR-1992; 92US-0845893.
XX 05-NOV-1993; 93US-0147364.
XX
XX (GETH ) GENENTECH INC.
XX
XX Derynck RMA, Goeddel DV;
XX
XX WPI; 1996-076891/08.
XX P-PSDB; AAR90827.
XX
XX New recombinant human transforming growth factor-beta prods. - produced
XX using Chinese hamster ovary cells, for use in diagnostic applications
XX or in therapy
XX
XX Example 3; Fig 1; 26pp; English.
XX
XX The cDNA encodes the pre-transforming growth factor (TGF) beta 1 protein.
XX The nucleotide sequence was obtd. by an analysis of several overlapping
XX cDNAs and gene fragments. The DNA is useful for the recombinant
XX production of TGF beta 1, which can be used in, e.g. wound healing.
XX (Revised entry submitted to correct sequence analysis breakdown.)
XX
XX Sequence 2537 BP; 473 A; 893 C; 739 G; 432 T; 0 other;
XX
XX
XX Query Match 60.4%; Score 204.6; DB 17; Length 2537;
XX Best Local Similarity 75.2%; Pred. NO. 7.9e-49;
XX Matches 255; Conservative 0; Mismatches 84; Indels 0; Gaps 0;
XX
XX 1 gctttggacacaaattactgttcgcgaacttgaggagaactgtgtgtgccccctc 60
XX || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
Db 1676 gccctggacacaaattactgttcgcgaacttgaggagaactgtgtgtgccccctg 1735
XX
XX 61 tacattgacttcgcgacagatctgggctggaagtgggtccatgaacctaaagggtactat 120

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```

Db 1736 tacattgacttcgcgacagacctcgcgtggaagtggatccacagagcccaagggtaccat 1795
Qy 121 gcaacttctgtcagcccttgcctaccatcctcgcagtcgacagacacacccacagcacg 180
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1796 gcaacttctgtcagccctcgcctaccatcctcgcagtcgacagacagcagtcacagcaag 1855
Qy 181 gtctgggactgtacaacactgtgaacctgaagcctcgcctcgcctcgcctcgcctcgcctcgc 240
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1856 gtctggcctgtacaaccagcataaccggcgccctcgcgcgcgcgcgcgcgcgcgcgcgcgcg 1915
Qy 241 caggacctggagccctcgcctcgcctcgcctcgcctcgcctcgcctcgcctcgcctcgcctcgc 300
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1916 caggcctggagcctcgcctcgcctcgcctcgcctcgcctcgcctcgcctcgcctcgcctcgc 1975
Qy 301 ctctcaacatggtgtggaagtctttaaattgtagctga 339
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1976 ctgtccaacatgatgtgctcctcgcctcgcctcgcctcgcctcgcctcgcctcgcctcgcctcgc 2014

RESULT 50
AAV52933
ID AAV52933 standard; cDNA; 2537 BP.
XX
AC AAV52933;
XX
DT 21-DEC-1998 (first entry)
XX
DE Human pre-transforming growth factor-beta 1 cDNA.
XX
KW Transforming growth factor-beta 1; TGF-beta 1; human; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 842..2014
FT /*tag= a
FT mat_peptide 1676..2011
FT /*tag= b
FT stem_loop 37..113
FT /*tag= b
FT /*note= "putative stable hairpin loop"
FT misc_feature 2015..2100
FT /*tag= c
FT /*note= "GC-rich sequence"
FT polyA_signal 2514..2520
FT /*tag= d
XX
XX US5801231-A.
XX
XX 01-SEP-1998.
XX
XX 22-MAR-1985; 85US-0715142.
XX
XX 13-MAR-1987; 87US-0025423.
XX 22-MAR-1985; 85US-0715142.
XX 04-AUG-1989; 89US-0389929.
XX 04-MAR-1992; 92US-0845893.
XX 05-NOV-1993; 93US-0147364.
XX 30-MAY-1995; 95US-0454468.
XX
XX (GETH ) GENENTECH INC.
XX
XX Derynck RMA, Goeddel DV;
XX
XX WPI; 1998-494840/42.
XX P-PSDB; AAW78785.
XX
XX DNA encoding transforming growth factor-beta precursor sequence -
XX useful for analysis to perform manipulations to increase yield of
XX recombinant production of the protein
XX
XX Example 3; Fig 1B 1-3; 26pp; English.
XX
XX PS

```

```

XX This nucleotide sequence codes for the human transforming growth
CC factor-beta 1 precursor (preTGF-beta 1, see AAW78785). It is a
CC composite of overlapping cDNA clones isolated from different cDNA
CC libraries (placenta, A172 glioblastoma, HT1080 fibroblastoma) using
CC TGF-beta exon (see AAV52936) restriction fragments as probes.
CC The 3' region of the sequence was determined using cloned genomic
CC DNA. The invention relates to the recombinant production of
CC TGF-beta. Biologically active TGF-beta is defined as being capable
CC of inducing EGF-potentiated anchorage independent growth of target
CC cell lines and/or growth inhibition of neoplastic cell lines.
CC Nucleic acids encoding TGF-beta have been isolated and cloned into
CC vectors which are replicated in bacteria and expressed in
CC eukaryotic cells. TGF-beta recovered from transformed cells is
CC used in known therapeutic applications. TGF-beta nucleic acids are
CC also useful in diagnosis and identification of TGF-beta clones.
XX
SQ Sequence 2537 BP; 475 A; 895 C; 736 G; 431 T; 0 other;

Query Match          60.4%; Score 204.6; DB 19; Length 2537;
Best Local Similarity 75.2%; Pred. No. 7.9e-49;
Matches 255; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

QY 1 gctttgacacacattactgtctccgaacttgaggagagaactgctgtgccccctc 60
   || ||||| ||||| || ||||| || ||||| || ||||| || ||||| ||
Db 1676 gccttgacacacattgtcttcagctccacggagagaactgctgctggcagctg 1735

QY 61 tacattgacttcgcagacagatctggctggaagtgggtccatgaacctaaaggctactat 120
   || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
Db 1736 tacattgacttcgcagacagatctggctggaagtgggtccatgaacctaaaggctactat 1795

QY 121 gccaaacttctgctcagcccttgcacatcctccgactgcagtcagacacacacacagcag 180
   || ||||| ||||| || ||||| || ||||| || ||||| || ||||| ||
Db 1796 gccaaacttctgctcagcccttgcacatcctccgactgcagtcagacacacacacagcag 1855

QY 181 gtgctgggactgtacacactctgaaccttgaaactctgcctcgcctgtcgtgcccc 240
   || ||||| ||||| || ||||| || ||||| || ||||| || ||||| ||
Db 1856 gtctggcctgtacacacagataaccggcgccctcggcgccgctgctgctgcccc 1915

QY 241 caggacctggacctgacctctactatgttgggaggaccccccaagtggagcag 300
   || ||||| ||||| || ||||| || ||||| || ||||| || ||||| ||
Db 1916 caggcgtggagcgtgcccactgtactacgtggcgcgaagcccaagtgggagcag 1975

QY 301 ctctccacacatggtgtagctgttaagtcttaagttagctga 339
   || ||||| ||||| || ||||| || ||||| || ||||| || ||||| ||
Db 1976 ctgtccacacatgctgctcctcgaagtgcagctga 2014

RESULT 51
AAT05876
ID AAT05876 standard; cDNA; 2745 BP.
XX
AC AAT05876;
XX
XX 25-JUN-1996 (first entry)
XX
DE cDNA encoding transforming growth factor-beta 1.
XX
KW macrophage inducible nitric oxide synthase; iNOS; constitutive NOS;
KW interleukin-1-beta; transforming growth factor-beta; TGF-beta; IL1-beta;
KW nitric oxide production; hypotension; inflammation; septic shock;
KW treatment; ds.
XX
OS Mammalian sp.
XX
FH Key Location/Qualifiers
FT CDS 842..2017
FT /tag= a
FT /product= transforming growth factor-beta 1
XX
PN W09526745-A1.
XX

```

```

PD 12-OCT-1995.
XX
XX 05-APR-1994; 94WO-US03705.
XX
XX 05-APR-1994; 94WO-US03705.
XX
XX (HARD ) HARVARD COLLEGE.
XX
XX Lee M, Perrella MA;
XX
XX WPI; 1995-358443/46.
XX
XX P-PSDB; AAR83054.
XX
XX Treatment of hypotension, esp. in septic shock - by administering
XX transforming growth factor-beta e.g. to inhibit inducible nitric
XX oxide synthase gene transcription
XX
XX Disclosure; Fig 15; 52pp; English.
XX
XX The cDNA encodes transforming growth factor-beta 1 (TGF-beta 1) which
XX has been found to inhibit inducible nitric oxide synthase (iNOS) gene
XX transcription, esp. in interleukin-1-beta (IL1-beta) stimulated rat
XX smooth muscle cells, and at a dose which does not inhibit constitutive
XX NOS. TGF-beta 1 or 2 (AAR83055) or their active fragments, can be used
XX in the treatment of hypotension, such as that associated with severe
XX inflammation or septic shock.
XX
XX Sequence 2745 BP; 527 A; 938 C; 801 G; 479 T; 0 other;

Query Match          60.4%; Score 204.6; DB 16; Length 2745;
Best Local Similarity 75.2%; Pred. No. 8e-49;
Matches 255; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

QY 1 gctttgacacacattactgtctccgaacttgaggagagaactgctgtgccccctc 60
   || ||||| ||||| || ||||| || ||||| || ||||| || ||||| ||
Db 1679 gccctggacacacactattgttcagctccacggagagaactgctgctggcagctg 1738

QY 61 tacattgacttcgcagacagatctggctggaagtgggtccatgaacctaaaggctactat 120
   || ||||| ||||| || ||||| || ||||| || ||||| || ||||| ||
Db 1739 tacattgacttcgcagacagatctggctggaagtgggtccatgaacctaaaggctactat 1798

QY 121 gccaaacttctgctcagcccttgcacatcctccgactgcagtcagacacacacacagcag 180
   || ||||| ||||| || ||||| || ||||| || ||||| || ||||| ||
Db 1799 gccaaacttctgctcagcccttgcacatcctccgactgcagtcagacacacacagcag 1858

QY 181 gtgctgggactgtacacacactctgaaccttgaaactctgcctcgcctgtgctgcccc 240
   || ||||| ||||| || ||||| || ||||| || ||||| || ||||| ||
Db 1859 gtctggcctgtacacacagataaccggcgccctcggcgccgctgctgctgcccc 1918

QY 241 caggacctggacctgacctctactatgttgggaggaccccccaagtggagcag 300
   || ||||| ||||| || ||||| || ||||| || ||||| || ||||| ||
Db 1919 caggcgtggagcgtgcccactgttactacgtgggcccgaagcccaagtgggagcag 1978

QY 301 ctctccacacatggtgtagctgttaagtcttaagttagctga 339
   || ||||| ||||| || ||||| || ||||| || ||||| || ||||| ||
Db 1979 ctgtccacacatgctgctcctcgaagtgcagctga 2017

RESULT 52
AAT16516
ID AAT16516 standard; DNA; 3541 BP.
XX
XX AAT16516;
XX
XX 01-OCT-1996 (first entry)
XX
XX Collagen A1/TGF-beta-1 chimeric gene.
XX
XX Transforming growth factor; TGF-beta-1; collagen IA; osteogenesis;
XX bone formation; tissue repair; ds.
XX
XX Synthetic.
XX

```



```
SQ      Sequence 3541 BP; 504 A; 1145 C; 1188 G; 704 T; 0 other;

Query Match      60.4%; Score 204.6; DB 21; Length 3541;
Best Local Similarity 75.2%; Pred. No. 8.9e-49;
Matches 255; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

QY      1 gctttggacacaaattactgtctccgaacttggagagaaactgctgtgccccctc 60
Db      || ||||| ||||| || ||||| ||||| || ||||| ||||| || ||||| ||
QY      3197 gccctggacacaaactattgttcagctccacgagagaagaactgctgctggcgagctg 3256
Db      || ||||| ||||| || ||||| ||||| || ||||| ||||| || ||||| ||
QY      61 tacattgacttcgacagatctggctggaagtgggtccatgaacctaaaggctactat 120
Db      || ||||| ||||| || ||||| ||||| || ||||| ||||| || ||||| ||
QY      3257 tacattgacttcggaaggaactcgcctggaagtggatccacgagcccaaggctaccat 3316
Db      || ||||| ||||| || ||||| ||||| || ||||| ||||| || ||||| ||
QY      121 gcaaatcttctgcagcccttgcctacccctcgcagtcgagtcagacacacacagcacg 180
Db      || ||||| ||||| || ||||| ||||| || ||||| ||||| || ||||| ||
QY      3317 gccaaacttgcctggcgccttgcctacatttgagcctggacacgcaagtacagcaag 3376
Db      || ||||| ||||| || ||||| ||||| || ||||| ||||| || ||||| ||
QY      181 gtgctgggactgtacaaactctgaacctgaacctgaacctgtcctgcctgtgctgctgcc 240
Db      || ||||| ||||| || ||||| || ||||| || ||||| ||||| || ||||| ||
QY      3377 gtccctggcctgtacaaaccagataaccggcgctcgcgcgcgcgtgctgctgccc 3436
Db      || ||||| ||||| || ||||| || ||||| || ||||| ||||| || ||||| ||
QY      241 caggaaactggacccctgaccatctgtactatgttggaggagcccccaagtgagcag 300
Db      || ||||| ||||| || ||||| || ||||| || ||||| ||||| || ||||| ||
QY      3437 caggcctggagccgctgcctcgtgtactacgtggcgcgaagcccaaggtggagcag 3496
Db      || ||||| ||||| || ||||| || ||||| || ||||| ||||| || ||||| ||
QY      301 ctctccaaactggtggaagcttgaatgtatgtactga 339
Db      || ||||| ||||| || ||||| || ||||| || ||||| ||||| || ||||| ||
QY      3497 ctgtccaaactgctgcctcctgcctgcaagtgcagctga 3535
Db      || ||||| ||||| || ||||| || ||||| || ||||| ||||| || ||||| ||

RESULT 54
AAQ55624
ID      AAQ55624 standard; DNA; 4105 BP.
XX
AC      AAQ55624;
XX
DT      12-JUL-1994 (first entry)
XX
DE      TGFbeta1 5'-UTR-CDS-3'-UTR.
XX
KW      Transforming Growth Factor beta 1; TGF; non-coding region;
KW      coding region; resonance; interaction; optimisation; ss.
XX
OS      Homo sapiens.
XX
FH      Key
FH      Location/Qualifiers
FT      mRNA
FT      1..4105
FT      /tag= a
FT      /note= "the inventor has used T instead of U in
FT      the TGFbeta1 full-length mRNA"
FT
FT      5'UTR
FT      1..2202
FT      /tag= b
FT      enhancer
FT      231..631
FT      /tag= c
FT      misc_RNA
FT      1..230
FT      /tag= d
FT      /note= "N1 region"
FT      misc_RNA
FT      632..910
FT      /tag= e
FT      /note= "N2 region"
FT      misc_RNA
FT      911..1039
FT      /tag= f
FT      /note= "P region"
FT      CDS
FT      2203..3378
FT      /tag= g
FT      /product= TGFbeta1
FT      3379..4105
FT      3'UTR
FT      /tag= h
FT      /note= "the N residues at positions 3464 and
FT      3465 each appear as the letter F in
FT      the specification"
FT
```

```
XX      FR2692594-A.
PN
XX
PD      24-DEC-1993.
XX
PF      22-JUN-1992; 92FR-0007571.
XX
PR      22-JUN-1992; 92FR-0007571.
XX      (PERE/) PEREZ J.
PA
XX      Perez J;
PI
XX      WPI; 1994-028256/04.
DR
XX      Application of optimised gene expression - for scientific,
PT      industrial and therapeutic purposes
XX
PS      Disclosure; Fig 1; 110pp; French.
XX
CC      The TGFbeta1 mRNA was divided into 3 regions (i.e. 5'-UTR, CDS and
CC      3'-UTR) for various "perturbation" experiments. The relative order
CC      of the 3 regions was altered, e.g. the 3'-UTR was positioned
CC      upstream of the CDS and the 5'-UTR was positioned downstream of the
CC      CDS. The experiments showed that interactions between coding and non-
CC      coding regions are destroyed by such perturbations.
XX
SQ      Sequence 4105 BP; 744 A; 1407 C; 1201 G; 751 T; 2 other;

Query Match      60.4%; Score 204.6; DB 15; Length 4105;
Best Local Similarity 75.2%; Pred. No. 8.9e-49;
Matches 255; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

QY      1 gctttggacacaaattactgtctccgaacttggagagaaactgctgtgccccctc 60
Db      || ||||| ||||| || ||||| || ||||| || ||||| ||||| || ||||| ||
QY      3040 gccctggacacaaactattgttcagctccacgagagaagaactgctgctgagcagctg 3099
Db      || ||||| ||||| || ||||| || ||||| || ||||| ||||| || ||||| ||
QY      61 tacattgacttcgacagatctggctggaagtgggtccatgaacctaaaggctactat 120
Db      || ||||| ||||| || ||||| || ||||| || ||||| ||||| || ||||| ||
QY      3100 tacattgacttcggaaggaactcgcctggagtggtatccacgagcccaaggctaccat 3159
Db      || ||||| ||||| || ||||| || ||||| || ||||| ||||| || ||||| ||
QY      121 gcaaatcttctgcagcccttgcctacccctcgcagtcgagtcagacacacacacagcacg 180
Db      || ||||| ||||| || ||||| || ||||| || ||||| ||||| || ||||| ||
QY      3160 gccaaacttctgcctcggcgcctgcctacatttgagcctggacacagcagtcacagcaag 3219
Db      || ||||| ||||| || ||||| || ||||| || ||||| ||||| || ||||| ||
QY      181 gtgctgggactgtacaaactctgaacctgtgaacctgaacctgtcctgtgctgctgcc 240
Db      || ||||| ||||| || ||||| || ||||| || ||||| ||||| || ||||| ||
QY      3220 gtccctggcctgtacaaaccagataaccggcgctcgcgcgcgcgtgctgctgccc 3279
Db      || ||||| ||||| || ||||| || ||||| || ||||| ||||| || ||||| ||
QY      241 caggaaactggagcccttgaccatctgtactatgttggaggagcccccaagtgagcag 300
Db      || ||||| ||||| || ||||| || ||||| || ||||| ||||| || ||||| ||
QY      3280 caggcctggagccgctgcccactgctactacgtggcgcgaagcccaagtgagcag 3339
Db      || ||||| ||||| || ||||| || ||||| || ||||| ||||| || ||||| ||
QY      301 ctctccaaactggtggaagcttgaatgttgaatgtactga 339
Db      || ||||| ||||| || ||||| || ||||| || ||||| ||||| || ||||| ||
QY      3340 ctgtccaaactgctgctgctcctgcctgcaagtgcagctga 3378
Db      || ||||| ||||| || ||||| || ||||| || ||||| ||||| || ||||| ||

RESULT 55
AAQ11993
ID      AAQ11993 standard; cDNA; 339 BP.
XX
AC      AAQ11993;
XX
DT      29-AUG-1991 (first entry)
XX
DE      Transforming Growth Factor beta 1.
XX      TGF-beta1; biologically active protein production; ss.
XX      Homo sapiens.
XX
```



```
QY 241 caggacctgagccctgaccatctgtactatgttggaggagaccaccccaagtgagcag 300
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 241 caggcgctggagccgctgccatctgtactacgtggtgcgcaagcccaagtgagcag 300
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 301 ctctccaacatggtggaagctcttgaatgtagctga 339
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 301 ctgtccaacatgatgtgcgtctctcaagtcaggtga 339
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 57
ID AAN81085
XX AAN81085 standard; DNA; 1569 BP.
AC AAN81085;
XX
DT 09-OCT-1990 (first entry)
DE Coding sequence of human transforming growth factor-beta 1.
XX
KW Transforming growth factor-beta 1; tumour treatment; ss cDNA.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 267..1442
    /*tag= a
FT sig_peptide 288..329
    /*tag= b
FT mat_peptide 1104..1442
    /*tag= c
FT
XX
PN EP293785-A.
XX
PD 07-DEC-1988.
XX
PF 27-MAY-1988; 88EP-0108528.
XX
PR 29-MAY-1987; 87US-0055662.
PR 25-JAN-1988; 88US-0147842.
XX
PA (ONCO-) ONCOGEN.
XX
PI Purchio AF, Gentry L, Twardzik D;
XX
DR WPI: 1988-347488/49.
DR P-PSDB; AAP81362.
XX
PT Prodn. of simian transforming growth factor beta-1 - by culturing
PT transfected eucaryotic cells, and new precursor proteins, useful for
PT treating tumours.
XX
PS Disclosure; ; pp; English.
XX
XX cDNA is human and mature human TGF-beta 1 has 100% homology with mature
CC simian TGF-beta 1.
XX
SQ Sequence 1569 BP; 295 A; 563 C; 445 G; 266 T; 0 other;

Query Match 59.9%; Score 203; DB 9; Length 1569;
Best Local Similarity 74.9%; Pred. No. 2e-48;
Matches 254; Conservative 0; Mismatches 85; Indels 0; Gaps 0;

QY 1 gtttggacaccaatactgttcgcgaacttgagagaactgtgtgcgccccctc 60
    || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1104 gccctggacaccaactattgtctcagtcacgagagaactgtcgtgcgcgagctg 1163
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 61 tacattgacttcgcacagatctggctggaagtgggtccatgaacctaaaggctactat 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1164 tacattgacttcgcgaagacacctcggctggaagtggatccacgagcccaagggtaccat 1223
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 121 gccaaacttctgcaggcccttgccatccttcgcagtcagtcagacacacccacagcag 180
```

```
Db 1224 gccaaacttctgcaggccctgtccctacatttggagcctggacacagcagtcagcag 1283
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 181 gtgctggactgtacaacactctgaacctctgaacctctgctcgccttgcgtgcgtgcc 240
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1284 gtctggccctgtacaaccagcataaaccggcgctcgcggcgccgtgctgcgtgccg 1343
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 241 caggacctggagccctgaccatctgtactatgttggaggagaccaccccaagtgagcag 300
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1344 caggcgctggagccgctgccatctgttactacgtggcgcaagcccaagtgagcag 1403
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 301 ctctccaacatggtggaagctcttgaatgtagctga 339
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1404 ctgtccaacatgatcgtgcgtcctcctgaaagtgcagctga 1442
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 58
AAQ41602
ID AAQ41602 standard; cDNA; 336 BP.
XX
AC AAQ41602;
XX
DT 26-AUG-1993 (first entry)
DE Transforming Growth Factor-beta1(44/45)beta2 hybrid.
XX
KW hTGF-beta1; hTGF-beta2; hybrid protein; wound healing;
KW cancer treatment; bone repair; growth regulation; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT mat_peptide 1..336
    /*tag= a
FT
FT /note= "TGF-beta1-1-132, TGF-beta2-133-336"
XX
PN EP542679-A.
XX
PD 19-MAY-1993.
XX
PF 03-NOV-1992; 92EP-0810845.
XX
PR 11-NOV-1991; 91EP-0810870.
XX
PA (CIBA ) CIBA GEIGY AG.
XX
PI McMaster GK, Cox D, Cerletti N, Kuhla J;
XX
XX WPI; 1993-161126/20.
DR DR
DR P-PSDB; AAR39641.
XX
XX New hybrid transforming growth factor-beta molecules - comprise
PT portions of mature TGF-beta isoforms; useful as wound healants,
PT cardioprotective, antiinflammatory and immunosuppressive agents etc.
XX
PS Claim 8; Page 25-26; 48pp; English.
XX
XX The invention covers hybrid TGF-beta molecules consisting of parts
CC of the human isoforms TGF-beta1, TGF-beta2 and TGF-beta3 (see AAQ41599,
CC AAQ41600 and AAQ41601, respectively). The hinge points between parts
CC derived from different parent isoforms are pref. between amino acids
CC 44 and 45, 56 and 57, 79 and 80, 90 and 91, or 22 and 23. Of the 30
CC possible hybrids using these hinge points and one part each
CC from two of the isoforms, 6 are preferred including the hybrid
CC TGF-beta1(44/45)beta2. The hybrid molecules promote cell migration,
CC inhibit the growth of A375 melanoma cells, accelerate the healing of
CC partial-thickness burn wounds and full-thickness incisional wounds and
CC increase formation of fibrous granular tissue.
CC See also AAQ41603-041607 for the other pref. hybrids.
XX
SQ Sequence 336 BP; 90 A; 92 C; 72 G; 82 T; 0 other;
```



```
XX New chimeric transforming growth factor -
PT with TGF-beta biological activity and increased secretion
PT efficiency.
XX
XX Clam 2; Fig 1; 18pp; English.
XX
CC Chimeric gene has TGF activity and may be more desirable than its
CC parents TGF-beta1 and TGF-beta2. CHO cells expressing the product
CC from a plasmid vector (p5beta/dhfr) are 2.5 times more bioactive
CC than normal. The product is useful in treatment of cancer and wound
CC healing.
CC See also EP-373994.
XX
XX Sequence 1561 BP; 304 A; 543 C; 443 G; 271 T; 0 other;
SQ
Query Match 57.5%; Score 195; DB 11; Length 1561;
Best Local Similarity 73.5%; Pred. No. 3.7e-46;
Matches 249; Conservative 0; Mismatches 90; Indels 0; Gaps 0;
QY 1 gcttggacacaaactactgctcccgcaacttgaggagaaactgctgtgcccctc 60
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1096 gccttgacacaaactactgctccgaataatgacagataattgctgctacgtccgctt 1155
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 61 tacattgacttcgacagatctgggctggaagtgggtccatgaacctaaaggctactat 120
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1156 tacattgacttcagaggacctcggtggaagtggatccacgagcccaagggtaccat 1215
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 121 gcaacttctgctcagggccctgcccatacctccgacgtgacagacacacccacagcag 180
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1216 gcaacttctgctgggcccctgtccctacatttggagctggacacgcagtagcagaag 1275
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 181 gtgctgggactgtacaaactctgaacctgaacctgaacctgacctgctgctgctgccc 240
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1276 gtctggccctgtataccacagataaccgcggcctcggcgccctgctgctgctgccc 1335
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 241 caggacctggagccctgacctctgtactatgttggaggaccaccccaagtggagcag 300
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1336 caggcgctggagccactgcccactgctgtactacgtggtggcgcaagcccaagtggagcag 1395
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 301 ctctccaacatggtggtgaagctctgttaaatgtagctga 339
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1396 ctgtccaacatgatgtgctgctccgtccgtcaaatgacgtga 1434
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
RESULT 61
AAQ29177
ID AAQ29177 standard; DNA; 1561 BP.
XX
AC AAQ29177;
XX
XX 10-MAR-1993 (first entry)
XX
DE TGF-beta 1/beta 2 chimeric gene.
XX
XX Transforming growth factor; TGF; TGF-beta; TGF-5 beta; simian;
KW Simian virus 40; SV40; expression vector; Chinese Hamster ovary; CHO;
KW vascular endothelial cell; ss.
XX
OS Synthetic.
XX
XX Key Location/Qualifiers
FH CDS 262..1434
FT /*tag= a
FT mat_peptide 1096..1431
FT /*tag= b
FT /*note= "Mature TGF-5 beta"
FT sig_peptide 262..348
FT /*tag= c
FT /*note= "TGF-5 beta pre-pro-protein"
FT precursor_RNA 349..1095
FT /*tag= d
```

```
FT mutation /note= "TGF-5 beta pro-protein"
FT 1120..1122 /*tag= e
FT /label= S9R
FT 1123..1125 /*tag= f
FT /label= S10N
FT mutation 1126..1128 /*tag= g
FT /label= T11V
FT mutation 1129..1131 /*tag= h
FT /label= E12Q
FT mutation 1132..1134 /*tag= i
FT /label= K13D
FT mutation 1144..1146 /*tag= j
FT /label= V17L
FT mutation 1150..1152 /*tag= k
FT /label= Q19P
FT mutation 1168..1170 /*tag= l
FT /label= R25K
FT mutation 1171..1173 /*tag= m
FT /label= K26R
FT old_sequence 1120..1155 /*tag= n
FT /*note= "Mutagenic linker"
FT 179..200 /*tag= o
FT /note= "Feature not labelled in the specification"
XX
PN WO9216228-A.
XX
PD 01-OCT-1992.
XX
PF 13-MAR-1992; 92WO-USO1993.
XX
PR 14-MAR-1991; 91US-0669171.
XX
XX (BRIM ) BRISTOL-MYERS SQUIBB CO.
XX
XX Madisen L, Merwin J, Purchio AF;
XX
XX WPI; 1992-348938/42.
DR P-PSDB; AAR27522.
XX
XX Compn. comprising new chimeric TGF-B (TGF-beta 1-beta 2) -
PT inhibits proliferation of vascular endothelial cells, useful for
XX treating cancer and to promote wound healing
XX
XX Disclosure; Fig 1; 45pp; English.
XX
XX The sequence given encodes a hybrid transforming growth factor
CC (TGF)-beta termed TGF-beta 1/beta 2 (or TGF-5 beta). The mutations
CC indicated in the features table represent replacements of TGF-beta 1
CC bases with those from the corresponding positions of TGF-beta 2.
CC Simian codon usage was maintained. This DNA sequence could be placed
CC under the control of Simian virus 40 (SV40) expression regulatory
CC region within an expression vector and used to transfect Chinese
CC Hamster ovary (CHO) cells. CHO transfectants can be seen to synthesize
CC and secrete high levels of mature TGF-5 beta. TGF-5 beta induces
CC effects on the proliferation of vascular endothelial cells equivalent
CC to those produced by TGF-beta 1.
XX
XX Sequence 1561 BP; 306 A; 541 C; 443 G; 271 T; 0 other;
SQ
Query Match 57.5%; Score 195; DB 13; Length 1561;
Best Local Similarity 73.5%; Pred. No. 3.7e-46;
```



```
XX PA (CIBA ) CIBA GEIGY AG.
XX PI Cerletti N;
XX DR WPI; 1996-116999/12.
XX DR P-PSDB; AAR91957.
XX PT Prodn. of dimeric, biologically active transforming growth factor
XX PT beta - by refolding denatured monomer in buffer contg. mild
XX PT detergent and specific organic solvents to improve yields
XX PS Example 1; Page 34-35; 59pp; English.
XX CC AAT15462-T15464 encode transforming growth factor (TGF) beta-1,
XX CC TGF beta-2 and TGF beta-3 which are produced using recombinant
XX CC DNA technology and used to produce TGF beta-like proteins in
XX CC dimeric form. The TGF beta-like proteins produced are hybrids of
XX CC 2 different types of TGF beta e.g. TGF beta-1-3, TGF beta-2-3, etc,
XX CC or bone morphogenic proteins e.g. BMP-2. The TGF beta hybrids were
XX CC made using a new process of producing dimeric, biologically active
XX CC TGF beta-like proteins. The new process involves treating denatured
XX CC TGF beta monomers with folding buffer contg. a mild detergent (CHAPS,
XX CC CHAPSO or digitonin) and at least one of the solvents DMSO (dimethyl
XX CC sulphoxide), DMSO2 (dimethylsulphone) and DMF (dimethyl formamide).
XX CC The detergent allows folding of the monomer such that, after
XX CC dimerisation, the TGF beta-like protein retains biological activity
XX CC and remains in soluble form. The method allows relatively high yields
XX CC of biologically active TGF beta-like proteins in their native dimeric
XX CC form. TGF-beta like proteins are multifunctional regulators of
XX CC cellular activity and a typical use is to stimulate wound healing.
XX SQ Sequence 339 BP; 98 A; 77 C; 70 G; 94 T; 0 other;

Query Match 53.7%; Score 182.2; DB 17; Length 339;
Best Local Similarity 71.1%; Pred. No. 1.le-42;
Matches 241; Conservative 0; Mismatches 98; Indels 0; Gaps 0;

Qy 1 gctttggacacaaattactgtctccgcaactggaggagaactgctgtgctgccccctc 60
Db 1 gctttggatggcgcctattgtttagaattgtcagggaataattgctgctacgtccact 60

Qy 61 tacattgacttcagacaggtatctgggtggagtggtccatgaacctaaagggctactat 120
Db 61 tacattgattcaagaggatctagggtggaatggatacagacacccaagggtacaat 120

Qy 121 gccaaactctgcagagccctggccatcacctccgcagtcagacacacccaagcagc 180
Db 121 gccaaactctgtgtggagcatgccgctatttatgagttcagacactcagcagcag 180

Qy 181 gtgctgggactgtacaacactctgaacctgaacctgaagcatcctgctgctgctgcc 240
Db 181 gctctgagctatataaccataaataccagaagcatcgtctctctgtgctgtgcc 240

Qy 241 caggacctggagccctgaccatctgtactatgttggaggagacccccaagtgagcag 300
Db 241 caagattgagaacctctaacattctctactacattggaacacccaagattgaacag 300

Qy 301 ctctccacatcgttggtgaagtcttggtaaatgtagtga 339
Db 301 ctctcctaataatgattgtaaaagtcttgcaaatgcagctaa 339

RESULT 66
AAT42772
ID AAT42772 standard; cDNA; 339 BP.
XX AC AAT42772;
XX AC
XX DT 26-AUG-1997 (first entry)
XX DE TGF active fragment of a TGF-beta fusion protein encoding cDNA.
```

```
XX KW Transforming growth factor-beta fusion protein; wound healing;
XX KW artificial skin; surgery recovery time; ss.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT CDS 1..339
XX FT /*tag= a
XX FT /function= TGF active fragment
XX PN WO9639430-A1.
XX PD 12-DEC-1996.
XX PF 05-JUN-1996; 96WO-US08973.
XX PR 06-JUN-1995; 95US-0470837.
XX PA (CHEU/) CHEUNG D T.
XX PA (HALL/) HALL F L.
XX PA (NIMN/) NIMNI M E.
XX PA (TUAN/) TUAN T.
XX PA (WULL/) WU L.
XX PI Cheung DT, Hall FL, Nimni ME, Tuan T, Wu L;
XX WPI; 1997-043065/04.
XX P-PSDB; AAW08174.
XX PT Prepn. of transforming growth factor-beta fusion protein - useful to
XX PT reduce surgery recovery time and to prepare artificial skin
XX PS Disclosure; Page 46-47; 59pp; English.
XX CC A novel transforming growth factor-beta (TGF-beta) fusion protein
XX CC comprises a purification tag and a TGF active fragment. The present
XX CC sequence encodes a specifically claimed TGF active fragment.
XX CC Additionally, the fusion protein may comprise proteinase-sensitive
XX CC linker sites and binding domain so the protein sequence may contain
XX CC some or all of the following elements: purification tag:proteinase
XX CC site:ECM binding site:proteinase site:TGF-beta. TGF-beta promotes
XX CC wound healing, and the fusion protein can be used to reduce surgery
XX CC recovery time and in the preparation of artificial skin. The inclusion
XX CC of a purification tag facilitates purification of the fusion protein.
XX CC The proteinase site is included to permit cleavage and release of the
XX CC purification tag after purification if desired. The extracellular
XX CC matrix binding site facilitates delivery of the fusion protein to the
XX CC desired site of action. Delivery of the TGF-beta to the site to be
XX CC treated reduces the amount of TGF-beta required to be administered to
XX CC be effective and reduces the concentration of circulating TGF-beta
XX CC which may result in undesirable effects.
XX SQ Sequence 339 BP; 98 A; 77 C; 70 G; 94 T; 0 other;
```

Query Match 53.7%; Score 182.2; DB 18; Length 339;
Best Local Similarity 71.1%; Pred. No. 1.le-42;
Matches 241; Conservative 0; Mismatches 98; Indels 0; Gaps 0;

```
Qy 1 gctttggacacaaattactgtctccgcaactggaggagaactgctgtgctgccccctc 60
Db 1 gctttggatggcgcctattgtttagaattgtcagggaataattgctgctacgtccact 60

Qy 61 tacattgacttcagacaggtatctgggtggagtggtccatgaacctaaagggctactat 120
Db 61 tacattgattcaagaggatctagggtggaatggatacagacacccaagggtacaat 120

Qy 121 gccaaactctgcagagccctggccatcacctccgcagtcagacacacccaagcagc 180
Db 121 gccaaactctgtgtggagcatgccgctatttatgagttcagacactcagcagcag 180

Qy 181 gtgctgggactgtacaacactctgaacctgaacctgaagcatcctgctgctgctgcc 240
```



```
CC healing or bone growth.
XX
SQ Sequence 339 BP; 98 A; 77 C; 70 G; 94 T; 0 other;

Query Match      53.7%; Score 182.2; DB 20; Length 339;
Best Local Similarity 71.1%; Pred. No. 1.1e-42;
Matches 241; Conservative 0; Mismatches 98; Indels 0; Gaps 0;

Qy 1 gctttggacacaaattactgtctccgcaacttggagggagaactgctgtgtgccccctc 60
    ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| |||
Db 1 gctttggatggcgcctattgtctttgaaatgtgcagataattgtcgtcaagtcacatt 60
    ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| |||

Qy 61 tacattgacttcacagagatgggtggagtggtgggtccatgaacccaagggctactat 120
    ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| |||
Db 61 tacattgattccaagggataggtggaaatggatcacagacccaagggatacaat 120
    ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| |||

Qy 121 gccaaactctgtcagggcccttggccatcccgactggaagtcagacacacacacagcag 180
    ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| |||
Db 121 gccaaactctgtcggagcatgcccgtatttatggattcagacactcagcacagcagg 180
    ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| |||

Qy 181 gtgctgggactgtacacacactctgaacctgaagcatctgctcgccttgcgtgcgtgcc 240
    ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| |||
Db 181 gtcctgagcttataataaccataaataccagaagcatctgctccttgcgtgcgtgcc 240
    ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| |||

Qy 241 caggacctggagccctgacacatcctgtactatgtttgggaggaccccccaagtgagcag 300
    ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| |||
Db 241 caagatttagaacctctaaccattctactacattggaacaccccaagattgaacag 300
    ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| |||

Qy 301 ctctccaacatggtgtgaagtcttgaataatgaactga 339
    ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| |||
Db 301 ctcttaatatgattgtaagtcttgaataatgaactga 339
    ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| |||

RESULT 69
AAT05877
ID AAT05877 standard; cDNA; 1695 BP.
XX AC
XX AAT05877;
XX
XX 25-JUN-1996 (first entry)
XX
XX cDNA encoding transforming growth factor-beta 2.
XX
XX macrophage inducible nitric oxide synthase; iNOS; constitutive NOS;
KW interleukin-1-beta; transforming growth factor-beta; TGF-beta; IL1-beta;
KW nitric oxide production; hypotension; inflammation; septic shock;
KW treatment; ds.
XX
XX Mammalian sp.
XX
XX Key Location/Qualifiers
XX CDS 182..1426
XX /*tag= a
XX /product= transforming growth factor-beta 2
XX
XX W09526745-A1.
XX
XX 12-OCT-1995.
XX
XX 05-APR-1994; 94WO-US03705.
XX
XX 05-APR-1994; 94WO-US03705.
XX
XX (HARD ) HARVARD COLLEGE.
XX
XX Lee M, Ferrella MA;
XX PI
XX WPI: 1995-358443/46.
XX P-PSDB; AAR83055.
XX
XX Treatment of hypotension, esp. in septic shock - by administering
PT transforming growth factor-beta e.g. to inhibit inducible nitric
```

```
PT oxide synthase gene transcription
XX
XX Disclosure; Fig 16; 52pp; English.
XX
XX The cDNA encodes transforming growth factor-beta 2 (TGF-beta 2) which
CC has been found to inhibit inducible nitric oxide synthase (iNOS) gene
CC transcription, esp. in interleukin-1-beta (IL1-beta) stimulated rat
CC smooth muscle cells, and at a dose which does not inhibit constitutive
CC NOS. TGF-beta 1 or 2 (AAR83055) or their active fragments, can be used
CC in the treatment of hypotension, such as that associated with severe
CC inflammation or septic shock.
XX
XX Sequence 1695 BP; 523 A; 386 C; 354 G; 432 T; 0 other;

Query Match      53.7%; Score 182.2; DB 16; Length 1695;
Best Local Similarity 71.1%; Pred. No. 1.1e-42;
Matches 241; Conservative 0; Mismatches 98; Indels 0; Gaps 0;

Qy 1 gctttggacacaaattactgtctccgcaacttggagggagaactgctgtgtgccccctc 60
    ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| |||
Db 1088 gctttggatggcgcctattgtctttgaaatgtgcagataattgtcgtcacttccactt 1147
    ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| |||

Qy 61 tacattgacttcacagagatgggtggagtggtgggtccatgaacccaagggctactat 120
    ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| |||
Db 1148 tacattgattccaagggatctaggtggaaatggatcacagacccaagggatacaat 1207
    ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| |||

Qy 121 gccaaactctgtcagggcccttggccatcccgactggaagtcagacacacacacagcag 180
    ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| |||
Db 1208 gccaaactctgtcggagcatgcccgtatttatggattcagacactcagcacagcag 1267
    ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| |||

Qy 181 gtgctgggactgtacacacactctgaacctgaagcatctgctcgccttgcgtgcgtgcc 240
    ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| |||
Db 1268 gtctgagcttataataaccataaataccagaagcatctgctccttgcgtgcgtgcc 1327
    ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| |||

Qy 241 caggacctggagccctgacacatcctgtactatgtttgggaggaccccccaagtgagcag 300
    ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| |||
Db 1328 caagatttagaacctctaaccattctactacattggaacacccaagattgaacag 1387
    ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| |||

Qy 301 ctctccaacatggtgtgaagtcttgaataatgaactga 339
    ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| |||
Db 1388 ctcttaatatgattgtaagtcttgaataatgaactga 1426
    ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| |||

RESULT 70
AAQ20291
ID AAQ20291 standard; cDNA; 2208 BP.
XX AC
XX AAQ20291;
XX
XX 16-APR-1992 (first entry)
XX
XX Sequence encoding hybrid transforming growth factor (TGF)-
DE beta-1/beta-2.
XX
XX Hypertension therapy; hypotensive agent; blood pressure modulator;
KW ss.
XX
XX Homo sapiens and monkey.
XX
XX Key Location/Qualifiers
XX CDS 262..282
XX /*tag= a
XX sig_peptide 283..324
XX /*tag= b
XX CDS 325..1095
XX /*tag= c
XX mat_peptide 1096..1434
XX /*tag= d
XX polyA_site 2208
XX /*tag= e
XX
XX W09119513-A.
```



```

XX WPI: 1989-138796/19.
XX P-PSDB; AAP91889.
XX
XX New DNA sequence encoding transforming growth factor beta 2 -
XX used for large scale expression in eucaryotic cells
XX
XX Disclosure; Fig 1a; 27pp; German.
XX
XX PolyA-RNA was isolated from the tamoxifen-treated, human prostatic
XX adenocarcinoma cell line PC-3 and converted to cDNA. TGF DNA is used
XX for control of the SV40 promoter and expressed in CHO cells. The simian
XX SQ is also claimed.
XX
XX Sequence 2568 BP; 772 A; 597 C; 513 G; 586 T; 0 other;

Query Match      53.7%; Score 182.2; DB 10; Length 2568;
Best Local Similarity 71.1%; Pred. No. 1.8e-42;
Matches 241; Conservative 0; Mismatches 98; Indels 0; Gaps 0;

Qy 1 gcttggacacaaattactgtccgaacttggaggagaaactgtgtgccccctc 60
Db ||||| || ||||| || ||||| || ||||| || ||||| || |||||
Qy 61 tacattgacttcgacagagatcgtggctggaagtgggtccatgaacctaaagggtactat 120
Db ||||| || ||||| || ||||| || ||||| || ||||| || |||||
Qy 121 gccaaactctcagcccttgcacactccacccagtcagacacacacacagcagc 180
Db ||||| || || ||||| || || ||||| || || ||||| || |||||
Qy 1576 gccaaactctgtcgtggagcgtccgtattatggagttcagacactcagcagcag 1635
Db || || || || || || || || || || || || || || || || || || || || || ||
Qy 181 gtctgggactgtacacactctgaacctgaacctgtcctgccttgcctgtgcgtgcc 240
Db || || || || || || || || || || || || || || || || || || || || || ||
Qy 1636 gtcctgagcttataataaccataataaccagaagcatcgtctccttgcgtgtcc 1695
Db || || || || || || || || || || || || || || || || || || || || || ||
Qy 241 caggacctggagccctgacctcgtactatgttggaggagcccccaagtggagcag 300
Db || || || || || || || || || || || || || || || || || || || || || ||
Qy 1696 caagatttagaacctctaaccattctactacattggcgaacaccccccaagattgaacag 1755
Db || || || || || || || || || || || || || || || || || || || || || ||
Qy 301 ctctccaacatgggtgaagtcttgaatgtagctga 339
Db || || || || || || || || || || || || || || || || || || || || || ||
Qy 1756 ctttctaataatgatgtgaagcttgcgaatgcagctaa 1794
Db || || || || || || || || || || || || || || || || || || || || || ||

RESULT 72
AAQ05126
ID AAQ05126 standard; DNA; 2569 BP.
XX
XX AAQ05126;
XX
XX 02-NOV-1990 (first entry)
XX
XX Human TGF-Beta2-442 precursor cDNA.
XX
XX Human TGF-Beta2 precursor; cancer; tumorcide; ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX CDS 467..1792
XX FT /*tag= a
XX mat_peptide 1457..1792
XX FT /*tag= b
XX
XX EP376785-A.
XX
XX 04-JUL-1990.
XX
XX 14-DEC-1989; 89EP-0403480.
XX
XX 16-DEC-1988; 88US-0285140.

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PR 05-DEC-1989; 89US-0446020.
XX (ONCO-) ONCOGEN LTD PARTNER.
XX
XX Purchio AF, Madisen L, Webb N;
XX
XX WPI: 1990-203127/27.
XX P-PSDB; AAR05748.
XX
XX Cloning and expression of transforming growth factor beta 2 -
XX used for treatment of tumors or for augmenting wound healing.
XX
XX Claim 1; Fig 1a; 58pp; English.
XX
XX TGF-Beta2 may be used in treatment of tumors at effective doses,
XX and may also be useful in augmenting wound healing by stimulating
XX cell proliferation. The growth factor can be produced at high
XX levels from a CHO expression system.
XX
XX Sequence 2569 BP; 772 A; 598 C; 512 G; 687 T; 0 other;

Query Match      53.7%; Score 182.2; DB 11; Length 2569;
Best Local Similarity 71.1%; Pred. No. 1.8e-42;
Matches 241; Conservative 0; Mismatches 98; Indels 0; Gaps 0;

Qy 1 gcttggacacaaattactgtctccgaacttggaggagaaactgtgtgccccctc 60
Db ||||| || ||||| || ||||| || ||||| || ||||| || |||||
Qy 1457 gcttggatgcgcctattgtccttagaattgtgcagataattgctgctacgtccactt 1516
Db ||||| || ||||| || ||||| || ||||| || ||||| || |||||
Qy 61 tacattgacttcgacagagatcgtggctggaagtgggtccatgaacctaaagggtactat 120
Db ||||| || ||||| || ||||| || ||||| || ||||| || |||||
Qy 1517 tacattgattccaagggagctataggtggaatgatacacgaaccccaagggtacaat 1576
Db ||||| || ||||| || ||||| || ||||| || ||||| || |||||
Qy 121 gccaaactctcagcccttgcacactccacccagtcagacacacacacagcagc 180
Db ||||| || || ||||| || || ||||| || || ||||| || |||||
Qy 1577 gccaaactctgtcgtggagcgtccgtattatggagttcagacactcagcagcag 1636
Db || || || || || || || || || || || || || || || || || || || || || ||
Qy 181 gtctgggactgtacacactctgaacctgaacctgtcctgcctcgtcgtgcgtgcc 240
Db || || || || || || || || || || || || || || || || || || || || || ||
Qy 1637 gtcctgagcttataataaccataataaccagaagcatcgtctccttgcgtgtcc 1696
Db || || || || || || || || || || || || || || || || || || || || || ||
Qy 241 caggacctggagccctgacctcgtactatgttggaggagcccccaagtggagcag 300
Db || || || || || || || || || || || || || || || || || || || || || ||
Qy 1697 caagatttagaacctctaaccattcttattattattggcgaacaccccccaagattgaacag 1756
Db || || || || || || || || || || || || || || || || || || || || || ||
Qy 301 ctctccaacatgggtgaagtcttgaatgtagctga 339
Db || || || || || || || || || || || || || || || || || || || || || ||
Qy 1757 ctttctaataatgatgtgaagcttgcgaatgcagctaa 1795
Db || || || || || || || || || || || || || || || || || || || || || ||

RESULT 73
AAQ20290
ID AAQ20290 standard; cDNA; 2569 BP.
XX
XX AAQ20290;
XX
XX 16-APR-1992 (first entry)
XX
XX Sequence encoding human transforming growth factor (TGF)-
XX beta-2-442.
XX
XX Hypertension therapy; hypotensive agent; blood pressure modulator;
XX ss.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 467..475
XX FT /*tag= a
XX sig_peptide 478..525
XX FT /*tag= b
XX CDS 526..1456

```

```

FT mat_peptide /*tag= c
FT 1457..1792
FT /*tag= d
FT 2569
FT polyA_site /*tag= e
XX
XX WO9119513-A.
XX
XX 26-DEC-1991.
XX
XX 20-JUN-1991; 91WO-US04449.
XX
XX 20-JUN-1990; 90US-0541221.
XX
XX (BRIM ) BRISTOL-MYERS SQUIB.
XX
XX Oleson FB, Comerreski CR;
XX
XX WPI; 1992-024199/03.
XX P-PSDB; AAR20125.
XX
XX Use of transforming growth factor (TGF)-beta and their
XX antagonists - for modulating blood pressure, for treating
XX hypertension and hypotension
XX
XX Disclosure; Fig 2; 42pp; English.
XX
XX A new method for treating hypertension comprises administering a
XX transforming growth factor (TGF)-beta to an individual at a dose
XX effective for lowering blood pressure; the TGF-beta may be e.g.
XX mature TGF-beta, TGF-beta2, a mature TGF-beta1/beta2 hybrid, TGF-
XX beta1 precursor, a latent TGF-beta2 precursor, hybrid TGF-beta1/TGF-
XX beta2 precursor, a latent TGF-beta1 complex or a latent TGF-beta2
XX complex.
XX
XX Sequence 2569 BP; 772 A; 598 C; 513 G; 686 T; 0 other;

Query Match 53.7%; Score 182.2; DB 13; Length 2569;
Best Local Similarity 71.1%; Pred. No. 1.8e-42;
Matches 241; Conservative 0; Mismatches 98; Indels 0; Gaps 0;

QY 1 gcttggacacaaattactgctccgcaacttgagagaaactgctgtgctgccccctc 60
Db 1457 gcttggatgcggcctattgcttagaataatgacagataattgctgctacgtccactt 1516

QY 61 tacattgactccgacagatctggctggaagtgggtccatgaaacctaaagggtactat 120
Db 1517 tacattgattcaaggaggtatagtggtgaaatggatcacacgaacccaagggtacaat 1576

QY 121 gccaaactctgctcaggcccttgcccatacctccgagtgacagacacacccaagcagc 180
Db 1577 gccaaactctgctcaggagcatgcccgtattatgaggttcagacactcagcagcagc 1636

QY 181 gtgctgggactgtacaaactctgaacctgaagcatctgctcgcttgcctgcgtgccc 240
Db 1637 gctctgagcttataataaccataaatcagaagcatctgcttctcttgcgtgctgcc 1696

QY 241 caggacctggagccctgacctctctactatgtttgggagaccccccaaaagtggagcag 300
Db 1697 caagatttagaaccttaacctctctactacatctggaacacacccaagattgaacg 1756

QY 301 cctctcaacatggttggtgaagtcttgataatgtactga 339
Db 1757 cttcttaatatgatgtgaagtcttgcaaatgcagctaa 1795

RESULT 74
AAR04116
ID AAT04116 standard; cDNA; 2592 BP.
XX
XX AAT04116;
XX

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DT 28-MAY-1996 (first entry)
XX
XX Human transforming growth factor-2 cDNA.
XX
XX TGF-beta1; TGF-beta2; transforming growth factor; protein;
XX cell differentiation; cell proliferation; CHO; Chinese hamster;
XX ovary; COS; monkey kidney; animal; mammal; ss.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX sig_peptide 503..550
XX /*tag= a
XX mat_peptide 1484..1819
XX /*tag= b
XX misc_feature 553
XX /*tag= c
XX /*note= "putative signal sequence cleavage site"
XX
XX EP676474-A1.
XX
XX 11-OCT-1995.
XX
XX 14-DEC-1989; 89EP-0104223.
XX
XX 05-DEC-1989; 89US-0446020.
XX 16-DEC-1988; 88US-0285140.
XX
XX (ONCO ) ONCOGEN LP.
XX
XX Madisen L, Purchio AF, Webb N;
XX
XX WPI; 1995-346094/45.
XX P-PSDB; AAR79922.
XX
XX Hybrid transforming growth factor beta-1/TGF-beta-2 precursor - used
XX to produce biologically active, mature TGF-beta-2
XX
XX Disclosure; Fig.1a; 52pp; English.
XX
XX This DNA sequence is expressed in a host cell, preferably a
XX COS or CHO cell, containing a recombinant vector encoding this
XX sequence under the control of a 2nd nucleotide sequence that
XX regulates gene expression, preferably the SV40 promoter, so the host
XX cell produces active TGF-beta2. The produced TGF-beta2 protein can
XX be used to regulate cellular differentiation and proliferation.
XX
XX Sequence 2592 BP; 772 A; 613 C; 516 G; 691 T; 0 other;

Query Match 53.7%; Score 182.2; DB 16; Length 2592;
Best Local Similarity 71.1%; Pred. No. 1.8e-42;
Matches 241; Conservative 0; Mismatches 98; Indels 0; Gaps 0;

QY 1 gcttggacacaaattactgctccgcaacttgagagaaactgctgtgctgccccctc 60
Db 1484 gcttggatgcggcctattgcttagaataatgacagataattgctgctacgtccactt 1543

QY 61 tacattgactccgacagagatctggctggaagtgggtccatgaacctaaagggtactat 120
Db 1544 tacattgattcaaggaggtatctaggtggaaatggatcacgaacccaaggtacaat 1603

QY 121 gccaaactctgctcaggcccttgcccatacctccgagtgacagacacacccaagcagc 180
Db 1604 gccaaactctgctgagcatgcccgtattatggagttcagacactcagcagcagc 1663

QY 181 gtgctgggactgtacaaactctgaacctgaagcatctgctcgcttgcctgcgtgccc 240
Db 1664 gtctgagcttataataaccataaatcagaagcatctgcttctcttgcgtgctgcc 1723

QY 241 caggacctggagccctgacctctgactatgtttgggagaccccccaaaagtggagcag 300
Db 1724 caagatttagaaccttaacctctctactactatgttgcaaaacacccaagattgaacg 1783

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QY 61 tacattgacttcgcacagatctggctggaagtggtggtccatgaacctaaagggtactat 120
    ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| |||||
Db 1154 tacattgatttcaaggaggtatctagggtggaattgatacacgaacccaagggtacaat 1213
    ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| |||||
QY 121 gcaacttctgctcagggcccttgccataacctccgcagtcagtcagacacacccacagcag 180
    ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| |||||
Db 1214 gcaacttctgctgagcatgcccgtatttatggagttcagacactcagcagcag 1273
    ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| |||||
QY 181 gtgctgggactgtacaaactctgaacctgaagcctgcctgcctgcctgctgctgccc 240
    ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| |||||
Db 1274 gtccgagcttataataaccataaaatccagaagcattctctctctctgctgctgctcc 1333
    ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| |||||
QY 241 caggacctggagccctcaccatctgtactatgttggaggagcccccacaaagtggagcag 300
    ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| |||||
Db 1334 caagatttagaaccttaaccattctctactacattggcaaacacccaagattgaacag 1393
    ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| |||||
QY 301 ctctcaacatggtggtgaagcttctgtaaatgtagctga 339
    ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| |||||
Db 1394 ctctcaatgatgtgaagcttgcgaatgcagctaa 1432
    ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| |||||

RESULT 77
AAQ03511
ID AAQ03511 standard; DNA; 2207 BP.
XX
AC AAQ03511;
XX
DT 14-AUG-1990 (first entry)
XX
DE Hybrid transforming growth factor TGF-beta1/beta2.
XX
KW HIV; AIDS; SIV; vaccine; AZT; CD4; cytokines; growth
KW factors; ds.
XX
FH Key Location/Qualifiers
FT CDS 267..1437
FT FT /*tag= a
FT mat_peptide 1103..1437
FT FT /*tag= b
XX
PN EP356935-A.
XX
XX
PD 07-MAR-1990.
XX
PF 25-AUG-1989; 89EP-0115719.
XX
PR 25-AUG-1988; 88US-0236698.
XX
PA (ONCO-) ONCOGEN LTD PARTNER.
XX
PI Brankovan V, Lioubin M, Purchio A;
XX
WPI; 1990-068723/10.
DR P-PSDB; AAR05666.
XX
XX
PT Compsns. contg. transforming growth factor beta -
PT used for inhibitions of HIV infection and replication in vivo.
XX
XX
CC TGF-beta may be used in vivo to prevent formation of synctia and
CC inhibit HIV infection. TGF may also be used with other HIV treatments
CC (AZT, soluble CD4 etc.).
XX
PS Disclosure; Fig 3; 20pp; English.
XX
SQ Sequence 2207 BP; 600 A; 576 C; 532 G; 499 T; 0 other;

Query Match 53.3%; Score 180.6; DB 11; Length 2207;
Best Local Similarity 70.8%; Pred. No. 5e-42;
Matches 240; Conservative 0; Mismatches 99; Indels 0; Gaps 0;

QY 1 gctttggacacacaaattactgtctccgcaacttgaggaggaactgtgtgtgccccctc 60

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Db 1095 gctttggatccgcgcctattgttttagaaatgtgcagcataattgtgctcactccactt 1154
    ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| |||||
QY 61 tacattgaacttccacagagatctggctggaagtggtccatgaacctaaagggtactat 120
    ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| |||||
Db 1155 tacattgatttcaaggaggtatctagggtggaattgatacacgaacccaagggtacaat 1214
    ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| |||||
QY 121 gccaaacttctgctcagggcccttgccataacctccgcagtcagtcagacacacccacagcag 180
    ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| |||||
Db 1215 gccaaacttctgctgagcatgcccgtatttatggagttcagacactcagcagcag 1274
    ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| |||||
QY 181 gtgctgggactgtacaaactctgaacctcgaacctgaagcctgcctgcctgctgctgccc 240
    ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| |||||
Db 1275 gtccgagcttataataaccataaaatccagaagcattctctctctctgctgctgctcc 1334
    ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| |||||
QY 241 caggacctggagccctcaccatctgtactatgttggaggagcccccacaaagtggagcag 300
    ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| |||||
Db 1335 caagatttagaacctcctcaaccattctctactacattggcaaacacccaagattgaacag 1394
    ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| |||||
QY 301 ctctcccaacatggtggtgaagcttctgtaaatgtagctga 339
    ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| |||||
Db 1395 ctctcaatgatgtgaagcttgcgaatgcagctaa 1433
    ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| |||||

RESULT 78
AAQ05127
ID AAQ05127 standard; DNA; 2207 BP.
XX
AC AAQ05127;
XX
DT 02-NOV-1990 (first entry)
XX
DE Human TGF-Betal/TGF-Beta2 hybrid precursor cDNA expressing
DE TGF-Beta2.
XX
KW Human TGF-Beta2 precursor; cancer; tumorcide; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT CDS 261..1430
FT FT /*tag= a
FT mat_peptide 1092..1430
FT FT /*tag= b
XX
PN EP376785-A.
XX
XX
PD 04-JUL-1990.
XX
PF 14-DEC-1989; 89EP-0403480.
XX
PR 16-DEC-1988; 88US-0285140.
PR 05-DEC-1989; 89US-0446020.
XX
XX
PA (ONCO-) ONCOGEN LTD PARTNER.
XX
PI Purchio AF, Madisen L, Webb N;
XX
WPI; 1990-203127/27.
DR P-PSDB; AAR05749.
XX
XX
PT Cloning and expression of transforming growth factor beta 2 -
PT used for treatment of tumors or for augmenting wound healing.
XX
PS Claim 15; Fig 1b; 58pp; English.
XX
CC TGF-Beta2 may be used in treatment of tumors at effective doses,
CC and may also be useful in augmenting wound healing by stimulating
CC cell proliferation. The growth factor can be produced at high
CC levels from a CHO expression system.
XX
SQ Sequence 2207 BP; 600 A; 577 C; 532 G; 498 T; 0 other;

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FT      /*tag= b
FT      /note= "Simian TGF-beta1 precursor"
FT      1085..1423
FT      /*tag= c
FT      /note= "human TGF-beta2 precursor"
FT      278..319
FT      /*tag= d
XX      EP676474-A1.
PN
XX
XX      11-OCT-1995.
XX
XX      14-DEC-1989; 89EP-0104223.
XX
XX      05-DEC-1989; 89US-0446020.
XX      16-DEC-1988; 88US-0285140.
XX      (ONCO ) ONCOGEN LP.
XX
XX      Madisen L, Purchio AF, Webb N;
PI
XX
XX      WPI; 1995-346094/45.
XX      P-PSDB; AAR79921.
XX
XX      Hybrid transforming growth factor beta-1/TGF-beta-2 precursor - used
XX      to produce biologically active, mature TGF-beta-2
XX
XX      Claim 1, 2 and 3; Fig.1b; 52pp; English.
XX
XX      This hybrid DNA sequence is expressed in a host cell, preferably a
XX      COS or CHO cell, containing a recombinant vector encoding this
XX      sequence under the control of a 2nd nucleotide sequence that
XX      regulates gene expression, preferably the SV40 promoter, so the host
XX      cell produces active TGF-beta2. The produced TGF-beta2 protein can
XX      be used to regulate cellular differentiation and proliferation.
XX
XX      Sequence 2200 BP; 597 A; 588 C; 517 G; 498 T; 0 other;

Query Match      52.3%; Score 177.4; DB 16; Length 2200;
Best Local Similarity 70.2%; Pred. No. 4e-41;
Matches 238; Conservative 0; Mismatches 101; Indels 0; Gaps 0;

Qy      1 gcttggacacaaataactgctccgcaacttgaggagagaactgctgtgccccctc 60
Db      ||||| || || || || || || || || || || || || || || || || || ||
Dy      1088 gcttggatccccctattcttaccataatgagcagataattgctgctcacgtccact 1147

Qy      61 tacattgacttcgacagatctggctggaagtgggtccatgaacctaaagggtactat 120
Dy      ||||| || || || || || || || || || || || || || || || || || ||
Dy      1148 tacattgattcaagacgactaggtggaatgatacagacacccaaagggtacaat 1207

Qy      121 gcaactctgtcagggcccttgcccatcctccagtcagtcagacacacccacagcag 180
Dy      ||||| || || || || || || || || || || || || || || || || || ||
Dy      1208 gcaactctgtgctgagcagtcgctgattgagtgagtcagactcagcagcagcag 1267

Qy      181 gtgctggagactatacaactctgaacctgaacctgacctgctcctgctgctgccc 240
Dy      ||||| || || || || || || || || || || || || || || || || || ||
Dy      1268 gctcggagcttataataaccataataaccagagcactgctctcctgctgctgctc 1327

Qy      241 caggacctggagccctcaccatcctgtactatgttgaggaggaccacccaaagggtgagcag 300
Dy      ||||| || || || || || || || || || || || || || || || || || ||
Dy      1328 caagatttagaaccttaaccattctctactacattggaacacccaaaggattgaacg 1387

Qy      301 ctctccaaatggtggtgaagtctgttaaatgtagctga 339
Dy      || || || || || || || || || || || || || || || || || || || ||
Dy      1388 ctctctaataatgataagctctgcaaatgcagctaa 1426

RESULT 81
AAQ29178
ID      AAQ29178 standard; DNA; 1565 BP.
XX
XX      AAQ29178;

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XX      10-MAR-1993 (first entry)
XX      TGF-beta 1.
XX      Transforming growth factor; TGF; TGF-beta; TGF-5 beta; simian;
XX      Simian virus 40; SV40; expression vector; Chinese Hamster ovary; CHO;
XX      vascular endothelial cell; TGF-beta 1; TGF-beta 2; ss.
XX      Homo sapiens.
XX      Key Location/Qualifiers
XX      sig_peptide 269..355
XX      /tag= a
XX      precursor_RNA 356..1105
XX      /note= "Signal peptide, pre-pro-protein"
XX      /tag= b
XX      mat_peptide 1106..1438
XX      /note= "Pro-protein"
XX      /tag= c
XX      WO9216228-A.
XX      01-OCT-1992.
XX      13-MAR-1992; 92WO-US01993.
XX      14-MAR-1991; 91US-0669171.
XX      (BRIM ) BRISTOL-MYERS SQUIBB CO.
XX      Madisen L, Merwin J, Purchio AF;
XX      WPI; 1992-348938/42.
XX      P-PSDB; AAR29657.
XX      Compsn. comprising new chimeric TGF-B (TGF-beta 1-beta 2) -
XX      inhibits proliferation of vascular endothelial cells, useful for
XX      treating cancer and to promote wound healing
XX      Disclosure; Fig 1; 45pp; English.
XX      The sequence given encodes the human transforming growth factor
XX      (TGF)-beta 1. This was used within the scope of the invention to
XX      compare to a simian TGF hybrid termed TGF-beta 1/beta 2 (or TGF-5
XX      beta) (see also AAQ29177). the chimeric DNA sequence could be placed
XX      under the control of Simian virus 40 (SV40) expression regulatory
XX      region within an expression vector and used to transfect Chinese
XX      Hamster ovary (CHO) cells. CHO transfectants can be seen to synthesize
XX      and secrete high levels of mature TGF-5 beta. TGF-5 beta induces
XX      effects on the proliferation of vascular endothelial cells equivalent
XX      to those produced by TGF-beta 1.
XX      Sequence 1565 BP; 300 A; 553 C; 439 G; 273 T; 0 other;

Query Match      52.0%; Score 176.2; DB 13; Length 1565;
Best Local Similarity 72.3%; Pred. No. 8.1e-41;
Matches 245; Conservative 0; Mismatches 88; Indels 6; Gaps 1;

Qy      1 gcttggacacaaataactgctccgcaacttgaggagagaactgctgtgccccctc 60
Dy      || || || || || || || || || || || || || || || || || || || || ||
Dy      1106 gccctggacacaaataactgctccagaaatgagcagtaattgctcagctgcgctt 1165

Qy      61 tacattgacttcgacagatctggctggaagtgggtccatgaacctaaagggtactat 120
Dy      ||||| || || || || || || || || || || || || || || || || || ||
Dy      1166 tacattgatttc-----gatctagggtggaatgagtcacagacccaaagggtaccat 1219

Qy      121 gccaaactctgctcagggcccttgcccatcctccagtcagtcagacacacccacagcag 180
Dy      ||||| || || || || || || || || || || || || || || || || || ||
Dy      1220 gccaaactctgctcgggccccctgccccacatttgagcctgagcagcagtcagtcagcag 1279

Qy      181 gtgctggagactgtacaacacactctgaacctgaacctgaacctgctcctgctgctgcc 240

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PT useful for analysis to perform manipulations to increase yield of
 XX recombinant production of the protein

PS Example 2; Fig 2; 26pp; English.

XX This nucleotide sequence comprises a fragment of the human
 CC transforming growth factor-beta 1 (TGF-beta 1) gene incorporating
 CC an exon and flanking intron sequences. It was isolated from a
 CC human genomic library using probes based on a partial protein
 CC sequence of TGF-beta 1. The exon encodes amino acids 288-338
 CC (see AAU78788) of TGF-beta 1. Restriction fragments of the isolated
 CC exon were used as probes for the isolation of TGF-beta 1 cDNAs
 CC (see AAU52933). The invention relates to the recombinant production
 CC of TGF-beta. Nucleic acids encoding TGF-beta have been isolated
 CC and cloned into vectors which are replicated in bacteria and
 CC expressed in eukaryotic cells. TGF-beta recovered from transformed
 CC cells is used in known therapeutic applications. TGF-beta nucleic
 CC acids are also useful in diagnosis and identification of TGF-beta
 CC clones.

XX Sequence 975 BP; 274 A; 184 C; 338 G; 179 T; 0 other;

Query Match 28.6%; Score 96.8; DB 19; Length 975;
 Best Local Similarity 74.4%; Pred. No. 2.5e-18;
 Matches 122; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

QY 21 ctccgcaacttgaggagaactgctgtgtgcgccccctctacattgacttccgacagga 80

DB 341 ctgcagctccacgaggaagactgctgtgtgcgagctgtacattgacttccgacagga 400

QY 81 tctggctggaagtgggtccatgaacctaaagggtactatgccaaacttctgtctcaggccc 140

DB 401 cctcgctggaagtgtatccacagagcccaagggtaccatgccaaacttctgtctcaggccc 460

QY 141 ttgccatactccgagtgacagacacacacccacagcacggtgc 184

DB 461 ctgcccctacattggagctgacacgacgagtcacagcaaggtac 504

RESULT 88

AAQ56924

ID AAQ56924 standard; DNA; 975 BP.

XX AC AAQ56924;

DT 09-JUL-1994 (first entry)

XX Human pre-TGF-beta-1.

XX TGF-beta-1; TGF-beta-2; transforming growth factor beta-1;
 KW transforming growth factor beta-3; recombinant; wound healing;
 KW vulnerability.

OS Homo sapiens.

FH Key Location/Qualifiers

FT exon

FT 1..975 a

FT /codon_start= 348..350

XX US5284763-A.

XX 08-FEB-1994.

XX 22-MAR-1985; 85US-0715142.

XX 22-MAR-1985; 85US-0715142.

PR 13-MAR-1987; 87US-0025423.

PR 04-AUG-1989; 89US-0389929.

PR 04-MAR-1992; 92US-0845893.

XX (GETH) GENENTECH INC.

XX Derynk RMA, Goeddel DV;

XX WPI; 1994-056343/07.

DR P-PSDB; AAQ56924.

XX Nucleic acid sequences encoding transforming growth factor-beta -
 PT diagnostic probes, and for use in therapeutics

XX Disclosure; Fig 2; 25pp; English.

XX cDNA sequences were determined for human pre-TGF-beta-1 (AAQ56923),
 CC pig TGF-beta-3 (AAQ56925) and human TGF-beta-3 (AAQ56926), and the
 CC corresponding amino acid sequences were determined (AAR46227-29,
 CC respectively). A genomic fragment corresponding to a human TGF-
 CC beta-1 exon (AAQ56924) was also isolated and its amino acid sequence
 CC determined (AAR46230). The sequences have been used in the
 CC construction of vectors for the expression of recombinant TGF-
 CC beta.

XX Sequence 975 BP; 274 A; 181 C; 341 G; 179 T; 0 other;

Query Match 28.1%; Score 95.2; DB 15; Length 975;
 Best Local Similarity 73.8%; Pred. No. 7.1e-18;
 Matches 121; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

QY 21 ctccgcaacttgaggagaactgctgtgtgcgccccctctacattgacttccgacagga 80

DB 341 ctgcagctccacgaggaagactgctgtgtgcgagctgtacattgacttccgacagga 400

QY 81 tctggctggaagtgggtccatgaacctaaagggtactatgccaaacttctgtctcaggccc 140

DB 401 cctcgctggaagtgtatccacagagcccaagggtaccatgccaaacttctgtctcaggccc 460

QY 141 ttgccatactccgagtgacagacacacacccacagcacggtgc 184

DB 461 ctgcccctacattggagctgacacgacgagtcacagcaaggtac 504

RESULT 89

AAQ11775

ID AAQ11775 standard; DNA; 817 BP.

XX AC AAQ11775;

DT 23-JUL-1991 (first entry)

XX Encodes Fb-Fb-truncated "(8 Cys)"-TGF-beta.

XX Transforming Growth Factor beta; AIDS; ss.

XX Synthetic.

FH Key Location/Qualifiers

FT sig_peptide

FT /tag= a

FT /note= "modified trp-LE leader sequence"

FT 181..375

FT misc_RNA

FT /tag= b

FT /product= fragment B of Staphylococcal Protein A

FT /note= "directly linked to a second Fb fragment"

FT misc_RNA

FT /tag= c

FT /product= Fragment B of Staphylococcal Protein A

FT 553..564

FT misc_structure

FT /tag= d

FT /product= hinge region

FT 565..843

FT mat_peptide

FT /tag= e

FT /product= truncated TGF-beta containing 8 x Cys

FT /note= "only contains 6 Cys residues; sequence disclosed in specification omits 50 bases"

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XX PN W09105565-A.
XX PD 02-MAY-1991.
XX PF 18-OCT-1990; 90WO-US06006.
XX PR 18-OCT-1989; 89US-0422962.
XX PA (CREA-) CREATIVE BIOMOLECUL.
XX PI Cohen CM;
XX DR WPI; 1991-148530/20.
XX DR P-PSDB; AAR11957.
XX PT Recombinant truncated transforming growth factor-beta analogues -
XX PT capable of inducing an anti-proliferative effect in mammalian
XX PT epithelial cells in vitro
XX PS Claim 23; Fig 2B; 42pp; English.
XX PS This synthetic gene was designed based on reported sequence data,
XX CC codons inferred from known amino acid sequences and observations of
XX CC partial homology with known genes of the TGF-beta family. It was
XX CC assembled from chemically synthesised oligonucleotides and can be
XX CC expressed in prokaryotic host cells. The sequence is that given in
XX CC the specification, however, 50 bases should be inserted between
XX CC nucleotides 600 and 601 of this sequence; the two "missing" Cys
XX CC codons are presumably contained in the omitted sequence. The
XX CC truncated TGF-beta protein is cleaved from the Fb-Fb domain at the
XX CC hinge region to give the truncated product.
XX CC See also AAQ11774, AAR11942-7 and AAR11954.
XX SQ Sequence 817 BP; 207 A; 213 C; 219 G; 178 T; 0 other;

Query Match 21.6%; Score 73.2; DB 12; Length 817;
Best Local Similarity 61.6%; Pred. No. 1.2e-11;
Matches 117; Conservative 0; Mismatches 73; Indels 0; Gaps 0;

Qy 143 gccataactccgcagtgacagacacacacagacagcagtgctggtgactgtacacactc 202
Db 615 gtccgtacatctggtctggtatccacagctactccaagtgctgctctgtacacacg 674
Qy 203 tgaacctgaagcatctgcctgccttgcgtgcgtgccccaggaacctggagccctgacca 262
Db 675 ataacccggggctagcagcagctccgtgctgtgttccacagccttggaaccgctgcga 734
Qy 263 tctgtactatgttgggagaccacacaaagtggagcagctctccacacatggtggtgaagt 322
Db 735 tegtattacgtcggccgtaagcctaaggttgaaacagctgtctaactgattgtgcga 794
Qy 323 cttgtaaatg 332
Db 795 gttgcaagtg 804

RESULT 90
AAQ23678
ID AAQ23678 standard; DNA; 894 BP.
XX AC AAQ23678;
XX DT 17-SEP-1992 (first entry)
XX DE Encodes C-terminal portion of bovine BMP-6.
XX KW bovine bone morphogenic protein-6; bone defects; cartilage defects;
XX KW wound healing; bone repair; cartilage formation;
XX KW periodontal disease; ss.
XX OS Synthetic.

```

```

XX FH Key Location/Qualifiers
XX FT CDS 1..669
XX FT /*tag= a
XX FT /product= C-terminal part of bovine BMP-6
XX PN W09205199-A.
XX PD 02-APR-1992.
XX PF 26-SEP-1991; 91WO-US07069.
XX PR 26-SEP-1990; 90US-0588227.
XX PA (GENE-) GENETICS INST INC.
XX PI Celeste A J, Rosen V A, Wang E A, Wozney J M;
XX DR WPI; 1992-132089/16.
XX PT New human bone morphogenic protein-5 derivs. - for treating bone
XX PT and/or cartilage defects, burns, incisions, ulcers, for wound
XX PT healing
XX PS Example 4; Page 25; 54pp; English.
XX PS This sequence was isolated from positive clones in a bovine lambda
XX CC gt10 library isolated with probes AAQ23673-6, which were then screened
XX CC with HELL5. One which hybridised positive was sequenced to yield the
XX CC given sequence. An inframe stop codon indicates it encodes the
XX CC C-terminal part of bovine BMP-6.
XX CC See also AAQ23773-81, and AAR22497-9.
XX SQ Sequence 894 BP; 169 A; 301 C; 277 G; 147 T; 0 other;

Query Match 16.1%; Score 54.6; DB 13; Length 894;
Best Local Similarity 51.9%; Pred. No. 2.4e-06;
Matches 179; Conservative 0; Mismatches 154; Indels 12; Gaps 2;

Qy 7 gacaccaatactgcttcgcgaacttgaggagagaactgctgtgtgcgccctctacatt 66
Db 325 gctcagactacaacagcagcgagctgaagacgctgcgcgaagcatgagcttactcgtg 384
Qy 67 gacttcgacaggaatctggctggaagtgggtccatgaacctaaaggctactatgccaac 126
Db 385 agcttcaggaacctgggtggcaggactggatcatgcccccaaggctcgtgccaac 444
Qy 127 ttctgctcaggcccttgcccataccctcccgagtgccagac-----acaacccacgc 177
Db 445 tactgtgacggagaaatgttcttcctctcaacgcacacatgaacgtaccacacatgcc 504
Qy 178 acggtgtgggactgtacaaacctgaacctgaacctgaagcatctgctcgtcgttgcgtg 237
Db 505 atcgtgcagacctggttcacctcatgaaccgcgagtaoctcccaaacgctgtgcgcg 564
Qy 238 cccacaggaactggagccctcgaccctctactatgttggggaggacc---cccaaatg 294
Db 565 ccacgaaactgaacgccatctcgtgtctactctgcagacacacactccaatgctcctg 624
Qy 295 gacgagctctccaaacatgggtgggtgaagtcttgaatgttagctga 339
Db 625 aagaagtaccggaaacatggtcgtacgagcgtgtgggtgccactga 669

RESULT 91
AAQ37567
ID AAQ37567 standard; DNA; 894 BP.
XX AC AAQ37567;
XX DT 22-JUN-1993 (first entry)
XX DE

```


CC include epidermis, nerve, muscle, liver, lung, cardiac, pancreas and
CC kidney. Osteoarthritis and osteoporosis can also be treated. It is useful
CC for healing bone fractures and cartilage defects in humans and other
CC animals, particularly domestic animals and thoroughbred horses and also
CC has uses in cosmetic plastic surgery. The composition may increase
CC neuronal survival and be useful in transplantation and the treatment of
CC conditions which exhibit a decrease in neuronal survival. The present
CC sequence represents a DNA encoding the carboxy-terminal part of bovine
CC BMP-6 protein.
XX
SQ Sequence 894 BP; 169 A; 301 C; 277 G; 147 T; 0 other;

Query Match 16.1%; Score 54.6; DB 20; Length 894;
Best Local Similarity 51.9%; Pred. No. 2.4e-06;
Matches 179; Conservative 0; Mismatches 154; Indels 12; Gaps 2;
QY 7 gacacaattactgtccgaacttgagagagaactgtgtgtgccccctctacatt 66
DB 325 gctcagactacaacagcagcagctgaagacgctgcggaagcatgagctctacgtg 384
QY 67 gactccgacagagatctggctggagtggtccatgaacctaaaggctactatgccaac 126
DB 385 agcttcaggaactgggtggcaggactggtatgtgcccccaagggtcacgtgccaac 444
QY 127 ttctgtcagggcccttgccatactctccgactgcagac-----acaacccacagc 177
DB 445 tactgtgacggagaatgttcctctcctcaacgcacacataaagcgtaccacatgcc 504
QY 178 acggtgctgggactgtacaacactctgaacctgaagcatctgctcgtgctgctgctg 237
DB 505 atcgtgcagacctggttcacatcatgaacctgaacctgacgtcccaaacgctgctg 564
QY 238 ccccgagacctgagccctaccatcctgtactatgttgaggagacc---cccaaatgtg 294
DB 565 cccaggaactgaagccatctcgtgctcctacttcgacgacaactcccaatgtcatcctg 624
QY 295 gacgactctcccaacatggtgtgaagtctgttaaatgtagtga 339
DB 625 aagaagtaccggaacatggtctagcagcgtgtggtgccactga 669

RESULT 93
AAN91769
ID AAN91769 standard; DNA; 454 BP.
AC AAN91769;
XX
DT 22-MAR-1990 (first entry)
XX
DE Consensus gene/probe to osteogenic protein OP1.
XX
KW Periodontal; osteoarthritis
XX
OS Mammal.
XX
PN W08909787-A.
XX
PD 19-OCT-1989.
XX
PF 07-APR-1989; 89WO-US01453.
XX
PR 08-APR-1988; 88US-0179406.
XX
PA (CREA) CREATIVE BIOMOLECUL.
XX
PI Kuberasampath T, Oppermann H, Rueger DC, Ozkaynak E;
XX
DR WPI: 1989-324202/44.
DR P-PSDB; AAP91200.
XX
PT Osteogenic devices comprising matrix contg. osteogenic protein - useful
for inducing endochondral bone growth eg in non-union fractures

XX Disclosure; fig 1B; 104pp; English.
PS This is a synthetic consensus gene sequence, used as a probe to isolate
CC natural genes of proteins that induce endochondral bone formation.
XX
SQ Sequence 454 BP; 101 A; 146 C; 121 G; 86 T; 0 other;
Query Match 15.8%; Score 53.4; DB 10; Length 454;
Best Local Similarity 53.2%; Pred. No. 4.3e-06;
Matches 142; Conservative 0; Mismatches 116; Indels 9; Gaps 1;
QY 51 gcqcccccttacatgacttccgacaggaatctggtgggaagtgggtcccatgaacacaa 110
DB 79 gcacgagctgtagtacgttccgagacctggctggcaggactggatcatcgccgtga 138
QY 111 gggtactatgccaaacttctgcaggcccttgccataacctc-----cgcagtg 161
DB 139 agacttcgacgctactactgtcccgagcgtgcaggttccctctcgggatcacttcaa 198
QY 162 agacacaaacccacagcagctgctgggactgtacaacactctgaacctgaagcatctgc 221
DB 199 cagcacaacacgcgcgtggtgcagacctggtgaacaacatgaaccccgcaaggtacc 258
QY 222 ctgccttgcgtgctgcccagacgtgagccctgagccctgacctctgtactatgttgagg 281
DB 259 caagcctgctgctgcccacagctgtccgcacatgctgcacatgctgtacctggacgaga 318
QY 282 gacccccaaagtggagcagctctccaa 308
DB 319 ttccaccgtggtgctgaagaactacca 345
RESULT 94
AAT11062
ID AAT11062 standard; DNA; 630 BP.
AC AAT11062;
XX
DT 15-APR-1996 (first entry)
XX
DE Murine growth differentiation factor-11 (GDF-11) coding sequence.
XX
KW Growth differentiation factor-11; GDF-11; antibody; detection;
KW disorder; muscle; antisense; suppression; vector; liposome;
KW targeting; ss.
XX
OS Mus musculus.
XX
FH Key Location/Qualifiers
FT CDS 198..578
FT /*tag= a
FT /product= Murine growth differentiation factor-11.
XX
PN W09601845-A1.
XX
PD 25-JAN-1996.
XX
PF 07-JUL-1995; 95WO-US08543.
XX
PR 08-JUL-1994; 94US-0272763.
XX
PA (UYJO) UNIV JOHNS HOPKINS SCHOOL MED.
XX
PI Lee S, Mcpherron AC;
XX
DR WPI: 1996-097589/10.
DR P-PSDB; AAR88554.
XX
PT New Growth Differentiation Factor-11 (GDF-11) - with tissue-specific
expression in muscle, neural and uterine cells, for detecting cell
proliferation disorders

XX	Claim 3; Page 38-39; 67pp; English.
XX	
XX	Antibodies directed against the growth differentiation factor (GDF)
CC	are useful for detecting cell proliferative disorders when contacted
CC	with a specimen from a subject suspected of having a GDF-11
CC	associated disorder. Antibody binding constitutes a positive result.
CC	Detection is performed in muscle cells in vitro or in vivo.. The
CC	antibodies may also be used in the treatment of such disorders by
CC	suppressing GDF-11 activity. Antisense GDF-11 reagents may also be
CC	used. Vectors are utilised in the treatment process e.g. colloidal
CC	dispersion systems such as liposomes which are target specific and
CC	either anatomically or mechanistically targetted.
XX	
XX	Sequence 630 BP; 155 A; 173 C; 159 G; 143 T; 0 other;
XX	
XX	Query Match 15.6%; Score 52.8; DB 17; Length 630;
XX	Best Local Similarity 55.4%; Pred. No. 7e-06;
XX	Matches 102; Conservative 0; Mismatches 82; Indels 0; Gaps 0;
XX	
QY	17 actgcttcgcgaacttgaggagaactgctgtgtgcccctctacattgacttccgac 76
Db	
Db	262 actgcgatgaacctcagtgagtcgcgcgtgctgccgatctctctcacagtgacttg 321
QY	77 aggatctgggtgaaagtgggtccatgaacctaaagggtctactatgccaaacttctgctcag 136
Db	
Db	322 aggcctttgctggagctgactgatctgcacctaaagcgtacaaaggccaactactgctcg 381
QY	137 gcccttgccatacctccgcagtcgagacacacccacagcacggtgctggagactgtaca 196
Db	
Db	382 gccagtcggaatacatgttcatgcataaagtatccacacacccacttggtgcaacaggcca 441
QY	197 acac 200
Db	
Db	442 accc 445
XX	
XX	RESULT 95
XX	AAV07556
ID	AAV07556 standard; DNA; 630 BP.
XX	
XX	AAV07556;
XX	
XX	09-NOV-1998 (first entry)
XX	
DE	Mouse growth differentiation factor-11 DNA fragment.
XX	
KW	Growth differentiation factor-11; GDF-11; mouse; transgenic animal;
KW	transforming growth factor-beta; cell proliferation;
KW	neuromuscular disorder; muscular dystrophy; muscle atrophy; aging;
KW	obesity; therapy; ss.
XX	
OS	Homo sapiens.
XX	
XX	Key Location/Qualifiers
FT	198..578
FT	/*tag= a
XX	
XX	W09835019-A1.
XX	
XX	13-AUG-1998.
XX	
XX	06-FEB-1998; 98WO-US02310.
XX	
XX	06-FEB-1997; 97US-0795671.
XX	
XX	(UYJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
XX	
PI	Lee S, McPherron AC;
XX	
XX	WPI; 1998-447217/38.
DR	P-PSDB; AAW65459.
DR	

XX Transgenic animal growth differentiation factor-11 is inhibited - by
PT insertion of transgene, also use of GDF-11 inhibitors for treating
PT muscular wasting, neuromuscular disease, obesity
PT
PT
PS Example 1; Page 53-54; 89pp; English.
XX
XX This nucleotide sequence includes a region of an open reading frame
CC that codes for the C-terminal portion (see AAW65459) of murine growth
CC differentiation factor-11 (GDF-11), a new member of the transforming
CC growth factor-beta superfamily that is associated with various cell
CC proliferative disorders, especially those involving muscle, nerve
CC and adipose tissue. It was isolated from a murine genomic library
CC encoding murine GDF-8 as probe. A full-length sequence (see AAY07555)
CC encoding human GDF-11 (see AAW05458) is also provided. Claimed
CC transgenic animals, especially bovine, porcine, ovine or avian
CC animals, have been altered so that production of GDF-11 is reduced
CC or completely disrupted. Such animals have higher than normal
CC levels of muscle tissue, preferably without increased fat and/or
CC cholesterol levels, and are useful as food products. The invention
CC also provides methods for treating a muscle or adipose tissue
CC disorder in an animal, including humans. A GDF-11 antibody,
CC antisense molecule or dominant negative polypeptide (or a
CC polynucleotide encoding a dominant negative polypeptide) can be
CC administered to a patient to treat e.g. a muscle wasting disease,
CC a neuromuscular disorder, muscle atrophy, obesity or other
CC adipocyte cell disorders, and aging.
XX
SQ Sequence 630 BP; 155 A; 173 C; 159 G; 143 T; 0 other;

Query Match 15.6%; Score 52.8; DB 19; Length 630;
Best Local Similarity 55.4%; Pred. No. 7e-06;
Matches 102; Conservative 0; Mismatches 82; Indels 0; Gaps 0;

QY 17 actgtcttcgcgaacttgaggagaactgctgtgtgcgccctctacattgacttcgcac 76
||||| .||| .||| .||| .||| .||| .||| .||| .||| .|||
Db 262 actgcgatgaacctcagtgagtcgccgtgtgcgcatctctctccacgtgacttgc 321
||||| .||| .||| .||| .||| .||| .||| .||| .||| .|||
QY 77 aggattcggctggaagtgggtccattgaacctaaagggctactatgccaaacttctcag 136
||||| .||| .||| .||| .||| .||| .||| .||| .||| .|||
Db 322 aggccttggctgggactgcatcgcacctaaagcgtcacaaggcccaactctctccg 381
||||| .||| .||| .||| .||| .||| .||| .||| .||| .|||
QY 137 gcccttgcccatacctccgcagtcgacgacacacccacagcagctgctgggactgtaca 196
||||| .||| .||| .||| .||| .||| .||| .||| .||| .|||
Db 382 gccagtcgaatacatgttcatgcacaaagtatccacacacccacttggtgcacaggcca 441
||||| .||| .||| .||| .||| .||| .||| .||| .||| .|||
QY 197 acac 200
|||
Db 442 accc 445

RESULT 96
AAZ58970
ID AAZ58970 standard; DNA; 630 BP.
XX
AC AAZ58970;
XX
DT 08-MAY-2000 (first entry)
XX
DE Mouse growth differentiation factor-11 (GDF-11) encoding DNA.
XX
KW Growth differentiation factor-11; GDF-11; renal disease; cancer;
KW muscle associated disorder; AIDS; cell proliferation; immunologic; fat;
KW neurodegenerative disorder; adipose tissue disorder; animal food; muscle;
KW obesity; nephrotropic; cytostatic; anti-HIV; anorectic; mouse; ds.
XX
OS Mus sp.
XX
FH Key Location/Qualifiers
FT CDS 198..578
FT /tag= a
FT /product= "GDF-11"

```

FT XX /note= "the start codon is not indicated"
PN XX
PD PD WO2000067116-A1.
XX 10-FEB-2000.
XX 28-JUL-1999; 99WO-US17252.
XX 28-JUL-1998; 98US-0123929.
XX (UWJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
XX
XX Lee S, McPherron AC;
XX PI
XX WPI: 2000-195289/17.
XX P-PSDB; RAY77565.
XX
XX Preparation of transgenic animal food product useful for treating renal
XX and muscular disorders, comprises introducing transgene interfering
XX with expression of growth differentiation factor-11 into embryo
XX
XX Example 3; Fig 1A; 97pp; English.
XX
XX The invention relates to a method for producing animal food products with
XX increased ribs content. The method comprises: (a) introducing a transgene
XX which interferes with expression of growth differentiation factor-11
XX (GDF-11), into an embryo; (b) allowing the embryo to mature; (c) cross-
XX breeding the transgene-positive progeny; (d) processing these progeny to
XX obtain the foodstuff. Modulators of GDF-11 are useful for treating acute
XX or chronic renal disease, and various other muscle associated disorders
XX e.g cancer, AIDS; cell proliferative disorders, neurodegenerative
XX disorders; adipose tissue disorders and immunologic disorders. The animal
XX food product comprises large amounts of muscle and meagre amounts of fats
XX and cholesterol, hence useful in treating obesity and related disorders.
XX The present sequence represents a genomic DNA encoding a partial mouse
XX GDF-11 polypeptide.
XX
XX Sequence 630 BP; 155 A; 173 C; 159 G; 143 T; 0 other;

Query Match 15.6%; Score 52.8; DB 21; Length 630;
Best Local Similarity 55.4%; Pred. No. 7e-06;
Matches 102; Conservative 0; Mismatches 82; Indels 0; Gaps 0;

QY 17 actgcttcgcgaacttgaggagaaactgctgtgctgcccctctacattgacttcgcag 76
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 262 actcgcgatgaacactcgagtgcgcgcgtgctgcccgcatactcctcacagtgaacttg 321
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 77 aggaactcggctggaagtgggtccatgaaccatgaaggcgtactatgcgaactctgctcag 136
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 322 aggcctttgctgggactggatcatcgacccatgaagcgtacaaaggccaaactactgctccg 381
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 137 gcccttgcccatcctccgactgcagacacacacccacagcagcgtgctggactgtaca 196
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 197 acac 200
Db |||
QY 442 accc 445

RESULT 97
AAQ79444
ID AAQ79444 standard; DNA; 789 BP.
XX
XX AAQ79444;
XX
XX 10-AUG-1995 (first entry)
XX
XX Partial bovine bone morphogenetic protein-11 (BMP-11).
XX
XX Bone morphogenetic protein-11; BMP-11; TGF-beta superfamily; ss.
XX

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OS Bos taurus.
XX
XX Key Location/Qualifiers
FH CDS 324..704
FT /*tag= a
FT intron 322..323
FT /*tag= b
FT /note= "putative 3' end of intron"
FT mat_peptide 375..701
FT /*tag= c
XX
XX WO9426892-A.
XX
XX 24-NOV-1994.
XX
XX 12-MAY-1994; 94WO-US05288.
XX
XX 12-MAY-1993; 93US-0061464.
XX
XX (GEMY ) GENETICS INST INC.
XX
XX Celeste AJ, Wozney JM;
XX
XX WPI: 1995-006788/01.
XX P-PSDB; AAR66147.
XX
XX New DNA encoding bone morphogenetic protein 11 - and related
XX vectors, transformed cells and polypeptide(s), including
XX heterodimers, useful e.g. in fertility control bone and tissue
XX repair, etc.
XX
XX Claim 2; Page 40-41; 57pp; English.
XX
XX A bovine genomic library (strain Bovine Activin WC) in lambda EMBL3
XX was screened under low stringency conditions with a 1081-1403 base
XX fragment of human BMP-7 DNA. Positive clones were screened with BMP-
XX 5, -6, and -7 probes under high stringency conditions and one clone
XX reactive in the first screen but not in the second was selected. The
XX hybridisation characteristics were localised to a 0.5 kb fragment.
XX The partial sequence of this clone, lambda 7r-30 (ATCCD 75433) is
XX 079444. The 5' limit of this exon of the bovine BMP-11 gene is
XX difficult to define. Clone lambda 7r-30 contains at least one exon/
XX intron boundary. BMP-11 polypeptide exists as a dimer comprising two
XX of the mature protein AA sequences or as a heterodimer with one
XX mature sequence from BMP-11 and the other being any of BMP 1-10.
XX The predicted mol. wt. of the mature active species comprising two
XX mature protein sequences is approx. 12,000 daltons. Further active
XX species are contemplated comprising AAs 23-126. Primers C and D
XX are based on clone lambda 7r-30 (see Q79446, Q79447). Nts 375 or
XX 390-704 of Q79444 are claimed. AAs 18-126 of R66147 are claimed.
XX
XX Sequence 789 BP; 187 A; 213 C; 223 G; 166 T; 0 other;

Query Match 15.3%; Score 51.8; DB 16; Length 789;
Best Local Similarity 54.9%; Pred. No. 1.4e-05;
Matches 129; Conservative 0; Mismatches 97; Indels 9; Gaps 1;

QY 37 gagaactgctgtgtgcgcccctctacattgacttcgcagaggtatctggctggaagtgg 96
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 408 gagtcctcgtgtgcgctaccctcctcactgtgacttgaggctttgtgctggagactgg 467
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 97 gtccatgaacctaaagggtactatgtccaaactctctcctcagcccttgcccatcctccgc 156
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 468 atcatcgtctctaaacgctacaaggcccaactactgctccgcccagtcgagtacatgttt 527
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 157 agtgcagacacacacccacagcagcgtgctggactgtacaaacactctgaacctgaagca 216
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 528 atgcaaaagatctccgcacacccacttggcgcaacaggct-----aacccaagagc 578
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 217 tctgctgccttgcgtgcgtgccccaggagccttgaggccctgaccatcctgtact 271
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 579 tctcggggccctgctgcacaccacacgaagtgtccccaatacaatgctctact 633
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```


Db 468 atcatgctctcctaaacgctacaagccaactactgctccggccagtgcgagtacatgttt 527
QY 157 agtgcagacacacccacagcagcggtgctgggactgtacaacactctgaacctgaagca 216
Db 528 atgcaaaagtatccgcacacccacttgggtgcaacaggt-----aacccaagaggc 578
QY 217 tctgctcgccttgcgtgctgcccagcactggagccctgacctctgtact 271
Db 579 tctgcggggccctgctgcacacccacccaagaagtgcaccaatcaacatgctctact 633

RESULT 100
AAx58652
ID AAx58652 standard; DNA; 789 BP.
XX
AC AAx58652;
XX
DT 16-AUG-1999 (first entry)
XX
DE Bovine activin WC (BMP-11) partial DNA sequence.
XX
KW Activin WC; bone morphogenetic protein 11; BMP-11; cattle; bovine;
KW bone; cartilage; connective tissue; neuronal tissue;
KW wound healing; tissue repair; vulnery; contraceptive;
KW transforming growth factor-beta; ds.
XX
OS Bos taurus.
XX
FH Key
FT 322...323
FT intron
FT /*tag= a
FT /partial
FT /note= "putative 3' end of intron"
FT CDS 324..704
FT /*tag= b
FT mat_peptide 375..701
FT /*tag= c
XX
PN WO9924058-A2.
XX
PD 20-MAY-1999.
XX
PF 06-NOV-1998; 98WO-US23827.
XX
PR 07-NOV-1997; 97US-0966297.
XX
PA (GENEY) GENETICS INST INC.
XX
PI Celeste AJ, Thies SR, Wozney JM;
XX
DR WPI; 1999-327207/27.
XX
DR P-PSDB; AAY06096.
XX
PT Administration of human or bovine bone morphogenetic protein 11
XX
PS Example 1; Page 55; 62pp; English.

This is a partial nucleotide sequence of bovine activin WC, or bone morphogenetic protein 11 (BMP-11). The DNA was isolated by screening a bovine genomic library with a fragment of human BMP-7 DNA probe and with a mixed BMP-5, BMP-6 and BMP-7 probe; the recombinant hybridised positively to the BMP-7 probe under reduced stringency conditions and exhibited weak or no hybridisation to the mixed probe under high stringency conditions. The clone includes an open reading frame encoding at least 126 amino acids (see AAY06096) of the C-terminal portion of bovine BMP-11 protein. This is an example of a novel family of proteins of the transforming growth factor beta superfamily. BMP-11 proteins may be useful to induce bone and/or cartilage formation and in wound healing and tissue repair, or for augmenting the activity of other BMP proteins. BMP-11 may also be useful for regulating the production of follicle stimulating hormone (e.g. for contraception), to

CC stimulate haematopoiesis, to suppress the development of gonadal
CC tumours, and especially (claimed) to induce neuronal cell
CC formation, growth differentiation, proliferation and maintenance.
XX
SQ Sequence 789 BP; 187 A; 213 C; 223 G; 166 T; 0 other;

Query Match 15.3%; Score 51.8; DB 20; Length 789;
Best Local Similarity 54.9%; Pred. No. 1.4e-05;
Matches 129; Conservative 0; Mismatches 97; Indels 9; Gaps 1;

QY 37 gagaactgctgtgtgcccctctctacattgacttccgacaggaactctggtggaagtgg 96
Db 408 gagtccgctgttgcgcgtaccctctactgtgactttgaggcttttggctggactgg 467
QY 97 gtccatgaacctaaagggtactatgccaaacttctgcagggccttgcctatccatccgc 156
Db 468 atcatgctcctaaacgctacaaggccaactactgtcccgccagtgcgagtacatgttt 527
QY 157 agtgcagacacacccacagcagcggtgctgggactgtacaacactctgaacctgaagca 216
Db 528 atgcaaaagtatccgcacacccacttgggtgcaacaggt-----aacccaagaggc 578
QY 217 tctgctcgccttgcgtgctgccccaggaacctggagccccctgacctctgtact 271
Db 579 tctgcggggccctgctgcacacccacccaagaagtgcaccaatcaacatgctctact 633

Search completed: October 30, 2001, 10:56:53
Job time: 6181 sec

ALIGNMENTS

RESULT 1
US-08-486-057B-3
; Sequence 3, Application US/08486057B
; Patent No. 5650494
; GENERAL INFORMATION:
; APPLICANT: Cerletti, Nico
; APPLICANT: McMaster, Gary K.
; APPLICANT: Cox, David
; APPLICANT: Schmitz, Albert
; APPLICANT: Meyhack, Bernd
; TITLE OF INVENTION: Process for Refolding Recombinantly
; TITLE OF INVENTION: Produced TGF-beta-like Proteins
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Henry P. No. 5650494ak
; STREET: 520 White Plains Road, P.O. Box 2005
; CITY: Tarrytown
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10591-9005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,057B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/201,703
; FILING DATE: 25-FEB-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/960,309
; FILING DATE: 13-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/621,502
; FILING DATE: 03-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 8927546.5
; FILING DATE: 06-DEC-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5650494ak, Henry P.
; REGISTRATION NUMBER: 33200
; REFERENCE/DOCKET NUMBER: 4-17861/-/Cont3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 277-5110
; TELEFAX: (908) 277-4306
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 339 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..339
US-08-486-057B-3

Query Match 100.0%; Score 339; DB 1; Length 339;
Best Local Similarity 100.0%; Pred. No. 2.8e-87;
Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gctttggacacaaatctgtctccgaggaactgtgtgtgccccctc 60
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Db 1 GCTTTGGACACCAATCTGCTTCGCAACTTGGAGGAGAACTGTGTGCGCCCCCTC 60

QY 61 tacattgacttcgacaggatctgggctggaagtgggtccatgaacctaaaggctactat 120
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Db 61 TACATTGACTTCCGACAGGATCTGGGCTGGAAGTGGGTCCATGAACCTAAGGGCTACTAT 120
QY 121 gccaaattctgtcagggcccttgccataactccgcagtgagcagacacacacagcagc 180
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Db 121 GCCAACTTCTGCTCAGGCCCTTGCCCATAGCTCGCAGTGCAGACACAACCCACAGCAGC 180
QY 181 gtgctgggactgtacaacactctgaaccctgaagcagcatctacctgccttgcgtgccc 240
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Db 181 GTGCTGGGACTGTACAACACTCTGAACCCCTGAAGCATCTGCCTCGCCTTGTGCGTGCCC 240
QY 241 caggacctggagccctgaccatctgtactatgttgggagggacccccaaagtggagcag 300
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Db 241 CAGGACCTGGAGCCCTGACCATCTGTACTATGTGTGGGAGGACCCCAAGTGGAGCAG 300
QY 301 ctctccaaacatggtggtgaagtctttaaattagctga 339
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Db 301 CTCTCCAACATGGTGGTGAAGTCTTGTAAATGTAGCTGA 339
RESULT 2
US-08-470-837-33
; Sequence 33, Application US/08470837
; Patent No. 5800811
; GENERAL INFORMATION:
; APPLICANT: Nimmi, Marcel E.
; APPLICANT: Hall, Frederick L.
; APPLICANT: Tuan, Tai-Lan
; APPLICANT: Wu, Lingtao
; APPLICANT: Cheung, David T.
; TITLE OF INVENTION: Transforming Growth Factor B Fusion
; TITLE OF INVENTION: and
; TITLE OF INVENTION: Their Use in Wound Healing
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 11150 Santa Monica Boulevard, Suite 400
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90025-3395
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,837
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharp, Janice A.
; REGISTRATION NUMBER: 34,051
; REFERENCE/DOCKET NUMBER: 30630-1US01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 310-445-1140
; TELEFAX: 310-445-9031
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 339 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..336
; NAME/KEY: mat_peptide
; LOCATION: 1
US-08-470-837-33

Query Match 100.0%; Score 339; DB 1; Length 339;
Best Local Similarity 100.0%; Pred. No. 2.8e-87;
Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gcttggacacaaattactgctccgcaacttgagagaaactgctgtgagcccccctc 60
DB 1 GCTTTGGACACCAATTACTGCTTCCGCAACTTGGAGGAGAACTGCTGTGCGCCCCCTC 60

QY 61 tacattgactccgacagatgctggctggaagtgggtccatgaacctaaagggctactat 120
DB 61 TACATTGACTTCCGACAGGATCGGGCTGGAAGTGGGTCCATGAACCTTAAGGGCTACTAT 120

QY 121 gcaaatctgtcagagcccttgccatcacctccgagtcagacacaaacccacagcag 180
DB 121 GCCAACTTCTGCTAGGCGCTTGGCCATACCTCCGAGTGCAGACACAAACCCACAGCAG 180

QY 181 gtgctgggactgtacaacactctgaacctgaacctgaacctgacctgacctgacctg 240
DB 181 GTGCTGGGACTGTACAACACTCTGAACCCCTGAAGCACTGCGCTTGGCTGGCTGGCC 240

QY 241 caggacctggagccctgacctcctgtactatgttggaggagcccccacaaagtggagcag 300
DB 241 CAGGACCTGGAGCCCTGACCATCTGTACTATGTGTTGGAGGAGACCCCAAGTGGAGCAG 300

QY 301 ctctccaaatggtggtgaagtctgttaaatgtagctga 339
DB 301 CTCTCCAAATGGTGGTGAAGTCTTGTAAATGTAGCTGA 339

RESULT 3
US-08-789-588-3
; Sequence 3, Application US/08789588
; Patent No. 5922846
; GENERAL INFORMATION:
; APPLICANT: Cerletti, Nico
; APPLICANT: McMaster, Gary K.
; APPLICANT: Cox, David
; APPLICANT: Schmitz, Albert
; APPLICANT: Meyhack, Bernd
; TITLE OF INVENTION: Process for Refolding Recombinantly
; TITLE OF INVENTION: Produced TGF-beta-like Proteins
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Henry P. No. 5922846ak
; STREET: 520 White Plains Road, P.O. Box 2005
; CITY: Tarrytown
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10591-9005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/789,588
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/486,057
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/201,703
; FILING DATE: 25-FEB-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/960,309
; FILING DATE: 13-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/621,502
; FILING DATE: 03-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 8927546.5

FILING DATE: 06-DEC-1989
ATTORNEY/AGENT INFORMATION:
NAME: No. 5922846ak, Henry P.
REGISTRATION NUMBER: 33200
REFERENCE/DOCKET NUMBER: 4-17861/+ /Cont3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 277-5110
TELEFAX: (908) 277-4306
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 339 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..339
US-08-789-588-3

Query Match 100.0%; Score 339; DB 2; Length 339;
Best Local Similarity 100.0%; Pred. No. 2.8e-87;
Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gcttggacacaaattactgctccgcaacttgagagaaactgctgtgagcccccctc 60
DB 1 GCTTTGGACACCAATTACTGCTTCCGCAACTTGGAGGAGAACTGCTGTGCGCCCCCTC 60

QY 61 tacattgactccgacagatgctggctggaagtgggtccatgaacctaaagggctactat 120
DB 61 TACATTGACTTCCGACAGGATCGGGCTGGAAGTGGGTCCATGAACCTTAAGGGCTACTAT 120

QY 121 gcaaatctgtcagagcccttgccatcacctccgagtcagacacaaacccacagcag 180
DB 121 GCCAACTTCTGCTAGGCGCTTGGCCATACCTCCGAGTGCAGACACAAACCCACAGCAG 180

QY 181 gtgctgggactgtacaacactctgaacctgaacctgaacctgacctgacctgacctg 240
DB 181 GTGCTGGGACTGTACAACACTCTGAACCCCTGAAGCACTGCGCTTGGCTGGCTGGCC 240

QY 241 caggacctggagccctgacctcctgtactatgttggaggagcccccacaaagtggagcag 300
DB 241 CAGGACCTGGAGCCCTGACCATCTGTACTATGTGTTGGAGGAGACCCCAAGTGGAGCAG 300

QY 301 ctctccaaatggtggtgaagtctgttaaatgtagctga 339
DB 301 CTCTCCAAATGGTGGTGAAGTCTTGTAAATGTAGCTGA 339

RESULT 4
US-09-123-233-5
; Sequence 5, Application US/09123233
; Patent No. 6057430
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: No. 6057430el process for the production of
; TITLE OF INVENTION: biologically active dimeric protein
; NUMBER OF SEQUENCES: 14
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/123,233
; FILING DATE:
; CLASSIFICATION: 530
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 339 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double

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; TOPOLOGY: linear
; MOLECULE TYPE: CDNA to mRNA
; IMMEDIATE SOURCE:
; CLONE: E. coli LC137/pPLu.htGF-beta3 (DSM 5658)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..336
; OTHER INFORMATION: /product= "human TGF-beta3"
US-09-123-233-5

Query Match 100.0%; Score 339; DB 3; Length 339;
Best Local Similarity 100.0%; Pred. No. 2.8e-87;
Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gctttgacacaaattactctccgaacttgagagagaactgctgtgccccctc 60
DB 1 GCTTTGGACACAAATTACTGCTTCGCAACTTGGAGGAGAAGTGTGTGCGCCCCCTC 60
QY 61 tacattgactccgacagatctggctggaagtgggtcccatgaacctaaaggctactat 120
DB 61 TACATTGACTTCCGACAGACTGGGCTGGAAGTGGTCCATGAACCTAAGGGCTACTAT 120
QY 121 gccaaactctgctcaggcccttgcccatctccgcagctgcagacacacacagcagc 180
DB 121 GCCAAACTTCTGCTCAGGCCCTTGCCCATACCTCCGACGTGCAGACACAAACCCACAGCAG 180
QY 181 gtgctgggactgtacaacactctgaacctgaacctgaacctgctgcgctgtgctgccc 240
DB 181 GTGCTGGGACTGTACAACACTCTGAACCTGAACCTGAACCTGCTCGCCCTGTGCTGCGCC 240
QY 241 cagacctggagccctgaacctctgactatgttgaggagaccccaagtgagcag 300
DB 241 CAGGACCTGGAGCCCTGACCATCTCTGACTATGTGGGAGAGACCCCAAGTGGAGCAG 300
QY 301 ctctccaacatggtggaagtcttgtaaatgtagctga 339
DB 301 CTCTCCAACATGGTGGTGAAGTCTTGTAATGTAGCTGA 339

METHODS OF PR
; Sequence 1, Application PC/TUS9104541
; GENERAL INFORMATION:
; APPLICANT: Oncogene Science Inc.
; TITLE OF INVENTION: TISSUE DERIVED TUMOR GROWTH INHIBITORS
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/04541
; FILING DATE: 19910625
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 1919/22669-F-PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)977-9550
; TELEFAX: (212)664-0525
; TELEX: 422523 COOP UI
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:

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; LENGTH: 2529 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: N
; ANTI-SENSE: N
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Transforming Growth Factor-Beta 3
; IMMEDIATE SOURCE:
; CLONE: TGF-B3
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 263..1498
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 263..1498
; OTHER INFORMATION:
PCT-US91-04541-1

Query Match 100.0%; Score 339; DB 5; Length 2529;
Best Local Similarity 100.0%; Pred. No. 5.2e-87;
Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gctttgacacaaattactctccgaacttgagagagaactgctgtgccccctc 60
DB 1163 GCTTTGGACACAAATTACTGCTTCGCAACTTGGAGGAGAAGTGTGTGCGCCCCCTC 1222
QY 61 tacattgactccgacagatctggctggaagtgggtcccatgaacctaaaggctactat 120
DB 1223 TACATTGACTTCCGACAGGATCTGGGCTGGAAGTGGGTCCATGAACCTAAGGGCTACTAT 1282
QY 121 gccaaactctgctcaggcccttgcccatctccgcagctgcagacacacacagcagc 180
DB 1283 GCCAAACTTCTGCTCAGGCCCTTGCCCATACCTCCGACGTGCAGACACAAACCCACAGCAG 1342
QY 181 gtgctgggactgtacaacactctgaacctgaacctgaacctgctgcgctgtgctgccc 240
DB 1343 GTGCTGGGACTGTACAACACTCTGAACCTGAACCTGCGCTTCGCTTCGCTGCGGCC 1402
QY 241 caggacctggagccctgacctctgactatgttgaggagaccccaagtgagcag 300
DB 1403 CAGGACCTGGAGCCCTTGACCATCTCTGACTATGTGGGAGGAGACCCCAAGTGGAGCAG 1462
QY 301 ctctccaacatggtggaagtcttgtaaatgtagctga 339
DB 1463 CTCTCCAACATGGTGGTGAAGTCTTGTAATGTAGCTGA 1501

RESULT 6
5262319-1
; Patent No. 5262319
; APPLICANT: IWATA, KENNETH K.; FOULKES, J. GORDON; DIJKE,
; PETER T.; HALEY, JOHN D.
; TITLE OF INVENTION: METHOD FOR OBTAINING BONE MARROW FREE
; OF TUMOR CELLS USING TRANSFORMING GROWTH FACTOR B3
; NUMBER OF SEQUENCES: 9
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/543,341
; FILING DATE: 25-JUN-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 353,410
; FILING DATE: 17-MAY-1989
; APPLICATION NUMBER: 183,410
; FILING DATE: 20-APR-1988
; APPLICATION NUMBER: 111,022
; FILING DATE: 20-OCT-1987
; APPLICATION NUMBER: 922,121
; FILING DATE: 20-OCT-1986
; APPLICATION NUMBER: 847,931

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; FILING DATE: 07-APR-1986
; APPLICATION NUMBER: 725,003
; FILING DATE: 19-APR-1985
; SEQ ID NO:1:
; LENGTH: 2529
5262319-1

Query Match 100.0%; Score 339; DB 6; Length 2529;
Best Local Similarity 100.0%; Pred. No. 5.2e-87;
Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gctttgacacaaattactgtctccgaacttgagagaaactgtgtgccccctc 60
|||||
Db 1163 gctttgacacaaattactgtctccgaacttgagagaaactgtgtgccccctc 1222
|||||
QY 61 tacattgacttcgcagagatcgggtggaagtgggtccatgaacctaaagggtactat 120
|||||
Db 1223 tacattgacttcgcagagatcgggtggaagtgggtccatgaacctaaagggtactat 1282
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QY 121 gccaaattctgtcagggcccttgccataacctccgcagtgagacacaaacccagcag 180
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Db 1283 gccaaattctgtcagggcccttgccataacctccgcagtgagacacaaacccagcag 1342
|||||
QY 181 gtctgggactgtacaaactctgaaccttgaaacctgaagcatctgcctgcctgtgcgtgcc 240
|||||
Db 1343 gtctgggactgtacaaactctgaaccttgaaacctgaagcatctgcctgcctgtgcgtgcc 1402
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QY 241 caggacctggagccctgacctctgtactatgttgggagagaccccaagtgagcag 300
|||||
Db 1403 caggacctggagccctgacctctgtactatgttgggagagaccccaagtgagcag 1462
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QY 301 ctctccaaacatggtggtgaagtcttgttaaattgagctga 339
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Db 1463 ctctccaaacatggtggtgaagtcttgttaaattgagctga 1501
|||||

RESULT 7
5168051-10
; Patent No. 5168051
; APPLICANT: DERYNCK, RIK M.A.; GOEDDEL, DAVID V.
; TITLE OF INVENTION: NUCLEIC ACID ENCODING TGF-B ITS USES
; NUMBER OF SEQUENCES: 21
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/389,929
; FILING DATE: 04-AUG-1989
; SEQ ID NO:10:
; LENGTH: 2233
5168051-10

Query Match 96.0%; Score 325.4; DB 6; Length 2173;
Best Local Similarity 99.4%; Pred. No. 3.5e-83;
Matches 337; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 gctttgacacaaattactgtctccgaacttgagagaaactgtgtgccccctc 60
|||||
Db 278 gctttgacacaaattactgtctccgaacttgagagaaactgtgtgccccctc 337
|||||
QY 61 tacattgacttcgcagagatcgggtggaagtgggtccatgaacctaaagggtactat 120
|||||
Db 338 tacattgacttcgcagagatcgggtggaagtgggtccatgaacctaaagggtactat - 396
|||||
QY 121 gccaaattctgtcagggcccttgccataacctccgcagtgagacacaaacccagcag 180
|||||
Db 397 gccaaattctgtcagggcccttgccataacctccgcagtgagacacaaacccagcag 456
|||||
QY 181 gtctgggactgtacaaactctgaacctgaagcatctgcctgcctgtcgtgcc 240
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Db 457 gtctgggactgtacaaactctgaacctgaagcatctgcctgcctgtcgtgcc 516
|||||
QY 241 caggacctggagccctgacctctgtactatgttgggagagaccccaagtgagcag 300
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Db 517 caggacctggagccctgacctactgtactatgttgggagaccccaagtgagcag 576
QY 301 ctctccaaacatggtggtgaagtcttgaatgttagctga 339
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Db 577 ctctccaaacatggtggtgaagtcttgaatgttagctga 615
|||||

RESULT 8
5168051-9
; Patent No. 5168051
; APPLICANT: DERYNCK, RIK M.A.; GOEDDEL, DAVID V.
; TITLE OF INVENTION: NUCLEIC ACID ENCODING TGF-B ITS USES
; NUMBER OF SEQUENCES: 21
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/389,929
; FILING DATE: 04-AUG-1989
; SEQ ID NO:9:
; LENGTH: 2671
5168051-9

Query Match 89.1%; Score 302.2; DB 6; Length 2671;
Best Local Similarity 93.2%; Pred. No. 1.3e-76;
Matches 316; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 1 gctttgacacaaattactgtctccgaacttgagagaaactgtgtgccccctc 60
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Db 1159 gccctggacacaaactactgtctccgaatttgagagaaactgtgtgccccctc 1218
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QY 61 tacattgacttcgcagagatcgggtggaagtgggtccatgaacctaaagggtactat 120
|||||
Db 1219 tacattgacttcgcagagatcgggtggaagtgggtccatgaacctaaagggtactat 1278
|||||
QY 121 gccaaattctgtcagggcccttgccataacctccgcagtgagacacaaacccagcag 180
|||||
Db 1279 gccaaattctgtcagggcccttgccataacctccgcagtgagacacaaacccagcag 1338
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QY 181 gtctgggactgtacaaactctgaacctgaagcatctgcctgcctgtcgtgcc 240
|||||
Db 1339 gtctgggactgtacaaactctgaacctgaagcatctgcctgcctgtcgtgcc 1398
|||||
QY 241 caggacctggagccctgacctctgtactatgttgggagaccccaagtgagcag 300
|||||
Db 1399 caggacctggagccctgacctctgtactacgtcgggagaccccaagtgagcag 1458
|||||
QY 301 ctctccaaacatggtggtgaagtcttgttaaattgagctga 339
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Db 1459 ctctccaaacatggtggtgaagtcttgttaaattgagctga 1497
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RESULT 9
US-09-123-233-7
; Sequence 7, Application US/09123233
; Patent No. 6057430
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: No. 6057430el process for the production of
; biologically active dimeric protein
; NUMBER OF SEQUENCES: 14
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/123,233
; FILING DATE:
; CLASSIFICATION: 530
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 336 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double

TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "recombinant hybrid DNA of TGF-beta1 and TGF-beta3 DNA"
IMMEDIATE SOURCE:
CLONE: E. coli LC137/pPLMu.TGF-beta1(44/45)beta3
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 1..132
OTHER INFORMATION: /product= "N-terminal 44 amino acids of human TGF-beta1"
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 133..336
OTHER INFORMATION: /product= "C-terminal 68 amino acids of human TGF-beta3"
FEATURE:
NAME/KEY: CDS
LOCATION: 1..336
OTHER INFORMATION: /product= "hybrid TGF-beta named TGF-beta1-3"
US-09-123-233-7

Query Match 87.8%; Score 297.6; DB 3; Length 336;
Best Local Similarity 92.9%; Pred. No. 1.4e-75;
Matches 312; Conservative 0; Mismatches 24; Indels 0; Gaps 0;
QY 1 gctttggacacaaattactgttcgcgaacttgaggagaaactgtgtgtgccccctc 60
Db 1 GCCCTGGACACCACTATTGCTTCAAGCTCCACGGAGAAAGAACTGCTGCGCGGAGCTG 60
QY 61 tacattgtactccgacagatctggctgggaagtgggtccatgaacctaaaggtactat 120
Db 61 TACATTGACTCCGCAAGAGACCTCGGCTGGAAAGTGGATCCAGACCCCAAGGGCTACCAT 120
QY 121 gccaaactctgtcagggcccttgccacatacctccgcagtgagacacacacacagcag 180
Db 121 GCCAACTTCTGCTCAGGCCCCITGCCCATACCTCCGAGTGAGACACACACACAGCAGC 180
QY 181 gtgctggagactgtacaaacactctgaacctgaagcatctgctcgcctgtgctgcccc 240
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QY 241 caggaactggagccctgaacctctgtactatgttgaggagaccccccaaaagtggagcag 300
Db 241 CAGGACCTGGAGCCCTGACCATCTGTACTATGTGGGAGGAGACCCCAAAAGTGGAGCAG 300
QY 301 ctctccaaacatggtggaagtctgtgaaatgtagc 336
Db 301 CTCCTCAACATGGTGTGAAGTCTTGTAAATGTAGC 336

RESULT 10
US-09-123-233-9
Sequence 9, Application US/09123233
Patent No. 6057430
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: No. 6057430el process for the production of biologically active dimeric protein
NUMBER OF SEQUENCES: 14
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/123,233
FILING DATE:
CLASSIFICATION: 530
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:

LENGTH: 336 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "recombinant hybrid DNA of TGF-beta1 and TGF-beta3"
IMMEDIATE SOURCE:
CLONE: E. coli LC137/pPLMu.TGF-beta2(44/45)beta3
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 1..132
OTHER INFORMATION: /product= "N-terminal 44 amino acids of human TGF-beta2"
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 133..336
OTHER INFORMATION: /product= "C-terminal 68 amino acids of human TGF-beta3"
FEATURE:
NAME/KEY: CDS
LOCATION: 1..336
OTHER INFORMATION: /product= "hybrid TGF-beta2-3"
US-09-123-233-9
Query Match 81.7%; Score 276.8; DB 3; Length 336;
Best Local Similarity 89.0%; Pred. No. 1.1e-69;
Matches 299; Conservative 0; Mismatches 37; Indels 0; Gaps 0;
QY 1 gctttggacacaaattactgttcgcgaacttgaggagaaactgtgtgtgccccctc 60
Db 1 GCTTTGGATGCGGCCCTATTGCTTTAGAAATGTGCAGGATAATTGCTGCTACGTCACCTT 60
QY 61 taactgtactccgacagatctggctgggaagtgggtccatgaacctaaaggtactat 120
Db 61 TACATTGATTTCAAGAGGGATCTAGGGTGAATGGATACACGAACCCCAAAAGGTACAAT 120
QY 121 gccaaactctgtcagggcccttgccacatacctccgcagtgagacacacacacagcag 180
Db 121 GCCAACTTCTGCTCAGGCCCCITGCCCATACCTCCGAGTGAGACACACACACAGCAGC 180
QY 181 gtgctggagactgtacaaacactctgaacctgaagcatctgctcgcctgtgctgcccc 240
Db 181 GTGCTGGAGCTGTACAACTCTGAACCTCTGAACCTCTGCGCTGCTGCTGCGCTGCC 240
QY 241 caggaactggagccctgaacctctgtactatgttgaggagaccccccaaaagtggagcag 300
Db 241 CAGGACCTGGAGCCCTGACCATCTGTACTATGTGGGAGGAGACCCCAAAAGTGGAGCAG 300
QY 301 ctctccaaacatggtggaagtctgtgaaatgtagc 336
Db 301 CTCCTCAACATGGTGTGAAGTCTTGTAAATGTAGC 336
RESULT 11
US-09-123-233-11
Sequence 11, Application US/09123233
Patent No. 6057430
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: No. 6057430el process for the production of biologically active dimeric protein
NUMBER OF SEQUENCES: 14
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/123,233
FILING DATE:
CLASSIFICATION: 530

INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 336 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "recombinant hybrid DNA
DESCRIPTION: coding for hybrid TGF-beta3-2"
IMMEDIATE SOURCE:
CLONE: E. coli LC137/pPLu.TGF-beta3(44/45)beta2
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 1..132
OTHER INFORMATION: /product= "N-terminal 44 amino
OTHER INFORMATION: acids of human TGF-beta3"
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 133..336
OTHER INFORMATION: /product= "C-terminal 68 amino
OTHER INFORMATION: acids of human TGF-beta2"
FEATURE:
NAME/KEY: CDS
LOCATION: 1..336
OTHER INFORMATION: /product= "hybrid TGF-beta3-2"
US-09-123-233-11

Query Match 70.8%; Score 240; DB 3; Length 336;
Best Local Similarity 82.1%; Pred. No. 2.7e-59;
Matches 276; Conservative 0; Mismatches 60; Indels 0; Gaps 0;
QY 1 gcttggacacaaattactgtccgcaacttgagagaaactgtgtgccccctc 60
DB 1 GCTTGGACACCAATTACTGCTCCCACTTGGAGAGAACTGTGTGCCCCCTC 60
QY 61 tacattgactccgacagatctgggtcggaagtgggtccatgaacctaaaggtactat 120
DB 61 TACATTGACTTCGACAGGATCTGGGCTGGAAGTGGTCCATGAACCTAAGGGCTACTAT 120
QY 121 gcaacttctgctcagcccttgccatccctccgagtcgagacacacacacagcag 180
DB 121 GCCAATTCTGTGCTGGAGCATGCCGCTATTTATGGAGTTTCAGACACTCAGACAGCAGG 180
QY 181 gtctggagacttacacactctgaacctgaacctgaacctgtcctgcctgtgtgcccc 240
DB 181 GTCCTGAGCTTATATAATACCATAAATCCAGAAAGCATCTGCTTCTCTCTGCTGCGTGTC 240
QY 241 caggacctggagcccttgacctctgtactatgttggaggagaccccccaagtgagcag 300
DB 241 CAAGATTAGAACCTTAACCAATCTCTACTACATTGGGCAAAACACCCCAAGATTGAACAG 300
QY 301 ctctccacatggtggtgaagtctgttaaatgtagc 336
DB 301 CTTTCTAATATGATTGATAAAGTCTTGCAATGCAGC 336

RESULT 12
US-08-470-837-29
Sequence 29, Application US/08470837
Patent No. 5800811
GENERAL INFORMATION:
APPLICANT: Nimni, Marcel E.
APPLICANT: Hall, Frederick L.
APPLICANT: Tuan, Tai-Lan
APPLICANT: Wu, Lingtao
APPLICANT: Cheung, David T.
TITLE OF INVENTION: Transforming Growth Factor B Fusion
TITLE OF INVENTION: and
TITLE OF INVENTION: Their Use in Wound Healing
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant & Gould

STREET: 11150 Santa Monica Boulevard, Suite 400
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90025-3395
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,837
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Sharp, Janice A.
REGISTRATION NUMBER: 34,051
REFERENCE/DOCKET NUMBER: 30630-1US01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 310-445-1140
TELEFAX: 310-445-9031
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 339 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..333
FEATURE:
NAME/KEY: CDS
LOCATION: 1..336
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 1
US-08-470-837-29

Query Match 60.8%; Score 206.2; DB 1; Length 339;
Best Local Similarity 75.5%; Pred. No. 9.7e-50;
Matches 256; Conservative 0; Mismatches 83; Indels 0; Gaps 0;

QY 1 gcttggacacaaattactgtccgcaacttgagagaaactgtgtgccccctc 60
DB 1 GCCCTGGACACCACTATTGCTTTCAGCTCCACGGAGAAAGAACTGTGCTGGCGGAGCTG 60
QY 61 tacattgactccgacagatctgggtcggaagtgggtccatgaacctaaaggtactat 120
DB 61 TACATTGACTTCCGCAAGGACCTCGGCTGGAAGTGGATCCATGAGCCCAAGGGCTACCAT 120
QY 121 gcaacttctgctcagcccttgcccatccctccagtcgagacacacacacagcagc 180
DB 121 GCCAATTCTGCTCGGGCCCTGCCCTTACATTTGAGCCCTGGACACGACGACTACAGCAAG 180
QY 181 gtctgggactgtacacactctgaacctgaacctgaacctgtcctgtgtgcccc 240
DB 181 GTCTGGCCCTGTACAAACACAGCATAAACCCGGCGCCTCGGGCGGCCGCTGCTGCGTGCGG 240
QY 241 caggacctggagcccttgacctctgtactatgttggaggagaccccccaagtgagcag 300
DB 241 CAGCGCTGGAGCGCTGCCCATCTGTGTACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 300
QY 301 ctctccacatggtggtgaagtctgttaaatgtagctga 339
DB 301 CTGTCCCAACATGATCTGCGCTCTCTGCAAGTGCAGCTGA 339

RESULT 13
US-08-486-057B-1
Sequence 1, Application US/08486057B
Patent No. 5650494

```

; GENERAL INFORMATION:
; APPLICANT: Cerletti, Nico
; APPLICANT: McMaster, Gary K.
; APPLICANT: Cox, David
; APPLICANT: Schmitz, Albert
; APPLICANT: Meyhack, Bernd
; TITLE OF INVENTION: Process for Refolding Recombinantly
; TITLE OF INVENTION: Produced TGF-beta-like Proteins
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Henry P. No. 5650494ak
; STREET: 520 White Plains Road, P.O. Box 2005
; CITY: Tarrytown
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10591-9005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,057B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/201,703
; FILING DATE: 25-FEB-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/960,309
; FILING DATE: 13-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/621,502
; FILING DATE: 03-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 8927546.5
; FILING DATE: 06-DEC-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5650494ak, Henry P.
; REGISTRATION NUMBER: 33200
; REFERENCE/DOCKET NUMBER: 4-17861/+ /Cont3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 277-4306
; TELEFAX: (908) 277-4306
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 339 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..339
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..339
; US-08-486-057B-1

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Query Match      60.4%; Score 204.6; DB 1; Length 339;
Best Local Similarity 75.2%; Pred. No. 2.7e-49;
Matches 255; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

Qy 1 gcttggacacaaattactgttcgcgaactggaggagaactgtgtgtgccccctc 60
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
Db 1 GCCCTGGACACAACTATTGCTTACGTCACGGAGAGAAGAACTGCTGCGGCGAGCTG 60
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||

Qy 61 tacattgactccgacagatctgggtgggaagtgggtccatgaacctaaagggctactat 120
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
Db 61 TACATTGACTTCCGACGAGACTCGGCTGGAAGTGGATCCACAGAGCCCAAGGGCTACCAT 120
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||

Qy 121 gccaaactctgctaggcccttgccatacctccgcaagtgcagacacacacacagcagc 180

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Db 121 GCCAACTTCTGCTGGGCCCTGCCCCCTACATTTGAGGCTTGACACGCGAGTACAGCAAG 180
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
Qy 181 gtgctgggagctgtacaacactctgaacactctgaacactctgcctcgtctgctgctgccc 240
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
Db 181 GTCTGGCCCTGTACACACAGCATAAACCGGGGCCCTCGGGCGCGCGCTGCTGCGTGCCG 240
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
Qy 241 caggacctggagccctcgaccatcctgtactatgttggaggagccccccaaagtggagcag 300
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
Db 241 CAGGCGCTGGAGCCGCTGCCCATCGTGTACTAGTGTGGCGGCGCAAGCCCAAGGTGGAGCAG 300
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
Qy 301 ctctccacatggtggtgaagtcttgttaataatgtagctga 339
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
Db 301 CTGTCCACATGATGCTGCGCTCCTGCAAGTGCAGCTGA 339
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||

RESULT 14
US-08-789-588-1
; Sequence 1, Application US/08789588
; Patent No. 5922846
; GENERAL INFORMATION:
; APPLICANT: Cerletti, Nico
; APPLICANT: McMaster, Gary K.
; APPLICANT: Cox, David
; APPLICANT: Schmitz, Albert
; APPLICANT: Meyhack, Bernd
; TITLE OF INVENTION: Process for Refolding Recombinantly
; TITLE OF INVENTION: Produced TGF-beta-like Proteins
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Henry P. No. 5922846ak
; STREET: 520 White Plains Road, P.O. Box 2005
; CITY: Tarrytown
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10591-9005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/789,588
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/486,057
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/201,703
; FILING DATE: 25-FEB-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/960,309
; FILING DATE: 13-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/621,502
; FILING DATE: 03-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 8927546.5
; FILING DATE: 06-DEC-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5922846ak, Henry P.
; REGISTRATION NUMBER: 33200
; REFERENCE/DOCKET NUMBER: 4-17861/+ /Cont3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 277-4306
; TELEFAX: (908) 277-4306
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 339 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)

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; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..339
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..339
US-08-789-588-1

Query Match 60.4%; Score 204.6; DB 2; Length 339;
Best Local Similarity 75.2%; Pred. No. 2.7e-49;
Matches 255; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

QY 1 gcttggacacaaattactgttccgcaacttggagagaactgtgtgtgcgccccctc 60
Db 1 GCCCTGGACACCAACTATTGCTTCAGCTCCACGGAGAAAGTGTGCGTGGCGAGCTG 60

QY 61 tacattgacttccgacagatctggctgggaagtgggtccatgaacctaaaggctactat 120
Db 61 TACATTGACTTCCGCAAGGACCTCGGCTGGAAGTGATCCAGAGCCCAAGGCGCTACCAT 120

QY 121 gcaacttctgtcagggcccttgccatacctccgagtcagacacacacacagcag 180
Db 121 GCCAACTTCTGCCCTGGGCGCCCTGCCCCATACATTTGGAGCTGGACACGAGTACAGCAAG 180

QY 181 gtctgggactgtacaacactctgaacctgaacctgaacctgtgctgctgctgctgcc 240
Db 181 GTCTGGCCCTGTACAACACAGCATAACCCGGCGCCTCGGGCGCGCTGCTGCGTGGCG 240

QY 241 caggacctggagccctgacctctgtactatgttgaggagaccccccaaaagtggagcag 300
Db 241 CAGGCGCTGGAGCGCTGCCCCATGCTGTACTACTGTGGGCGCGCAAGCCCAAGGTGGAGCAG 300

QY 301 ctctccacatgtgtggaagtctttaaattagctga 339
Db 301 CTGTCCAACATGATCGTGGCGCTCTCTGCAAGTGCAGCTGA 339

RESULT 16
US-07-669-171-1
; Sequence 1, Application US/07669171
; Patent No. 5304541
; GENERAL INFORMATION:
; APPLICANT: PURCHIO, ANTHONY F.
; APPLICANT: MADISEN, LINDA
; APPLICANT: MERWIN, JUNE RAE
; TITLE OF INVENTION: TGF-b1/b2: A NOVEL CHIMERIC TRANSFORMING
; TITLE OF INVENTION: GROWTH FACTOR-BETA
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS
; STREET: 1155 AVENUE OF THE AMERICAS
; CITY: NEW YORK
; STATE: N.Y.
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07669,171
; FILING DATE: 19910314
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MISROCK, S. LESLIE
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 5624-159-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-9741
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1560 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..336
; OTHER INFORMATION: /product= "human TGF-beta1"
US-09-123-233-1

; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..339
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..339
US-08-789-588-1

Query Match 60.4%; Score 204.6; DB 2; Length 339;
Best Local Similarity 75.2%; Pred. No. 2.7e-49;
Matches 255; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

QY 1 gcttggacacaaattactgttccgcaacttggagagaactgtgtgtgcgccccctc 60
Db 1 GCCCTGGACACCAACTATTGCTTCAGCTCCACGGAGAAAGTGTGCGTGGCGAGCTG 60

QY 61 tacattgacttccgacagatctggctgggaagtgggtccatgaacctaaaggctactat 120
Db 61 TACATTGACTTCCGCAAGGACCTCGGCTGGAAGTGATCCAGAGCCCAAGGCGCTACCAT 120

QY 121 gcaacttctgtcagggcccttgccatacctccgagtcagacacacacacagcag 180
Db 121 GCCAACTTCTGCCCTGGGCGCCCTGCCCCATACATTTGGAGCTGGACACGAGTACAGCAAG 180

QY 181 gtctgggactgtacaacactctgaacctgaacctgtgctgctgctgctgctgcc 240
Db 181 GTCTGGCCCTGTACAACACAGCATAACCCGGCGCCTCGGGCGCGCTGCTGCGTGGCG 240

QY 241 caggacctggagccctgacctctgtactatgttgaggagaccccccaaaagtggagcag 300
Db 241 CAGGCGCTGGAGCGCTGCCCCATGCTGTACTACTGTGGGCGCGCAAGCCCAAGGTGGAGCAG 300

QY 301 ctctccacatgtgtggaagtctttaaattagctga 339
Db 301 CTGTCCAACATGATCGTGGCGCTCTCTGCAAGTGCAGCTGA 339

RESULT 15
US-09-123-233-1
; Sequence 1, Application US/09123233
; Patent No. 6057430
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: No. 6057430el process for the production of
; TITLE OF INVENTION: biologically active dimeric protein
; NUMBER OF SEQUENCES: 14
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09123,233
; FILING DATE:
; CLASSIFICATION: 530
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 339 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; IMMEDIATE SOURCE:
; CLONE: E. coli LC137/pPLMu.htGF-beta1 (DSM 5656)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..336
; OTHER INFORMATION: /product= "human TGF-beta1"
US-09-123-233-1
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Db	1919	CAGGCGCTGGAGCCGCTGCCCATCTGTACTACGTGGCCGCAAGCCCAAGGTGGAGCAG	1978
Qy	301	ctctccaacatggtggtagagtccttgtaaatgtagctga	339
Db	1799	CTGTCCAACATGATCTGCCTTCCTGCAAGTGCAGCTGA	2017

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RESULT 19
US-07-669-171-3
; Sequence 3, Application US/07669171
; Patent No. 5304541
; GENERAL INFORMATION:
; APPLICANT: PURCHIO, ANTHONY F.
; APPLICANT: MADISEN, LINDA
; APPLICANT: MERWIN, JUNE RAE
; TITLE OF INVENTION: TGF-b1/b2: A NOVEL CHIMERIC TRANSFORMING
; TITLE OF INVENTION: GROWTH FACTOR-BETA
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS
; STREET: 1155 AVENUE OF THE AMERICAS
; CITY: NEW YORK
; STATE: N.Y.
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/669,171
; FILING DATE: 19910314
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MISROCK, S. LESLIE
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 5624-159-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1569 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-07-669-171-3

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	Query Match	58.0%	Score 196.6;	DB 1;	Length 1569;
	Best Local Similarity	73.7%;	Pred. No. 7.9e-47;		
Matches	250; Conservative	0;	Mismatches 89;	Indels	Gaps
QY	1 gctttggacaccaattactgtcttcgcgaaccttgagagagaactcgtgtagccocctc	60			
DG					
Db	1104 GCCTGGACACCACATTTCGTTCAGAAATGTGCAGGATAATTGCTGCCCTACGTCCGCTT	1163			
QY	61 tacataggacttccgcagaggatctggcgtaagtgggtccaataaacctaagggtactatat	120			
DG					
Db	1164 TACATTGAATTTCAAGAGGGATCTAGCGTGGAAGTGGATCACAGGCCAACGGGCTACCAT	1223			
QY	121 gccaaacttgtctcagggcccttgcccatactccgcgagtgagacaaccacccacgacg	180			
DG					
Db	1224 GCCAACTTCTGCTCGGGCCTGCCCTTACATTGGAGCTGGACAGCAGTACAGCAAG	1283			
QY	181 gtctggggaactgtacaacactctgaaccctgaagcatctgcctcgcttgctgcgtgcccc	240			
DG					
Db	1284 GTCTGGCCCTGTACAACACAGCATAAACCGGGGGCCCTCGGGGGGCGCGTGGTGGTGCCG	1343			
QY	241 caggaactgtgagcccttgaccactcttatctatatttggagagaccccaaatgtgagcag	300			

Db	1344	CAGCGCGTGGAGCCGCTGCCATCGTGACTACGTGGGCGCAAGCCCAAGGTGGAGCAG	1403
Qy	301	ctctccacaatggtgggtgaagtctctgtaaatgtagctga	339
Db	1404	CTGTCCACACATGATCGTGGTCTCTGCAAGTGCAGCTGA	1442

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RESULT 20
US-08-486-057B-2
; Sequence 2, Application US/08486057B
; Patent No. 5650494
; GENERAL INFORMATION:
; APPLICANT: Cerletti, Nico
; APPLICANT: McMaster, Gary K.
; APPLICANT: Cox, David
; APPLICANT: Schmitz, Albert
; APPLICANT: Meyhack, Bernd
; TITLE OF INVENTION: Process for Refolding Recombinantly
; Produced TGF-beta-like Proteins
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Henry P. No. 5650494ak
; STREET: 520 White Plains Road, P.O. Box 2005
; CITY: Tarrytown
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10591-9005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,057B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/201,703
; FILING DATE: 25-FEB-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/960,309
; FILING DATE: 13-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/621,502
; FILING DATE: 03-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 8927546.5
; FILING DATE: 06-DEC-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5650494ak, Henry P.
; REGISTRATION NUMBER: 33200
; REFERENCE/DOCKET NUMBER: 4-17861/+ /Cont3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 277-5110
; TELEFAX: (908) 277-4306
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 339 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..339
US-08-486-057B-2

```

Query Match 53.7%; Score 182.2; DB 1; Length 339;
Best Local Similarity 71.1%; Pred. NO. 5.9e-43;
Matches 241; Conservative 0; Mismatches 98; Indels 0; Gaps 0;

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OY 1 gcttggacacaaattactgttcgcgaacttggaggaagaactgtgtgtgccccctc 60
Db 1 GCTTTGGATGCGGCTATTGCTTTAGAAATGTCAGGATAATTGCTGCTCCACTT 60
OY 61 tacattgacttccgacagatctggctggaagtgggtccatgaacctaaaggctactat 120
Db 61 TACATTGATTTCAAGAGGATCTAGGTGGAATGGATACAGAACCCCAAGGGTACAAT 120
OY 121 gcaacttctgtcagggcccttgcccatctccgcagtgccagacacacccacagcacg 180
Db 121 GCAAACTTCTGTGCTGGAGCATGCCGTATTATGGAGTTCAGACACTCAGCACAGCAG 180
OY 181 gtgctgggactgtacacactctgaacctgaagcatctgcctgcctgtcgtgcccc 240
Db 181 GTCTGAGCTTATATAATACCAATAATCCAGAAGCATCTGCTTCTCTGCTGCGTGC 240
OY 241 caggacctggagccctgacctctgtactatgttgaggagaccccccacaaagtggagcag 300
Db 241 CAAGATTTAGAACCTCTACCAATTCCTACTACATTGGCAAAACACCCAAGATTGAACAG 300
OY 301 ctctccaatggtgtggaagtcttggtaaatgtagctga 339
Db 301 CTTTCTAATATGATTGTAAGTCTTGCAAAATGCAGCTAA 339

RESULT 21
US-08-470-837-31
; Sequence 31, Application US/08470837
; Patent No. 5800811
; GENERAL INFORMATION:
; APPLICANT: Nimni, Marcel E.
; APPLICANT: Hall, Frederick L.
; APPLICANT: Tuan, Tai-Lan
; APPLICANT: Wu, Lingtao
; APPLICANT: Cheung, David T.
; TITLE OF INVENTION: Transforming Growth Factor B Fusion
; TITLE OF INVENTION: and
; TITLE OF INVENTION: Their Use in Wound Healing
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 11150 Santa Monica Boulevard, Suite 400
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90025-3395
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470.837
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharp, Janice A.
; REGISTRATION NUMBER: 34,051
; REFERENCE/DOCKET NUMBER: 30630-1US01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 310-445-1140
; TELEFAX: 310-445-9031
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 339 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..336
; FEATURE:
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; NAME/KEY: mat_peptide
; LOCATION: 1
; US-08-470-837-31

Query Match 53.7%; Score 182.2; DB 1; Length 339;
Best Local Similarity 71.1%; Pred. No. 5.9e-43;
Matches 241; Conservative 0; Mismatches 98; Indels 0; Gaps 0;

OY 1 gcttggacacaaattactgttcgcgaacttggaggaagaactgtgtgtgccccctc 60
Db 1 GCTTTGGATGCGGCTATTGCTTTAGAAATGTCAGGATAATTGCTGCTCCACTT 60
OY 61 tacattgacttccgacagatctggctggaagtgggtccatgaacctaaaggctactat 120
Db 61 TACATTGATTTCAAGAGGATCTAGGTGGAATGGATACAGAACCCCAAGGGTACAAT 120
OY 121 gcaacttctgtcagggcccttgcccatctccgcagtgccagacacacccacagcacg 180
Db 121 GCAAACTTCTGTGCTGGAGCATGCCGTATTATGGAGTTCAGACACTCAGCACAGCAG 180
OY 181 gtgctgggactgtacacactctgaacctgaagcatctgcctgcctgtcgtgcccc 240
Db 181 GTCTGAGCTTATATAATACCAATAATCCAGAAGCATCTGCTTCTCTGCTGCGTGC 240
OY 241 caggacctggagccctgacctctgtactatgttgaggagaccccccacaaagtggagcag 300
Db 241 CAAGATTTAGAACCTCTACCAATTCCTACTACATTGGCAAAACACCCAAGATTGAACAG 300
OY 301 ctctccaatggtgtggaagtcttggtaaatgtagctga 339
Db 301 CTTTCTAATATGATTGTAAGTCTTGCAAAATGCAGCTAA 339

RESULT 22
US-08-789-588-2
; Sequence 2, Application US/08789588
; Patent No. 5922846
; GENERAL INFORMATION:
; APPLICANT: Cerletti, Nico
; APPLICANT: McMaster, Gary K.
; APPLICANT: Cox, David
; APPLICANT: Schmitz, Albert
; APPLICANT: Meyhack, Bernd
; TITLE OF INVENTION: Process for Refolding Recombinantly
; TITLE OF INVENTION: Produced TGF-beta-like Proteins
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Henry P. No. 5922846ak
; STREET: 520 White Plains Road, P.O. Box 2005
; CITY: Tarrytown
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10591-9005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/789,588
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/486,057
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/201,703
; FILING DATE: 25-FEB-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/960,309
; FILING DATE: 13-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/621,502
```

Query Match 53.7%; Score 182.2; DB 3; Length 339;

Query Match	53.7%	Score 182.2	DB 3	Length 339
Best Local Similarity	71.1%	Pred. No. 5.9e-43		
Matches 241	Conservative 0	Mismatches 98	Indels 0	Gaps 0
1	gctttggacacaaattactcttcgcgaacttgaggagagactgcctgtgtgcgccccctc	60		
b	1	gctttggatgcgccctattgctttagaaatgacagatattgctgccttaccgtccactt	60	
61	tacattgactctgcacagatctggctgggaagtgggtccatgaacctaaagggtactat	120		
b	61	tacattgatttcaagaggagactctagggtggaaatggatcacgaacccaaagggtacaa	120	
121	gccaaactctgtcagggcccttgcccatactccgcagtgacagacaaacccacagcacg	180		
b	121	gccaaactctgtcgtggagcattgcccgtatttatatggagattcagacactcagacacagcag	180	
181	gtgctgggagctgtacaaactctgaacctgaacctgaacatctccctcgctctgctcgtgcc	240		
b	181	gttcctggagctgtatataataccataaattccagaagcattctgcctctcctgtcgggtgcc	240	
241	caggacctggagccctcgaccatctgactatgtttggggagacccccaaagtggagcag	300		
b	241	caagatttagaacctctacccattctctactacattggcraaacaccacaaagattgaacag	300	
301	ctctccaacatggtggtgaagctttgttaaatgtagtga	339		
301	cttttctaataatgatgttaaagctctgtgcaaatgacagttaa	339		

RESULT 24
CT-US94-03705-4
Sequence 4, Application PC/TUS9403705
GENERAL INFORMATION:
APPLICANT: Mu-En Lee
APPLICANT: Mark A. Perrella
TITLE OF INVENTION: TRANSFORMING GROWTH
FACTOR- INHIBITS
TITLE OF INVENTION: INDUCIBLE NITRIC OXIDE
SYNTHASE GENE
TITLE OF INVENTION: TRANSCRIPTION
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: Wordperfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/03705
FILING DATE: 5 April 1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:

```

; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Janis K. Eraser
; REGISTRATION NUMBER: Reg. No. 34,819
; REFERENCE/DOCKET NUMBER: 05433/007001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1695
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; PCT-US94-03705-4

Query Match 53.7%; Score 182.2; DB 5; Length 1695;
Best Local Similarity 71.1%; Pred. No. 9.6e-43;
Matches 241; Conservative 0; Mismatches 98; Indels 0; Gaps 0;

QY 1 gcttggacacaaattactgtctccgcaacttggagagaactgtgtgtgccccctc 60
Db 1088 GCTTTGGATGCGCCTATTGCTTAGAATGTGCAGGATAATTGCTGCTACGTCACATT 1147

QY 61 tacattgacttcgcagagatcgggctggaagtgggtccatgaacctaaagggtactat 120
Db 1148 TACATTTGATTTCAAGAGGATCTAGGGTGAATGGATACACGAAACCCAAAGGTACAAAT 1207

QY 121 gccaaacttctgagcccttgccatactccagcagtcgcagtcgcagacacacacagcag 180
Db 1208 GCCAACTTCTGTGCTGGAGCATGCCCGTATTATGGAGTTCAGACACTCAGCACAGCAGG 1267

QY 181 gtgctggagactcaacaactcgaacctgaacctgaacatcctgcctgcctgtgcgtgcc 240
Db 1268 GTCCTGAGCTTATATATACCAATTCAGGAAGCATCTCTCTCTCTGCTGCGGTGCC 1327

QY 241 caggacctggagccctgacctcctgtactatgttgggagagaccccaaaagtggagcag 300
Db 1328 CAAGATTTAGAACCTCTAACCATTCCTACTATACATTGGCAAAACCCCAAGATTGACAG 1387

QY 301 ctctccaaatggtggtgaagtctgtgtaaatgtagctga 339
Db 1388 CTTTCTAATATGATTGAAGTCTTGCAAAATGCAGTAA 1426

RESULT 25
5221620-1
; Patent No. 5221620
; APPLICANT: PURCHIO, ANTHONY F.; MADISEN, LINDA; WEBB, NANCY
; TITLE OF INVENTION: CLONING AND EXPRESSION OF TRANSFORMING
; GROWTH FACTOR BETA-2
; NUMBER OF SEQUENCES: 16
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/446,020
; FILING DATE: 05-DEC-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 285,140
; FILING DATE: 16-DEC-1988
; APPLICATION NUMBER: 234,065
; FILING DATE: 18-AUG-1988
; APPLICATION NUMBER: 148,267
; FILING DATE: 25-JAN-1988
; APPLICATION NUMBER: 106,752
; FILING DATE: 06-OCT-1987
; SEQ ID NO: 1:
; LENGTH: 2569
5221620-1

Query Match 53.7%; Score 182.2; DB 6; Length 2569;
Best Local Similarity 71.1%; Pred. No. 1.1e-42;
Matches 240; Conservative 0; Mismatches 99; Indels 0; Gaps 0;

QY 1 gcttggacacaaattactgtctccgcaacttggagagaactgtgtgtgccccctc 60
Db 1095 gcttggatcgccctattgtcttagaaatgtgcagataattgtgcttaccttccactt 1154

QY 61 tacattgacttcgcagagatcgggctggaagtgggtccatgaacctaaagggtactat 120
Db 1155 tacattgatttcaagagagatcctaggtggaaatggatatacacacaccccaagggtacaat 1214

QY 121 gccaaacttctgctcagggcccttgccatactccgcagtcgcagacacacacacagcag 180
Db 1215 gccaaacttctgctgagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 1274

QY 181 gtgctggagactgtacaacactcgaacctgaacctgaacatcctgcctgcctgtgcgtgcc 240
Db 1275 gtccgagcttataataaccataaacagagcagcagcagcagcagcagcagcagcagcagcag 1334

QY 241 caggacctggagccctgacctcctgtactatgttgggagagaccccaaaagtggagcag 300

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Matches 241; Conservative 0; Mismatches 98; Indels 0; Gaps 0;

QY 1 gcttggacacaaattactgtctccgcaacttggagagaactgtgtgtgccccctc 60
Db 1457 gcttggatcgccctattgtcttagaaatgtgcagataattgtgcttaccttccactt 1516

QY 61 tacattgacttcgcagagatcgggctggaagtgggtccatgaacctaaagggtactat 120
Db 1517 tacattgatttcaagagagatcctaggtggaaatggatatacacacaccccaagggtacaat 1576

QY 121 gccaaacttctgctcagggcccttgccatactccgcagtcgcagacacacacacagcag 180
Db 1577 gccaaacttctgctgagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 1636

QY 181 gtgctggagactgtacaacactcgaacctgaacctgaacatcctgcctgcctgtgcgtgcc 240
Db 1637 gtccgagccttataataaccataaacagagcagcagcagcagcagcagcagcagcagcagcag 1696

QY 241 caggacctggagccctgacctcctgtactatgttgggagaccccaaaagtggagcag 300
Db 1697 caagatttgaacctcctaaaccttctctattatttggcaaacacaccccaagattgaacag 1756

QY 301 ctctccaaatggtggtgaagtctgtgtaaatgtagctga 339
Db 1757 cttctaatatgattgttaaagtcttgcataatgcagctaa 1795

RESULT 26
5221620-3
; Patent No. 5221620
; APPLICANT: PURCHIO, ANTHONY F.; MADISEN, LINDA; WEBB, NANCY
; TITLE OF INVENTION: CLONING AND EXPRESSION OF TRANSFORMING
; GROWTH FACTOR BETA-2
; NUMBER OF SEQUENCES: 16
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/446,020
; FILING DATE: 05-DEC-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 285,140
; FILING DATE: 16-DEC-1988
; APPLICATION NUMBER: 234,065
; FILING DATE: 18-AUG-1988
; APPLICATION NUMBER: 148,267
; FILING DATE: 25-JAN-1988
; APPLICATION NUMBER: 106,752
; FILING DATE: 06-OCT-1987
; SEQ ID NO: 3:
; LENGTH: 2207
5221620-3

Query Match 53.3%; Score 180.6; DB 6; Length 2207;
Best Local Similarity 70.8%; Pred. No. 2.9e-42;
Matches 240; Conservative 0; Mismatches 99; Indels 0; Gaps 0;

QY 1 gcttggacacaaattactgtctccgcaacttggagagaactgtgtgtgccccctc 60
Db 1095 gcttggatcgccctattgtcttagaaatgtgcagataattgtgcttaccttccactt 1154

QY 61 tacattgacttcgcagagatcgggctggaagtgggtccatgaacctaaagggtactat 120
Db 1155 tacattgatttcaagagagatcctaggtggaaatggatatacacacaccccaagggtacaat 1214

QY 121 gccaaacttctgctcagggcccttgccatactccgcagtcgcagacacacacacagcag 180
Db 1215 gccaaacttctgctgagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 1274

QY 181 gtgctggagactgtacaacactcgaacctgaacctgaacatcctgcctgcctgtgcgtgcc 240
Db 1275 gtccgagcttataataaccataaacagagcagcagcagcagcagcagcagcagcagcagcag 1334

QY 241 caggacctggagccctgacctcctgtactatgttgggagagaccccaaaagtggagcag 300

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; LENGTH: 894 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: cdna to mRNA
; HYPOTHETICAL: NO
; FRAGMENT TYPE: C-terminal
; ORIGINAL SOURCE:
; ORGANISM: Bos taurus
; TISSUE TYPE: Fetal long bone
; IMMEDIATE SOURCE:
; LIBRARY: Bovine bone cdna library
; CLONE: HELI6
; POSITION IN GENOME:
; UNITS: bp
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..669
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 250..666
; FEATURE:
; NAME/KEY: mRNA
; LOCATION: 1..894
;
US-07-764-731B-3

Query Match 16.1%; Score 54.6; DB 1; Length 894;
Best Local Similarity 51.9%; Pred.No.9.1e-07;
Matches 179; Conservative 0; Mismatches 154; Indels 12; Gaps

QY 7 gacaccaattactgtctccgaacttggagagaactgtgtgtgcgccctctacatt 66
Db 325 GCCTCAGACTACAACAGCAGAGCTGAAGACGCGCTGCCGGAAGCATGAGCTCTACGTG 384
QY 67 gatttcgcacagatctgggctggaagtgggtccatgaacctaaagggttactatgccaa 126
Db 385 AGCTTCCAGGACCTGGGGTGGCAGGACTGGATCATTTGCCCCCAAGGCTACGCTGCCAAC 444
QY 127 ttctgtcaggcccttgccatactccgcagtcgagac-----acaaaccacagc 177
Db 445 TACTGTGACGGGAATGTTTCGTTCCCTCTCAACGCACACATGAACGCTACCAACCATGCC 504
QY 178 acggtgtcggactgtacaacactgtgaacctgaagcatctgtcctgcgcttgcgtgcgtg 237
Db 505 ATCGTGACAGCCCTGGTTCCACTCATATGAACCCGAGTACGTCGCCCAACCGTGTGCGG 564
QY 238 ccccgagacctgagccctcgacctcctgtactactgttggaggacc---cccaaaagtgc 294
Db 565 CCCAGAAACTGAACGCCCATCTCGTGTCTCTACTTCGAGGACAACCTCAATGTGTCATCCTG 624
QY 295 gacgactctccacatggtgtggaagtcttgtaaatgtagtga 339
Db 625 AAGAAGTACCGGAACATGGTGTGCTACGAGCGTGTGGGTGCCACTGA 669

RESULT 29
5187076-3
; Patent No. 5187076
; APPLICANT: WOZNEY, JOHN M.; WANG, ELIZABETH A.; ROSEN, VICKI A.;
; CELESTE, ANTHONY J.
; TITLE OF INVENTION: DNA SEQUENCES ENCODING BMP-6 PROTEINS
; NUMBER OF SEQUENCES: 16
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/490,033
; FILING DATE: 07-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 370,544
; FILING DATE: 23-JUN-1989
; APPLICATION NUMBER: 347,559
; FILING DATE: 04-MAY-1989
; APPLICATION NUMBER: 329,610
; FILING DATE: 28-MAR-1989

```


ATTORNEY/AGENT INFORMATION:
NAME: LAZAR, Steven R.
REGISTRATION NUMBER: 32,618
REFERENCE/DOCKET NUMBER: G15205-CIP
TELEPHONE: 617 876-1170
TELEFAX: 617 876-5851
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 789 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Bos Taurus
STRAIN: Bovine Activin WC
FEATURE:
NAME/KEY: CDS
LOCATION: 324..704
FEATURE:
NAME/KEY: misc_feature
LOCATION: 322..323
OTHER INFORMATION: /note= "putative 3' end of intron"
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 375..701
US-08-452-772-1

Query Match 15.3%; Score 51.8; DB 1; Length 789;
Best Local Similarity 54.9%; Pred. No. 5.4e-06;
Matches 129; Conservative 0; Mismatches 97; Indels 9; Gaps 1;

QY 37 gagaactgctgtgccccctctacattgacttccgacaggaattcgggtggaagtgg 96
Db 408 GAGTCCCGCTGTGGCGCTACCCCTCACTGTGGACTTTTGAGGCTTTTGGCTGGGACTGG 467

QY 97 gtccatgaacctaaagggctactatgcaacttctgctcaggcccttgccataccctccgc 156
Db 468 ATCATCGCTCTTAACGCTACAAGGCCAACTACTGCTCGGCCAGTGCAGAGTACATGTTT 527

QY 157 agtcgacacacacccacagcagcgtgtggtggaactgtacaacactctgaacctgaagca 216
Db 528 ATGCAAAAGTAGTCCGCACACACCCTTGGTGCAACAGGCT-----AACCCAAGAGGC 578

QY 217 tctgctcgctgtgctggtgccccagagacctggagccccctgaccatcctgtact 271
Db 579 TCTGGGGGGCCCTGCTGCACACCCCAAGATGTCCCAATCAACATGCTCTACT 633

RESULT 34
PCT-US94-05288-1
Sequence 1, Application PC/TUS9405288
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: BMP-11 COMPOSITIONS
NUMBER OF SEQUENCES: 11
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/05288
FILING DATE:
CLASSIFICATION:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 789 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Bos Taurus
STRAIN: Bovine Activin WC
FEATURE:
NAME/KEY: CDS
LOCATION: 324..704
FEATURE:
NAME/KEY: misc_feature
LOCATION: 322..323
OTHER INFORMATION: /note= "putative 3' end of intron"
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 375..701
PCT-US94-05288-1

Query Match 15.3%; Score 51.8; DB 5; Length 789;
Best Local Similarity 54.9%; Pred. No. 5.4e-06;
Matches 129; Conservative 0; Mismatches 97; Indels 9; Gaps 1;

QY 37 gagaactgctgtgccccctctacattgacttccgacaggaattcgggtggaagtgg 96
Db 408 GAGTCCCGCTGTGGCGCTACCCCTCACTGTGGACTTTTGAGGCTTTTGGCTGGGACTGG 467

QY 97 gtccatgaacctaaagggctactatgcaacttctgctcaggcccttgccataccctccgc 156
Db 468 ATCATCGCTCTTAACGCTACAAGGCCAACTACTGCTCGGCCAGTGCAGAGTACATGTTT 527

QY 157 agtcgacacacacccacagcagcgtgtggtggaactgtacaacactctgaacctgaagca 216
Db 528 ATGCAAAAGTAGTCCGCACACACCCTTGGTGCAACAGGCT-----AACCCAAGAGGC 578

QY 217 tctgctcgctgtgctggtgccccagagacctggagccccctgaccatcctgtact 271
Db 579 TCTGGGGGGCCCTGCTGCACACCCCAAGATGTCCCAATCAACATGCTCTACT 633

RESULT 35
US-07-841-646-33
Sequence 33, Application US/07841646
Patent No. 5266683
GENERAL INFORMATION:
APPLICANT: OPPERMAN, HERMANN
APPLICANT: OZKAYNAK, ENGIN
APPLICANT: KUBERASAMPATH, THANGAVEL
APPLICANT: RUEGER, DAVID C.
APPLICANT: PANG, ROY H.L.
TITLE OF INVENTION: OSTEOGENIC DEVICES
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: TESTA, HURWITZ & THIBEAULT
STREET: 53 STATE STREET
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: U.S.A.
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/841,646
FILING DATE: 19920221
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 810,560
FILING DATE: 20-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 827,052
FILING DATE: 28-JAN-1992
PRIOR APPLICATION DATA:

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; APPLICATION NUMBER: US 660,162
; FILING DATE: 22-FEB-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 621,988
; FILING DATE: 04-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 621,849
; FILING DATE: 04-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 616,374
; FILING DATE: 21-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 600,024
; FILING DATE: 18-OCT-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 599,543
; FILING DATE: 18-OCT-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 579,865
; FILING DATE: 07-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 483,913
; FILING DATE: 22-FEB-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 422,613
; FILING DATE: 17-OCT-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 315,342
; FILING DATE: 23-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 232,630
; FILING DATE: 15-AUG-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 179,460
; FILING DATE: 08-APR-1988
; FILING DATE: 08-APR-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: PITCHER, EDMUND R.
; REGISTRATION NUMBER: 27,829
; REFERENCE/DOCKET NUMBER: CRP-001CP6
; TELEPHONE: 617/248-7000
; TELEFAX: 617/248-7100
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 314 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: YES
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..314
; OTHER INFORMATION: /note= "CONSENSUS PROBE"
;
US-07-841-646-33

Query Match 15.2%; Score 51.6; DB 1; Length 314;
Best Local Similarity 55.2%; Pred. No. 4.7e-06;
Matches 149; Conservative 0; Mismatches 109; Indels 12; Gaps 2;

Qy 58 ctctacattgacttcgacgagctatcggtctgg---aagtgggtccatgaacctaaagggc 114
Db 13 CTGTAGTGGACTTCAGCGCGACGTGGCTGGGAGCTGGATCATCGCCCGCTCGAC 72
Qy 115 tactatgccaattctgtcagggcccttgccataacct-----cgagctgcagac 165
Db 73 TTCGAGCGCTACTACTGCTCCGAGCGCTGCGAGTTCCTCTCGGGATCATCTTCAACAGC 132

Qy 166 acaacccacagcacggtgctgtgggactgtgtaaacacactctgaacccctgaagcatctgctctg 225
Db 133 ACCAACACGCGCGTGGTGCAGACACCTGTGTGAACACATGAACCCCGCAAGGTACCCAG 192
Qy 226 ccttgctcggtgccccagagacctggagccctgaccatcctgtactatgttgagagacc 285
Db 193 CCCTGCTGGTGGTCCCGACGAGCTGCCGCCATCAGCATGCTGTACTGTGACGAGAAATTCC 252
Qy 286 cccaaagtggagcagctctcccaacatgggtg 315
Db 253 ACCGTGGTGTGAAGAACTACCAGGAGATG 282

RESULT 36
US-08-147-023-33
; Sequence 33, Application US/08147023
; Patent No. 5468845
; GENERAL INFORMATION:
; APPLICANT: OPPERMAN, HERMANN
; APPLICANT: OZKAYNAK, ENGIN
; APPLICANT: KUBERASAMPATH, THANGAVEL
; APPLICANT: RUEGER, DAVID C.
; APPLICANT: PANG, ROY H.L.
; TITLE OF INVENTION: OSTEOGENIC DEVICES
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TESTA, HURWITZ & THIBEAULT
; STREET: 53 STATE STREET
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: U.S.A.
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/147,023
; FILING DATE: 21-FEB-1992
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 810,560
; FILING DATE: 20-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 827,052
; FILING DATE: 28-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 660,162
; FILING DATE: 22-FEB-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 621,988
; FILING DATE: 04-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 621,849
; FILING DATE: 04-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 616,374
; FILING DATE: 21-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 600,024
; FILING DATE: 18-OCT-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 599,543
; FILING DATE: 18-OCT-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 579,865
; FILING DATE: 07-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 569,920
; FILING DATE: 20-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 483,913
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;
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: YES
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: misc-feature
; LOCATION: 1..314
; OTHER INFORMATION: /note= "CONSENSUS PROBE"
US-08-447-570-33

Query Match 15.2%; Score 51.6; DB 1; Length 314;
Best Local Similarity 55.2%; Pred. No. 4.7e-06;
Matches 149; Conservative 0; Mismatches 109; Indels 12; Gaps 2;

QY 58 ctctacattgactccagacagatctgggtgg---aagtgggtccatgaacctaaagggc 114
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 13 CTGTACGTGGATTCACGCGACGTGGGTGGGACGACATGCATCATCGCCCGCTCGAC 72
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 115 tactatgccaacttctgctcagcccttgcccatacctc-----cgagtcgagac 165
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 73 TTCGACGCCCTACTGCTCGGAGCCCTGCCAGTTCCTCTGCGGATCATTCAACAGC 132
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 166 acaaccacagacgggtgctggagctgtacaacactctgaacctgaagcatctgctcg 225
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 133 ACCAACACCGCGTGGTGCAGACCCCTGGTGTGAACAACATGAACCCCGCAAGTACC 192
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 226 ccttgctgctcccccagacctgagccctgacctgtactatgttggagagacc 285
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 193 CCTGCTGCTGCCACCGAGCTGTCCGCCATCAGCATGCTGTACTGTCGAGAGATTCC 252
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 286 cccaagtggagcagctctcccaacatgggtg 315
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Db 253 ACCGTGCTCTGAAGAATACACGAGGATG 282
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 38
US-08-449-700-33
; Sequence 33, Application US/08449700
; Patent No. 5863758
; GENERAL INFORMATION:
; APPLICANT: OPPERMANN, HERMANN
; APPLICANT: OZKAYNAK, ENGIN
; APPLICANT: KUBERASAMPATH, THANGAVEL
; APPLICANT: RUEGER, DAVID C.
; APPLICANT: PANG, ROY H. L.
; TITLE OF INVENTION: OSTEOGENIC DEVICES
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TESTA, HURWITZ & THIBEAULT
; STREET: 53 STATE STREET
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: U.S.A.
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/449,700
; FILING DATE: 21-FEB-1992
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 810,560
; FILING DATE: 20-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 827,052
; FILING DATE: 28-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 660,162
; FILING DATE: 22-FEB-1991

;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 621,988
; FILING DATE: 04-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 621,849
; FILING DATE: 04-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 616,374
; FILING DATE: 21-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 600,024
; FILING DATE: 18-OCT-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 599,543
; FILING DATE: 18-OCT-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 579,865
; FILING DATE: 07-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 569,920
; FILING DATE: 20-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 483,913
; FILING DATE: 22-FEB-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 422,613
; FILING DATE: 17-OCT-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 315,342
; FILING DATE: 23-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 232,630
; FILING DATE: 15-AUG-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 179,460
; FILING DATE: 08-APR-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: PITCHER, EDMUND R.
; REGISTRATION NUMBER: 27,829
; REFERENCE/DOCKET NUMBER: CRP-001CP6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/248-7000
; TELEFAX: 617/248-7100
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 314 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: YES
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: misc-feature
; LOCATION: 1..314
; OTHER INFORMATION: /note= "CONSENSUS PROBE"
US-08-449-700-33

Query Match 15.2%; Score 51.6; DB 2; Length 314;
Best Local Similarity 55.2%; Pred. No. 4.7e-06;
Matches 149; Conservative 0; Mismatches 109; Indels 12; Gaps 2;

QY 58 ctctacattgactccagacagatctgggtgg---aagtgggtccatgaacctaaagggc 114
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 13 CTGTACGTGGATTCACGCGACGTGGGTGGGACGACATGCATCATCGCCCGCTCGAC 72
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 115 tactatgccaacttctgctcagcccttgcccatacctc-----cgagtcgagac 165
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Db 73 TTCGACGCCCTACTGCTCGGAGCCCTGCCAGTTCCTCTGCGGATCATTCAACAGC 132
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QY 166 acaaccacagacgggtgctggagctgtacaacactctgaacctgaagcatctgctcg 225
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 133 ACCAACACCGCGTGGTGCAGACCCCTGGTGTGAACAACATGAACCCCGCAAGTACC 192
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 226 ccttgctgctcccccagacctgagccctgacctgtactatgttggagagacc 285
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 193 CCTGCTGCTGCCACCGAGCTGTCCGCCATCAGCATGCTGTACTGTCGAGAGATTCC 252
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 286 cccaagtggagcagctctcccaacatgggtg 315
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Db 253 ACCGTGCTCTGAAGAATACACGAGGATG 282
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Db 133 ACCAACCCGCGTGTGTGTCAGACCCCTGGTGAACACATGAACCCCGGCAAGGTACCCCAAG 192
Qy 226 ccttctgctgtccccagagacctgagccctgaccatcctgtactatatttgggagacc 285
Db 193 CCTGCTGCTGTCGCCACCGAGCTGTCGCCCATCAGCATGCTGTACCTGGACGAGAATTCC 252
Qy 286 cccaagtggagcagctctcccaacatggg 315
Db 253 ACCGTGGTGTGAAGAACTACCCAGGAGATG 282

RESULT 39
US-08-449-699A-33
; Sequence 33, Application US/08449699A
; Patent No. 5958441
; GENERAL INFORMATION:
; APPLICANT: OPPERMAN, HERMANN
; APPLICANT: OZKAYNAK, ENGIN
; APPLICANT: KUBERASAMPATH, THANGAVEL
; APPLICANT: RUEGER, DAVID C.
; APPLICANT: PANG, ROY H.L.
; TITLE OF INVENTION: ANTIBODIES TO OSTEOGENIC PROTEINS
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TESTA, HURWITZ & THIBEAULT
; STREET: 125 HIGH STREET
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: U.S.A.
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/449,699A
; FILING DATE: 24-MAY-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/147,023
; FILING DATE: 01-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: PITCHER, EDMUND R.
; REGISTRATION NUMBER: 27,829
; REFERENCE/DOCKET NUMBER: STK-001CP6CN
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/248-7000
; TELEFAX: 617/248-7100
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 314 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; HYPOTHETICAL: YES
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..314
; OTHER INFORMATION: /note= "CONSENSUS PROBE"
US-08-449-699A-33

Query Match 15.2%; Score 51.6; DB 2; Length 314;
Best Local Similarity 55.2%; Pred. No. 4.7e-06;
Matches 149; Conservative 0; Mismatches 109; Indels 12; Gaps 2;

Qy 58 ctctacattgacttcgacagagatctggctgg---aagtgggtccatgaacctaaagggc 114
Db 13 CTGTACGTGGACTTCCAGCGCGAGCTGGGCTGGGACGACTGGATCATCGCCCGCTCGAC 72

Qy 115 tactatgccaacttctgctcaggcccttgccataactc-----cgagtgcgagc 165
Db 73 TTGAGCGCCTACTACTACTTCTCCGAGCGCTGCCAGTTCCCTCTGGGATCACTTCAACAGC 132
Qy 166 acaaccacagcagcgtgctgggactgtacaacactctgaacctgaagcatctgctcg 225
Db 133 ACCAACCCGCGTGTGTGTCAGACCCCTGGTGAACAACTGAACCCCGGCAAGGTACCCCAAG 192
Qy 226 ccttctgctgtccccagagacctgagccctgaccatcctgtactatgttgggagacc 285
Db 193 CCTGCTGCTGTCGCCACCGAGCTGTCGCCCATCAGCATGCTGTACCTGGACGAGAATTCC 252
Qy 286 cccaagtggagcagctctcccaacatggg 315
Db 253 ACCGTGGTGTGAAGAACTACCCAGGAGATG 282

RESULT 40
5496552-1
; Patent No. 5496552
; APPLICANT: KUBERASAMPATH, THANGAVEL; RUEGER, DAVID C.
; TITLE OF INVENTION: OSTEOGENIC DEVICES
; NUMBER OF SEQUENCES: 25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/268,252
; FILING DATE: 29-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 103,604
; FILING DATE: 06-AUG-1993
; APPLICATION NUMBER: 827,052
; FILING DATE: 28-JAN-1992
; APPLICATION NUMBER: 579,865
; FILING DATE: 07-SEP-1990
; APPLICATION NUMBER: 179,406
; FILING DATE: 08-APR-1988
; SEQ ID NO: 1:
; LENGTH: 315
5496552-1

Query Match 15.2%; Score 51.6; DB 6; Length 315;
Best Local Similarity 55.2%; Pred. No. 4.7e-06;
Matches 149; Conservative 0; Mismatches 109; Indels 12; Gaps 2;

Qy 58 ctctacattgacttcgacagagatctggctgg---aagtgggtccatgaacctaaagggc 114
Db 13 ctgtacgtggacttcacgcgcagctgggtgggagcagctggtatcgcccccgtcgac 72
Qy 115 tactatgccaacttctgctcaggcccttgccataactc-----cgagtgcgagc 165
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Qy 166 acaaccacagcagcgtgctgggactgtacaacactctgaacctgaagcatctgctcg 225
Db 133 accaaccacgcgtgtgagaccctgtgaaacaatgaaccccggaaggtaccacaag 192
Qy 226 ccttctgctgtccccagagacctgagccctgaccatcctgtactatgttgggagacc 285
Db 193 ccttctgctgtccccacgcagctgtccgcacatcgatgtacctgtacacctgacgagaattcc 252
Qy 286 cccaagtggagcagctctcccaacatggg 315
Db 253 accgtgtgtgaagaactaccaggagatg 282

RESULT 41
US-07-718-274A-1
; Sequence 1, Application US/07718274A
; Patent No. 5284756
; GENERAL INFORMATION:
; APPLICANT: Grinna, Lynn
; APPLICANT: Parsons, Thomas F.
; APPLICANT: Theofan, Georgia

Db 386 GAAACATGGTG 396

RESULT 42

US-08-163-877-9

; Sequence 9, Application US/08163877

; Patent No. 5399677

; GENERAL INFORMATION:

; APPLICANT: McCoy, John

; APPLICANT: Murray, Beth

; APPLICANT: Wolfman, Neil

; TITLE OF INVENTION: MUTANTS OF BONE MORPHOGENIC PROTEINS

; NUMBER OF SEQUENCES: 10

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genetics Institute, Inc - Legal Affairs

; STREET: 87 CambridgePark Drive

; CITY: Cambridge

; STATE: Massachusetts

; COUNTRY: USA

; ZIP: 02140

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/163,877

; FILING DATE:

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Lazar, Steven R.

; REGISTRATION NUMBER: 32,618

; REFERENCE/DOCKET NUMBER: GI 5219

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 617 876-1170 x 8260

; TELEFAX: 617 876-5851

; INFORMATION FOR SEQ ID NO: 9:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 417 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

; ORIGINAL SOURCE:

; ORGANISM: bmp-7

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 1..417

US-08-163-877-9

Query Match	15.0%;	Score 51;	DB 1;	Length 417;	
Best Local Similarity	50.5%;	Pred. No. 7.5e-06;			
Matches 157;	Conservative	0;	Mismatches 145;	Indels 9;	Gaps 325
Qy	17	actgtctccgaacttgaggagaactgctgtgtgcgccctctctacattgactctccag	76		
Db	86	ACAGCAGCAGCGACGACGCCCTGTAAAGACGACGAGCTGTATGTACAGCTCCCGAG	145		
Qy	77	aggatctgggctggaagtgggtccatgaactgaagggtctactatgccaaactctctgctcag	136		
Db	146	ACCTGGGCTGGCAGGACTGGATCATCGCGCTTAGGGCTACGGCGCCTACTACTGTGAGG	205		
Qy	137	gccttggccat-----acctcggagtgacagacaaccaaccaacgaggtgctcg	187		
Db	206	GGGAGTGTGGCTTCCCTCTGAATCTCATATGAACGCCACCAACACGCCATCGTGCAGA	265		
Qy	188	gactgtacaactctgaaccctgaagcatctgcctgcgctgtgctgcgtgccccaggacc	247		
Db	266	CGTGGTCCACTTCATCAACCCGGAAACGGTGCCCAAGGCCCTGCTGTGGGCCACGCACG	325		
Qy	248	tggagcccttgaccatctgtactatgtttgggagagcccccaagtgggagcagctctcca	307		

Db 326 TCAATGCCATCTCCGTCCTACTTCCATGACAGCTCCAAAGCTCATCTCCTGAAGAAATACA 385
QY 308 acatggtggtg 318
| | | | |
Db 386 GAAACATGGTG 396
| | | | |
RESULT 43
US-08-149-106-1
; Sequence 1, Application US/08149106
; Patent No. 5411941
; GENERAL INFORMATION:
; APPLICANT: Grinna, Lynn
; APPLICANT: Parsons, Thomas F.
; APPLICANT: Theofan, Georgia
; TITLE OF INVENTION: Osteogenic Factor
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell
; STREET: Two First National Plaza, 20 South Clark
; STREET: Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/149,106
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/415,555
; FILING DATE: 04-OCT-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/256,034
; FILING DATE: 11-OCT-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharp, Jeffrey S.
; REGISTRATION NUMBER: 31,879
; REFERENCE/DOCKET NUMBER: 27129/9430
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 346-5750
; TELEFAX: (312) 984-9740
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 417 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..417
US-08-149-106-1
Query Match 15.0%; Score 51; DB 1; Length 417;
Best Local Similarity 50.5%; Pred. No. 7.5e-06;
Matches 157; Conservative 0; Mismatches 145; Indels 9; Gaps 1;
QY 17 actgttcctccgacttgaggagaaactgtgtgtcgccccctctacattgacttcgcac 76
| | | | |
Db 86 ACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 145
| | | | |
QY 77 aggatctgggtggaagtgggtccatgaacctaaagggtactatgccaaactctgtcag 136
| | | | |
Db 146 ACCTGGGTGGCAGGACTGGATCATCGCGCTGAAGGCTACGCGGCTACTACTGTGAGG 205
| | | | |

QY 137 gccttgcccat-----acctcgcgagtgagacacacacacacacgacggtgtg 187
| | | | |
Db 206 GGGAGTGTGCTTCCCTCTGAACCTCTTACATGAAGCGCCACCAACCGCCATCGTCAGA 265
| | | | |
QY 188 gactgtacacactctgaaccctgaagcatctgcctcgcttctgtgctgccccagacc 247
| | | | |
Db 266 CGTGTGTCACACTTCATCAACCCGGAACGGTGGCCCAAGCCCTGCTGTGCGCCACGAGC 325
| | | | |
QY 248 tggagccccctgaccatcctctactatgttgaggagaccccccaaaagtggagcagctctcca 307
| | | | |
Db 326 TCAATGCCATCTCCGTCCTACTTCCATGACAGCTCCAAAGCTCATCTCCTGAAGAAATACA 385
| | | | |
QY 308 acatggtggtg 318
| | | | |
Db 386 GAAACATGGTG 396
| | | | |
RESULT 44
US-08-298-021-1
; Sequence 1, Application US/08298021
; Patent No. 5508263
; GENERAL INFORMATION:
; APPLICANT: Grinna, Lynn
; APPLICANT: Parsons, Thomas F.
; APPLICANT: Theofan, Georgia
; TITLE OF INVENTION: Heterodimeric Osteogenic Factor
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-64023
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/298,021
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/149,106
; FILING DATE: 11-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/718,274
; FILING DATE: 20-JUN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/415,555
; FILING DATE: 04-OCT-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/256,034
; FILING DATE: 11-OCT-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharp, Jeffrey S.
; REGISTRATION NUMBER: 31,879
; REFERENCE/DOCKET NUMBER: 27129/32196
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 417 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS

```
; LOCATION: 1..417
US-08-298-021-1

Query Match          15.0%; Score 51; DB 1; Length 417;
Best Local Similarity 50.5%; Pred. No. 7.5e-06;
Matches 157; Conservative 0; Mismatches 145; Indels 9; Gaps 1;

QY 17 actgttcgcgaacttgaggagaactgtgtgccccctctacattgacttccgcag 76
   || || || || || || || || || || || || || || || || || || ||
Db 86 ACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 145

QY 77 aggatctgggtggaagtgggtccatgaacctaaagggctactatgccaaacttctgcag 136
   || || || || || || || || || || || || || || || || || || ||
Db 146 ACCTGGGTGGCAGGACTGGATCATCGCGCCTGAAGGCTACGCCGCTACTACTGTGAGG 205

QY 137 gcccttgcccat-----acctccgcagtgccagacacacccacagcaggtgctgg 187
   || || || || || || || || || || || || || || || || || || ||
Db 206 GGGAGTGTGCTTCCCTCTGAACTCTTACATGAAGACGCCACACCGCATCGTGCAGA 265

QY 188 gactgtacaacactctgaacctgaacctgtgctgccttgcctgtgctgccccagacc 247
   || || || || || || || || || || || || || || || || || || ||
Db 266 CGCTGGTCCACTCATCAACCCGGAACGGTGCCCAAGCCCTGCTGTGCCCCACGCAGC 325

QY 248 tggagccccctgacctctgtactatgttggaggagaccccccaaaagtggagcagctctcca 307
   || || || || || || || || || || || || || || || || || || ||
Db 326 TCAATGCCATCTCCGCTCTACTTCTGATGACAGCTCCAACTCATCTCTGAAGAAATACA 385

QY 308 acatggtggtg 318
Db 386 GAAACATGGTG 396

RESULT 45
US-08-360-914B-9
; Sequence 9, Application US/08360914B
; Patent No. 5756308
; GENERAL INFORMATION:
; APPLICANT: Neil M. Wolfman and John McCoy
; TITLE OF INVENTION: MUTANTS OF BONE MORPHOGENIC PROTEINS
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc - Legal Affairs
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/360.914B
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/163,877
; FILING DATE: December 7, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Lazar, Steven R.
; REGISTRATION NUMBER: 32,618
; REFERENCE/DOCKET NUMBER: GI 5219B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617 498-8260
; TELEFAX: 617 876-5851
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 417 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear

; MOLECULE TYPE: DNA
; ORIGINAL SOURCE:
; ORGANISM: bmp-7
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..417
US-08-360-914B-9

Query Match          15.0%; Score 51; DB 1; Length 417;
Best Local Similarity 50.5%; Pred. No. 7.5e-06;
Matches 157; Conservative 0; Mismatches 145; Indels 9; Gaps 1;

QY 17 actgttcgcgaacttgaggagaactgtgtgccccctctacattgacttccgcag 76
   || || || || || || || || || || || || || || || || || || ||
Db 86 ACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 145

QY 77 aggatctgggtggaagtgggtccatgaacctaaagggctactatgccaaacttctgcag 136
   || || || || || || || || || || || || || || || || || || ||
Db 146 ACCTGGGTGGCAGGACTGGATCATCGCGCCTGAAGGCTACGCCGCTACTACTGTGAGG 205

QY 137 gcccttgcccat-----acctccgcagtgccagacacacccacagcaggtgctgg 187
   || || || || || || || || || || || || || || || || || || ||
Db 206 GGGAGTGTGCTTCCCTCTGAACTCTTACATGAAGACGCCACACCGCATCGTGCAGA 265

QY 188 gactgtacaacactctgaacctgaacctgtgctgccttgcctgtgctgccccagacc 247
   || || || || || || || || || || || || || || || || || || ||
Db 266 CGCTGGTCCACTCATCAACCCGGAACGGTGCCCAAGCCCTGCTGTGCCCCACGCAGC 325

QY 248 tggagccccctgacctctgtactatgttggaggagaccccccaaaagtggagcagctctcca 307
   || || || || || || || || || || || || || || || || || || ||
Db 326 TCAATGCCATCTCCGCTCTACTTCTGATGACAGCTCCAACTCATCTCTGAAGAAATACA 385

QY 308 acatggtggtg 318
Db 386 GAAACATGGTG 396

RESULT 46
US-08-741-589A-9
; Sequence 9, Application US/08741589A
; Patent No. 5804416
; GENERAL INFORMATION:
; APPLICANT: Neil M. Wolfman and John McCoy
; TITLE OF INVENTION: MUTANTS OF BONE MORPHOGENIC PROTEINS
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc - Legal Affairs
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/741,589A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/163,877
; FILING DATE: December 7, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Lazar, Steven R.
; REGISTRATION NUMBER: 32,618
; REFERENCE/DOCKET NUMBER: GI 5219B-DIV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617 498-8260
; TELEFAX: 617 876-5851
; INFORMATION FOR SEQ ID NO: 9:
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; SEQUENCE CHARACTERISTICS:
; LENGTH: 417 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; ORIGINAL SOURCE:
; ORGANISM: bmp-7
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..417
US-08-741-589A-9

Query Match 15.0%; Score 51; DB 1; Length 417;
Best Local Similarity 50.5%; Pred. No. 7.5e-06;
Matches 157; Conservative 0; Mismatches 145; Indels 9; Gaps 1;

QY 17 actgtcttcgcaacttgaggagaaactgtgtgccccctctacattgacttccgac 76
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 86 ACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 145

QY 77 aggatctgggtggaagtgggtccatgaacctaaagggtactatgccaaattctgctcag 136
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 146 ACCTGGGCTGGCAGGACTGATCATCGCGCTGAAGGCTACGCCGCTACTACTGTGAGG 205

QY 137 gcccttgcccat-----acctcccgagtgacagacacacccacagcaggtgtggtg 187
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 206 GGGAGTGTGCCTTCCCTCTGAACCTCTATGAACGCCACCAACCAACCGCATCGTGCAGA 265

QY 188 gactgtacaaactctgaacctgaagcatctgcctgctgtgcgtgccccaggacc 247
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 266 CGCTGGTGCACCTTCATCAACCGGAAAGCGGTGCCCAAGCCCTGCTGTGCGCCACGCGAGC 325

QY 248 tggagccctgaccatctgtactatgttggaggagacccccaaagtggagcagctctcca 307
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 326 TCATGCCATCTCCGTCCTCTACTTCGATGACAGCTCCAACGTCATCTCTGAAGAAATACA 385

QY 308 acatggtggtg 318
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 386 GAAACATGGTG 396

RESULT 47
PCT-US94-13181-9
; Sequence 9, Application PC/TUS9413181
; GENERAL INFORMATION:
; APPLICANT: GENETICS INSTITUTE, INC.
; TITLE OF INVENTION: MUTANTS OF BONE MORPHOGENIC PROTEINS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc - Legal Affairs
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/13181
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/163,877
; FILING DATE: December 7, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Lazar, Steven R.
; REGISTRATION NUMBER: 32,618
; REFERENCE/DOCKET NUMBER: GI 5219-PCT

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; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617 498-8260
; TELEFAX: 617 876-5851
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 417 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; ORIGINAL SOURCE:
; ORGANISM: bmp-7
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..417
PCT-US94-13181-9

Query Match 15.0%; Score 51; DB 5; Length 417;
Best Local Similarity 50.5%; Pred. No. 7.5e-06;
Matches 157; Conservative 0; Mismatches 145; Indels 9; Gaps 1;

QY 17 actgtcttcgcaacttgaggagaaactgtgtgccccctctacattgacttccgac 76
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 86 ACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 145

QY 77 aggatctgggtggaagtgggtccatgaacctaaagggtactatgccaaattctgctcag 136
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 146 ACCTGGGCTGGCAGGACTGATCATCGCGCTGAAGGCTACGCCGCTACTACTGTGAGG 205

QY 137 gcccttgcccat-----acctcccgagtgacagacacacccacagcaggtgtggtg 187
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 206 GGGAGTGTGCCTTCCCTCTGAACCTCTATGAACGCCACCAACCAACCGCATCGTGCAGA 265

QY 188 gactgtacaaactctgaacctgaagcatctgcctgctgtgcgtgccccaggacc 247
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 266 CGCTGGTGCACCTTCATCAACCGGAAAGCGGTGCCCAAGCCCTGCTGTGCGCCACGCGAGC 325

QY 248 tggagccctgaccatctgtactatgttggaggagacccccaaagtggagcagctctcca 307
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 326 TCATGCCATCTCCGTCCTCTACTTCGATGACAGCTCCAACGTCATCTCTGAAGAAATACA 385

QY 308 acatggtggtg 318
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 386 GAAACATGGTG 396

RESULT 48
US-08-621-803-248
; Sequence 248, Application US/08621803
; Patent No. 5851802
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; TITLE OF INVENTION: Methods for Recombinant Microbial Production of
; TITLE OF INVENTION: Fusion Proteins and BPI-Derived Peptides
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/621,803
; FILING DATE: 22-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Borun, Michael F.

```

```
; REGISTRATION NUMBER: 25,447
; REFERENCE/DOCKET NUMBER: 27129/33199
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 248:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 557 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM:
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 66..548
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: residues 1-65
; OTHER INFORMATION: /label= EcoRI
; OTHER INFORMATION: /note="residues 1-65 comprise EcoRI site to beginning of pel B."
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: AA 1-22
; OTHER INFORMATION: /label= pel B
; OTHER INFORMATION: /note="pel B is the leader sequence from the pectate lyase gene of Erwinia carotovora."
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: AA 23-161
; OTHER INFORMATION: /label= "Bone D"
; OTHER INFORMATION: /note="Bone D is the subunit of human osteogenic protein (see U.S. Patent No. 5,284,756 e.g., Fig. 6, Example 9, Seq ID NOS: 1 and 2."
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: residues 549-557
; OTHER INFORMATION: /label= XhoI
; OTHER INFORMATION: /note="residues 549-557 comprise stop codon and XhoI site."
;
US-08-621-803-248
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Query Match 15.0%; Score 51; DB 2; Length 557;
Best Local Similarity 50.5%; Pred. NO. 8.2e-06;
Matches 157; Conservative 0; Mismatches 145; Indels 9; Gaps 1;

QY 17 actgtctccgcaacttgaggagaactgctgtgtgccccctctacattgacttcgcag 76
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 217 ACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 276

QY 77 aggatctgggtggaagtgggtccatgaacctaaagggtactatgccaacttctgctcag 136
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 277 ACCTGGCTGGCAGGACTGGATCATCGCGCTTGAAGCCTACGCCGCTACTACTGTGAGG 336

QY 137 gcccttgcccat-----acctccgagtgtagacacacacacacacacacacacac 187
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 337 GGAGGTGTGCTTCCCTCTCTGAACCTCTACATGAACGCCACCAACCGCATCGTGAGA 396

QY 188 gactgtacaactctgaacctgaagcattctgctgcttctgctgctgctgctgctgctg 247
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 397 CGTGTGTCACCTTCATCAACCGGAGCGGTGCGCCCAAGCCCTGCTGTGCGCCCAAGC 456

QY 248 tggagccctgaccatctgactatgttggaggagaccccaaaagtggagcagctctcca 307
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 457 TCAATGCCATCTCGTCCCTACTTCTGATGACAGCTCCACGCTCATCTCTGAAGAAATACA 516

QY 308 acatggtggtg 318
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 517 GAAACATGGTG 527
```

```
RESULT 49
US-09-271-970-1
; Sequence 1, Application US/09271970
; Patent No. 6242219
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Gavitt, Patrick D.
; TITLE OF INVENTION: Improved Methods for Recombinant Peptide Production
; FILE REFERENCE: 1103/11041US01
; CURRENT APPLICATION NUMBER: US/09/271,970
; CURRENT FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 1
; LENGTH: 557
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (66)..(548)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(65)
; OTHER INFORMATION: /label= EcoRI /note="residues 1-65 comprise EcoRI site to beginning of pel B."
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(22)
; OTHER INFORMATION: /label=pel B /note="pel B is the leader sequence from the pectate lyase gene of Erwinia carotovora."
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (23)..(161)
; OTHER INFORMATION: /label="Bone D" /note="Bone D is the subunit of human osteogenic protein (see, U.S. Patent No. 6242219)"
; OTHER INFORMATION: 5,284,756 e.g., Fig. 6, Example 9, Seq ID No. 6242219: 1
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (549)..(557)
; OTHER INFORMATION: /label=XhoI /note="residues 549-557 comprise stop codon and XhoI site."
;
US-09-271-970-1
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Query Match 15.0%; Score 51; DB 4; Length 557;
Best Local Similarity 50.5%; Pred. NO. 8.2e-06;
Matches 157; Conservative 0; Mismatches 145; Indels 9; Gaps 1;

QY 17 actgtctccgcaacttgaggagaactgctgtgtgccccctctacattgacttcgcag 76
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 217 ACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 276

QY 77 aggatctgggtggaagtgggtccatgaacctaaagggtactatgccaacttctgctcag 136
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 277 ACCTGGCTGGCAGGACTGGATCATCGCGCTTGAAGCCTACGCCGCTACTACTGTGAGG 336

QY 137 gcccttgcccat-----acctccgagtgtagacacacacacacacacacacacac 187
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 337 GGAGGTGTGCTTCCCTCTCTGAACCTCTACATGAACGCCACCAACCGCATCGTGAGA 396

QY 188 gactgtacaactctgaacctgaagcattctgctgcttctgctgctgctgctgctgctg 247
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 397 CGTGTGTCACCTTCATCAACCGGAGCGGTGCGCCCAAGCCCTGCTGTGCGCCCAAGC 456

QY 248 tggagccctgaccatctgactatgttggaggagaccccaaaagtggagcagctctcca 307
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 457 TCAATGCCATCTCGTCCCTACTTCTGATGACAGCTCCACGCTCATCTCTGAAGAAATACA 516

QY 308 acatggtggtg 318
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Db      517 gaaacatggtg 527
RESULT 50
US-09-271-970-7
; Sequence 7, Application US/09271970
; Patent No. 6242219
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Gavitt, Patrick D.
; TITLE OF INVENTION: Improved Methods for Recombinant Peptide Production
; FILE REFERENCE: 1103/11041US01
; CURRENT APPLICATION NUMBER: US/09/271,970
; CURRENT FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 610
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (66)..(599)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(65)
; OTHER INFORMATION: /label=EcoRI /note="residues 1-65 comprise EcoRI
; OTHER INFORMATION: site to beginning of pel B."
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(22)
; OTHER INFORMATION: /label=pel B /note="pel B is the leader sequence
; OTHER INFORMATION: from the pectate lyase gene of Erwinia
; OTHER INFORMATION: caratovora."
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (23)..(161)
; OTHER INFORMATION: /label="Bone D" /note="Bone D is the subunit of
; OTHER INFORMATION: human osteogenic protein (see, U.S. Patent No. 6242219
; OTHER INFORMATION: 5,284,756 e.g., Fig. 6, Example 9, Seq ID No. 6242219: 1
; OTHER INFORMATION: and 2."
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (162)..(166)
; OTHER INFORMATION: /label=cleavage linker /note="Ala-Leu-Asp-Pro-Pro
; OTHER INFORMATION: linking sequence with Asp-Pro cleavage site."
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (167)..(178)
; OTHER INFORMATION: /label=peptide sequence /note="BPI-derived
; OTHER INFORMATION: peptide."
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (600)..(610)
; OTHER INFORMATION: /label=xhoI /note="residues 600-610 comprise stop
; OTHER INFORMATION: codon and xhoI site."
US-09-271-970-7
Query Match      15.0%; Score 51; DB 4; Length 610;
Best Local Similarity 50.5%; Pred. No. 8.5e-06;
Matches 157; Conservative 0; Mismatches 145; Indels 9; Gaps 1;
Qy      17 actgttcgcgaacttgaggagaaactgtgtgtgcgccccctctacattgacttcgcag 76
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Db      217 acagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 276
      || || || || || || || || || || || || || || || || || || || || ||
Qy      77 aggaacttgagctggagtggtccatgaacctaaagggctactatgccaaactctgctcag 136
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      277 acctgggtggcaggactggatctgcgcctgaaggtacgcgccctactactgtgagg 336
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Qy      137 gcccttgcccat-----acctccgcagtgccagacacacccacagcagcggtgctgg 187
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Db      337 gggagtgcccttcctctgaactctctacatgaacgcccaacacagccatgctgcaga 396
Qy      188 gactgtacaacactctgaacccctgaagcatctgcctctgcctgtgctgctgccccagacc 247
      || | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      397 cgctggtccacttcatacccggaacaggtgcccaagccctgctgtgcgccccagcagc 456
Qy      248 tggagccccctgaccatcctgtactatgttgggaggagcccccaagtgaggagcagctctcca 307
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Db      457 tcaatgccatcctcgtcctctactctgatgacagctccaacgctcactctgaagaataca 516
Qy      308 acatggtggtg 318
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Db      517 gaaacatggtg 527
RESULT 51
US-08-621-803-256
; Sequence 256, Application US/08621803
; Patent No. 5851802
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; TITLE OF INVENTION: Methods for Recombinant Microbial Production of
; TITLE OF INVENTION: Fusion Proteins and BPI-Derived Peptides
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/621,803
; FILING DATE: 22-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Borun, Michael F.
; REGISTRATION NUMBER: 25,447
; REFERENCE/DOCKET NUMBER: 27129/33199
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 256:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 613 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 66..602
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: residues 1-65
; OTHER INFORMATION: /label=EcoRI
; OTHER INFORMATION: /note="residues 1-65 comprise EcoRI site to beginning of p
; OTHER INFORMATION: B."
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: AA 1-22
; OTHER INFORMATION: /label=pel B
; OTHER INFORMATION: /note="pel B is the leader sequence from the pectate lyase
; OTHER INFORMATION: gene of Erwinia caratovora."
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: AA 23-161
; OTHER INFORMATION: /label="Bone D"

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; OTHER INFORMATION: /product= "OPIB"
; OTHER INFORMATION: /note= "OPIB - FUSION"
US-08-449-699A-10

Query Match      15.0%; Score 51; DB 2; Length 1004;
Best Local Similarity 50.5%; Pred. No. 9.8e-06;
Matches 157; Conservative 0; Mismatches 145; Indels 9; Gaps 1;

Qy 17 actgttcgcgaacttgaggagaaactgtgtgctgcgcctctacattgacttccgac 76
Db 620 ACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 679
Qy 77 aggatctgggtggaagtgggtccatgaacctaaaggtactactatgccaaacttctgtcag 136
Db 680 ACCTGGGTGGCAGGACTGGATCATCGCGCCGTAAGAGCAGCAGCAGCAGCAGCAGCAG 739
Qy 137 gcccttgcccat-----acctccgcagtgscagacacacccacagcaggtgtg 187
Db 740 GGGAGTGTGCTTCCCTCTGAACCTCTATGATGAAGCCCAACCAACGCGCATCGTGCAGA 799
Qy 188 gactgtacaacactgaacctgaagcatctgcctgcctgtgctgctgctgctgctgctgctg 247
Db 800 CGCTGGTCACTTATCAACCCGGAACGGTCCCAAGCCCTGCTGTGGGCCCAACGCGCAGC 859
Qy 248 tggagccctgaccatctgtactatgtttgggagagaccccccacaaagtggagcagctctcca 307
Db 860 TCAATGCCATCTCCGCTCTCTACTTCTGATGACAGCTCCAACGTCATCTCTGAAGAAATACA 919
Qy 308 acatggtggtg 318
Db 920 GAAACATGGTG 930

RESULT 61
US-07-764-731B-9
; Sequence 9, Application US/07764731B
; Patent No. 5366875
; GENERAL INFORMATION:
; APPLICANT: Rosen, Vicki A.
; APPLICANT: Wang, Elizabeth A.
; APPLICANT: Wozney, John M.
; TITLE OF INVENTION: Methods for Producing BMP-7 Proteins
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Legal Affairs, Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07764.731B
; FILING DATE: 19910924
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Kapinos, Ellen J.
; REGISTRATION NUMBER: 32,245
; REFERENCE/DOCKET NUMBER: G15159B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-876-1170
; TELEFAX: 617-876-5851
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1259 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: circular

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; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; FRAGMENT TYPE: C-terminal
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; CELL LINE: U2-OS Osteosarcoma
; IMMEDIATE SOURCE:
; LIBRARY: U2-OS Human Osteosarcoma cDNA library
; CLONE: U2-5
; POSITION IN GENOME:
; UNITS: bp
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1200
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 783..1200
; FEATURE:
; NAME/KEY: mRNA
; LOCATION: 1..1259
US-07-764-731B-9

Query Match      15.0%; Score 51; DB 1; Length 1259;
Best Local Similarity 50.5%; Pred. No. 1.1e-05;
Matches 157; Conservative 0; Mismatches 145; Indels 9; Gaps 1;

Qy 17 actgttcgcgaacttgaggagaaactgtgtgctgcgcctctacattgacttccgac 76
Db 869 ACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 928
Qy 77 aggatctgggtggaagtgggtccatgaacctaaaggtactactatgccaaacttctgtcag 136
Db 929 ACCTGGGTGGCAGGACTGGATCATCGCGCTGAAGCAGCAGCAGCAGCAGCAGCAG 988
Qy 137 gcccttgcccat-----acctccgcagtgscagacacacccacagcaggtgtg 187
Db 989 GGGAGTGTGCTTCCCTCTGAACCTCTATGATGAAGCCCAACCAACGCGCATCGTGCAGA 1048
Qy 188 gactgtacaacacttgaaacctgaagcatctgcctgcctgtgctgctgctgctgctgctgctg 247
Db 1049 CGCTGGTCCACTTCATCAACCCGGAACGGTCCCAAGCCCTGCTGTGGGCCCAACGCGCAG 1108
Qy 248 tggagccctgaccatctgtactatgtttgggagagaccccccacaaagtggagcagctctcca 307
Db 1109 TCAATGCCATCTCCGCTCTCTACTTCTGATGACAGCTCCAACGTCATCTCTGAAGAAATACA 1168
Qy 308 acatggtggtg 318
Db 1169 GAAACATGGTG 1179

RESULT 62
US-07-841-646-14
; Sequence 14, Application US/07841646
; Patent No. 5266683
; GENERAL INFORMATION:
; APPLICANT: OPPERMANN, HERMANN
; APPLICANT: OKAYNAK, ENGIN
; APPLICANT: KUBERASAMPATH, THANGAVEL
; APPLICANT: RUEGER, DAVID C.
; APPLICANT: PANG, ROY H.L.
; TITLE OF INVENTION: OSTEOGENIC DEVICES
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TESTA, HURWITZ & THIBEAULT
; STREET: 53 STATE STREET
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: U.S.A.
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 621,849
FILING DATE: 04-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 616,374
FILING DATE: 21-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 600,024
FILING DATE: 18-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 599,543
FILING DATE: 18-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 579,865
FILING DATE: 07-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 569,920
FILING DATE: 20-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 483,913
FILING DATE: 22-FEB-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 422,613
FILING DATE: 17-OCT-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 315,342
FILING DATE: 23-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 232,630
FILING DATE: 15-AUG-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 179,460
FILING DATE: 08-APR-1988
ATTORNEY/AGENT INFORMATION:
NAME: PITCHER, EDMUND R.
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: CRP-001CP6
TELEPHONE: 617/248-7000
TELEFAX: 617/248-7100
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 1277 base pairs.
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: YES
ANTI-SENSE: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1224 /function= "OSTEOGENIC PROTEIN"
OTHER INFORMATION: /product= "Op1d"
OTHER INFORMATION: /note= "Op1d - FUSION"
US-08-147-023-14

Query Match 15.0%; Score 51; DB 1; Length 1277;
Best Local Similarity 50.5%; Pred. No. 1.1e-05;
Matches 157; Conservative 0; Mismatches 145; Indels 9; Gaps 1;
Qy 17 actgtttccgaacttgaggagaaactgtgtgtgcgcgcctctctacattgacttcagac 76
Db 893 ACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 952
Qy 77 aggatctgggctggagtggttccatgaacctaaaggctactatccaaacttctctcag 136
Db 953 ACCTGGGTCGAGCAGCTGATCATCGCCCTGAGGCTACCGCCGCTACTACTGTGAGG 1012
Qy 137 gcccttgcacat-----acctccgcagtcgagacacacacacagcaggtgtctgg 187
Db 1013 GGGAGTGTGCCTTCCTCTGAACTCCTACATGAACGCCACCAACACGCGCATCGTGACA 1072

Qy 188 gactgtacaacactctgaaccctgaagcatctgctgccttgcgtgcgtgcccagacc 247
Db 1073 CGCTGTCCACTTCATCAACCCGGAACGGTGCCTCAAGCCCTGCTGTGCGCCACGCGC 1132
Qy 248 tggagcccttgaccatctctgtactatgtttggaggagcccccaaaagtggagcagctctcca 307
Db 1133 TCAATGCCATCTCCGCTCTACTTCTGATGACAGCTCCAACGTCATCCTGAAGAAATACA 1192
Qy 308 acatggtggtg 318
Db 1193 GAAACATGGTG 1203
RESULT 64
US-08-447-570-14
Sequence 14, Application US/08447570
Patent No. 5714589
GENERAL INFORMATION:
APPLICANT: OPPERMAN, HERMANN
APPLICANT: OKAYNAK, ENGIN
APPLICANT: KUBERASAMPATH, THANGAVEL
APPLICANT: RUEGER, DAVID C.
APPLICANT: PANG, ROY H.L.
TITLE OF INVENTION: OSTEOGENIC DEVICES
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: TESTA, HURWITZ & THIBEAULT
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: U.S.A.
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/447,570
FILING DATE: 21-FEB-1992
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 810,560
FILING DATE: 20-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 827,052
FILING DATE: 28-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 660,162
FILING DATE: 22-FEB-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 621,988
FILING DATE: 04-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 621,849
FILING DATE: 04-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 616,374
FILING DATE: 21-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 600,024
FILING DATE: 18-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 599,543
FILING DATE: 18-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 579,865
FILING DATE: 07-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 569,920
FILING DATE: 20-AUG-1990
PRIOR APPLICATION DATA:

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; APPLICATION NUMBER: US 483,913
; FILING DATE: 22-FEB-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 422,613
; FILING DATE: 17-OCT-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 315,342
; FILING DATE: 23-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 232,630
; FILING DATE: 15-AUG-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 179,460
; FILING DATE: 08-APR-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: PITCHER, EDMUND R.
; REGISTRATION NUMBER: 27,829
; REFERENCE/DOCKET NUMBER: CRP-001CP6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/248-7000
; TELEFAX: 617/248-7100
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1277 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: YES
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1224
; OTHER INFORMATION: /function= "OSTEOGENIC PROTEIN"
; OTHER INFORMATION: /product= "Op1d"
; OTHER INFORMATION: /note= "Op1d - FUSION"
;
; US-08-447-570-14

Query Match 15.0%; Score 51; DB 1; Length 1277;
Best Local Similarity 50.5%; Pred. No. 1.1e-05;
Matches 157; Conservative 0; Mismatches 145; Indels 9; Gaps 1;

QY 17 actgtctccgaacttgaggaactgtgtgtgcgcgcctctacatgaacttcgac 76
   || || || || || || || || || || || || || || || || || || ||
Db 893 ACAGCAGCAGCGACGAGCGCCTGTGAAGAGCAGCAGCTGTATGTCAGCTCCGAG 952

QY 77 agaatctgggctggaagtgggtccatgaacctaaagggtactatgccaactctgtcag 136
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Db 953 ACCTGGGCTGGCAGGACTGGATCATCGCGCTGAAGGCTACGCGCCTACTACTGTGAGG 1012

QY 137 gcccttgccat-----acctcgcagtgacacacacacacacacggtgtgg 187
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Db 1013 GGGAGTGTGCTTCCCTCTGAATCTTACATGAACGCCACCAACGCGCATCGTGAGA 1072

QY 188 gactgtacaactctgaacctgaagcatctgctcgcctctgtcgtgccccaggacc 247
   || | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1073 CGTGTCTCACTTCATCAACCCGGAACGGTGCCCAAGCCTGCTGTGCGCCACGAGC 1132

QY 248 tggagcccttgaccatctctgtactatgtttggaggagacccccaaagtggagcgtctcca 307
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1133 TCAATGCATCTCCGTCCTCTACTTCGATGACAGCTCCAACGTCATCCTGAAGAAATACA 1192

QY 308 acatggtggtg 318
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Db 1193 GAAACATGGTG 1203

RESULT 65
US-08-449-700-14
; Sequence 14, Application US/08449700
; Patent No. 5863758
; GENERAL INFORMATION:
; TELECOMMUNICATION INFORMATION:
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; APPLICANT: OPPERMAN, HERMANN
; APPLICANT: OZKAYNAK, ENGIN
; APPLICANT: KUBERASAMPATH, THANGAVEL
; APPLICANT: RUEGER, DAVID C.
; APPLICANT: PANG, ROY H. L.
; TITLE OF INVENTION: OSTEOGENIC DEVICES
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TESTA, HURWITZ & THIBEAULT
; STREET: 53 STATE STREET
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: U.S.A.
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/449,700
; FILING DATE: 21-FEB-1992
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 810,560
; FILING DATE: 20-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 827,052
; FILING DATE: 28-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 660,162
; FILING DATE: 22-FEB-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 621,988
; FILING DATE: 04-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 621,849
; FILING DATE: 04-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 616,374
; FILING DATE: 21-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 600,024
; FILING DATE: 18-OCT-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 599,543
; FILING DATE: 18-OCT-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 579,865
; FILING DATE: 07-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 569,920
; FILING DATE: 20-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 483,913
; FILING DATE: 22-FEB-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 422,613
; FILING DATE: 17-OCT-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 315,342
; FILING DATE: 23-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 232,630
; FILING DATE: 15-AUG-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 179,460
; FILING DATE: 08-APR-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: PITCHER, EDMUND R.
; REGISTRATION NUMBER: 27,829
; REFERENCE/DOCKET NUMBER: CRP-001CP6
; TELECOMMUNICATION INFORMATION:
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Patent No. 5266683
GENERAL INFORMATION:
APPLICANT: OPPERMAN, HERMANN
APPLICANT: OZKAYNAK, ENGIN
APPLICANT: KUBERASAMPATH, THANGAVEL
APPLICANT: RUEGER, DAVID C.
APPLICANT: PANG, ROY H.L.
TITLE OF INVENTION: OSTEOGENIC DEVICES
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: TESTA, HURWITZ & THIBEAULT
STREET: 53 STATE STREET
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: U.S.A.
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/841,646
FILING DATE: 19920221
CLASSIFICATION: 530
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 810,560
FILING DATE: 20-DEC-1991
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 827,052
FILING DATE: 28-JAN-1992
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 660,162
FILING DATE: 22-FEB-1991
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 621,988
FILING DATE: 04-DEC-1990
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 621,849
FILING DATE: 04-DEC-1990
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 616,374
FILING DATE: 21-NOV-1990
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 600,024
FILING DATE: 18-OCT-1990
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 579,865
FILING DATE: 07-SEP-1990
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 569,920
FILING DATE: 20-AUG-1990
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 483,913
FILING DATE: 22-FEB-1990
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 422,613
FILING DATE: 17-OCT-1989
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 315,342
FILING DATE: 23-FEB-1989
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 232,630
FILING DATE: 15-AUG-1988
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 179,460
FILING DATE: 08-APR-1988
ATTORNEY/AGENT INFORMATION:
NAME: FITCHER, EDMUND R.
REGISTRATION NUMBER: 27,829

REFERENCE/DOCKET NUMBER: CRP-001CP6
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/248-7000
TELEFAX: 617/248-7100
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 1505 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: YES
ANTI-SENSE: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1452
OTHER INFORMATION: /function= "OSTEOGENIC PROTEIN"
OTHER INFORMATION: /product= "OPIC"
OTHER INFORMATION: /note= "OPIC - FUSION"
US-07-841-646-12
Query Match 15.0%; Score 51; DB 1; Length 1505;
Best Local Similarity 50.5%; Pred. No. 1.1e-05;
Matches 157; Conservative 0; Mismatches 145; Indels 9; Gaps 1;
Qy 17 actgtctccgaacttgaggagaaactgtgtgtcgccccctctacattgacttccgac 76
Db 1121 ACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1180
Qy 77 aggatctgggtggaagtgggtcccatgaacctaaagggtactatgccaacttctgtcag 136
Db 1181 ACCTGGGCTGGCAGGACTGGATCATCGCGCTGAAGGCTACGCCGCTACTACTGTGAGG 1240
Qy 137 gcccttgcccat-----acctccgcagtgacacaaacccacagacagtggtgctgg 187
Db 1241 GGGAGTGTGCCTTCCCTCTGAACTCTACATGAAGCCCAACCAACGCGCATCGTGCGAGA 1300
Qy 188 gactgtacacactctgaacctgaagcatctgcctgcctgtctgcgtgccccagacc 247
Db 1301 CGTGGTCCACTTCATCAACCCGGAAACGGTGCCCAAGCCCTGCTGTGCGCCACCGCAGC 1360
Qy 248 tggagcccttgaccatctgtactatgttgggagagaccccccaagtggagcagctctcca 307
Db 1361 TCAATGCCATCTCCGTCTCTACTTCGATGACAGCTCCAAACGTCATCTCTGAAGAAATA 1420
Qy 308 acatggtggtg 318
Db 1421 GAAACATGGTG 1431

RESULT 72
US-08-147-023-12
Sequence 12, Application US/08147023
Patent No. 5468845
GENERAL INFORMATION:
APPLICANT: OPPERMAN, HERMANN
APPLICANT: OZKAYNAK, ENGIN
APPLICANT: KUBERASAMPATH, THANGAVEL
APPLICANT: RUEGER, DAVID C.
APPLICANT: PANG, ROY H.L.
TITLE OF INVENTION: OSTEOGENIC DEVICES
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: TESTA, HURWITZ & THIBEAULT
STREET: 53 STATE STREET
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: U.S.A.
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

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1 OPERATING SYSTEM: PC-DOS/MS-DOS
2 SOFTWARE: PatentIn Release #1.0, Version #1.25
3 CURRENT APPLICATION DATA:
4 APPLICATION NUMBER: US/08/147,023
5 FILING DATE: 21-FEB-1992
6 CLASSIFICATION: 530
7 PRIOR APPLICATION DATA:
8 APPLICATION NUMBER: US 810,560
9 FILING DATE: 20-DEC-1991
10 PRIOR APPLICATION DATA:
11 APPLICATION NUMBER: US 827,052
12 FILING DATE: 28-JAN-1992
13 PRIOR APPLICATION DATA:
14 APPLICATION NUMBER: US 660,162
15 FILING DATE: 22-FEB-1991
16 PRIOR APPLICATION DATA:
17 APPLICATION NUMBER: US 621,988
18 FILING DATE: 04-DEC-1990
19 PRIOR APPLICATION DATA:
20 APPLICATION NUMBER: US 621,849
21 FILING DATE: 04-DEC-1990
22 PRIOR APPLICATION DATA:
23 APPLICATION NUMBER: US 616,374
24 FILING DATE: 21-NOV-1990
25 PRIOR APPLICATION DATA:
26 APPLICATION NUMBER: US 600,024
27 FILING DATE: 18-OCT-1990
28 PRIOR APPLICATION DATA:
29 APPLICATION NUMBER: US 599,543
30 FILING DATE: 18-OCT-1990
31 PRIOR APPLICATION DATA:
32 APPLICATION NUMBER: US 579,865
33 FILING DATE: 07-SEP-1990
34 PRIOR APPLICATION DATA:
35 APPLICATION NUMBER: US 569,920
36 FILING DATE: 20-AUG-1990
37 PRIOR APPLICATION DATA:
38 APPLICATION NUMBER: US 483,913
39 FILING DATE: 22-FEB-1990
40 PRIOR APPLICATION DATA:
41 APPLICATION NUMBER: US 422,613
42 FILING DATE: 17-OCT-1989
43 PRIOR APPLICATION DATA:
44 APPLICATION NUMBER: US 315,342
45 FILING DATE: 23-FEB-1989
46 PRIOR APPLICATION DATA:
47 APPLICATION NUMBER: US 232,630
48 FILING DATE: 15-AUG-1988
49 PRIOR APPLICATION DATA:
50 APPLICATION NUMBER: US 179,460
51 FILING DATE: 08-APR-1988
52 ATTORNEY/AGENT INFORMATION:
53 NAME: PITCHER, EDMUND R.
54 REGISTRATION NUMBER: 27,829
55 REFERENCE/DOCKET NUMBER: CRP-001CP6
56 TELECOMMUNICATION INFORMATION:
57 TELEPHONE: 617/248-7000
58 TELEFAX: 617/248-7100
59 INFORMATION FOR SEQ ID NO: 12:
60 SEQUENCE CHARACTERISTICS:
61 LENGTH: 1505 base pairs
62 TYPE: nucleic acid
63 STRANDEDNESS: single
64 TOPOLOGY: linear
65 MOLECULE TYPE: cDNA
66 HYPOTHETICAL: YES
67 ANTI-SENSE: NO
68 FEATURE:
69 NAME/KEY: CDS
70 LOCATION: 1..1452 /function= "OSTEOGENIC PROTEIN"
71 OTHER INFORMATION: /product= "OPIC"
72 OTHER INFORMATION: /note= "OPIC - FUSION"

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US-08-147-023-12

Query Match 15.0%; Score 51; DB 1; Length 1505;
Best Local Similarity 50.5%; Pred. No. 1.1e-05;
Matches 157; Conservative 0; Mismatches 145; Indels 9; Gaps 1;

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Qy	77	aggatctgggctgggaagtgggtcccatgaacctaaaggctactatgccaaacttctgctcag	136
Db	1181	ACCTGGGCTGGCAGGACTGGATCATCGGCGCTGAAGGCTACGCCGCTACTACTGTGAGG	1240
Qy	137	gccttggccat-----acctccgcagtgcagacacaaacccacagcacggtgctcg	187
Db	1241	GGAGTGTGGCTTCCCTCTGAACTCCTACATGACGCCCAACACCGCCATCGTGCAGA	1300
Qy	188	gactgtacaacactctgaaccttgaagcatctgcttcgcttgcgtgcccccaggacc	247
Db	1301	CGTGGTCCACTTCATCAACCCGGAAACGGTCCCAAGCCCTGCTGCGCCCAACGACG	1360
Qy	248	tggagcccttgaccatctctgttactatgtttggaggaccccccaaaagtggacagctctcca	307
Db	1361	TCAATGCCATCTCGGTCCCTCTACTTTCGATGACAGCTCCAAAGTATCCTCTGAAGAATAACA	1420
Qy	308	acatgggtggg	318
Db	1421	GAACAATGGT	1431

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RESULT 73
US-08-447-570-12
; Sequence 12, Application US/08447570
; Patent No. 5714589
; GENERAL INFORMATION:
; APPLICANT: OPPERMANN, HERMANN
; APPLICANT: OZKAYNAK, ENGIN
; APPLICANT: KUBERASAMPATH, THANGAVEL
; APPLICANT: RUEGER, DAVID C.
; APPLICANT: PANG, ROY H.L.
; TITLE OF INVENTION: OSTROGENIC DEVICES
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TESTA, HURWITZ & THIBEAULT
; STREET: 53 STATE STREET
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: U.S.A.
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/447,570
; FILING DATE: 21-FEB-1992
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 810,560
; FILING DATE: 20-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 827,052
; FILING DATE: 28-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 660,162
; FILING DATE: 22-FEB-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 621,988
; FILING DATE: 04-DEC-1990
; PRIOR APPLICATION DATA:

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APPLICANT: OZAKAYNAK, ENGIN
TITLE OF INVENTION: PROSTHETIC DEVICES HAVING ENHANCED
TITLE OF INVENTION: OSTEOGENIC PROPERTIES
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: TESTA, HURWITZ & THIBEAULT
STREET: EXCHANGE PLACE, 53 STATE STREET
CITY: BOSTON
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/901.703
FILING DATE: 19920616
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: PITCHER, ESO, EDMUND R
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: STK-057
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/248-7000
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1822 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: HOMO SAPIENS
TISSUE TYPE: HIPPOCAMPUS
FEATURE:
NAME/KEY: CDS
LOCATION: 49..1341
IDENTIFICATION METHOD: experimental
OTHER INFORMATION: /function= "OSTEOGENIC PROTEIN"
OTHER INFORMATION: /product= "Op1"
OTHER INFORMATION: /evidence= EXPERIMENTAL
OTHER INFORMATION: /standard_name= "Op1"
US-07-901-703-1

Query Match 15.0%; Score 51; DB 1; Length 1822;
Best Local Similarity 50.5%; Pred. No. 1.2e-05;
Matches 157; Conservative 0; Mismatches 145; Indels 9; Gaps 1;
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Qy 77 aggatctgggtgggaagtgggtlccatgaacctaaagggtactatgccaaactctgtcag 136
Db 1070 ACTTGGGCTGGCAGGACTGGATCATCGGCGCTGAAGGCTAGCCGCCVACTACTGTGAGG 1129
Qy 137 gcccttgcccat-----acctcccgagtgagacacccacagcaggtgtctgg 187
Db 1130 GGGAGTGTGCCTTCCCTCTGAACCTCTACATGAAGCGCCACCAACCGCCATCGTGCAGA 1189
Qy 188 gactgtacaacacttgaaacctgaagatctgtcgtcgttgctgctgccccagacc 247
Db 1190 CGTGGTCCACTTCATCAACCGGAAACGGTGCCCAACCCCTGTGTGCGCCACGACG 1249
Qy 248 tggagccctgaccatctgtactatgttggaggagcccccaagtgagcagctctcca 307
Db 1250 TCATGGCATCTCCGTCTCTACTTCGATGACAGCTCAACGTATCTCTGAAGAAATACA 1309

Qy 308 acatggtggtg 318
Db 1310 GAAACATGGTG 1320
RESULT 78
US-08-147-023-1
Sequence 1, Application US/08147023
Patent No. 5468845
GENERAL INFORMATION:
APPLICANT: OPPERMAN, HERMANN
APPLICANT: OZKAYNAK, ENGIN
APPLICANT: KUBERASAMPATH, THANGAVEL
APPLICANT: RUEGER, DAVID C.
APPLICANT: PANG, ROY H.L.
TITLE OF INVENTION: OSTEOGENIC DEVICES
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: TESTA, HURWITZ & THIBEAULT
STREET: 53 STATE STREET
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: U.S.A.
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/147,023
FILING DATE: 21-FEB-1992
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 810,560
FILING DATE: 20-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 827,052
FILING DATE: 28-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 660,162
FILING DATE: 22-FEB-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 621,988
FILING DATE: 04-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 621,849
FILING DATE: 04-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 616,374
FILING DATE: 21-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 600,024
FILING DATE: 18-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 599,543
FILING DATE: 18-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 579,865
FILING DATE: 07-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 569,920
FILING DATE: 20-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 483,913
FILING DATE: 22-FEB-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 422,613
FILING DATE: 17-OCT-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 315,342
FILING DATE: 23-FEB-1989
PRIOR APPLICATION DATA:


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; NAME/KEY: CDS
; LOCATION: 49..1341
; OTHER INFORMATION: /function= "OSTEOGENIC PROTEIN"
; OTHER INFORMATION: /product= "hOPI-pp"
; OTHER INFORMATION: /note= "hOPI cDNA"
US-08-479-666-3

Query Match 15.0%; Score 51; DB 1; Length 1822;
Best Local Similarity 50.5%; Pred. No. 1.2e-05;
Matches 157; Conservative 0; Mismatches 145; Indels 9; Gaps

QY 17 actgcttcgcgaacttgagagagaactgctgtgtgcgccccctctacattgacttcgcac 76
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Db 1010 ACAGCAGCAGCAGCAGCAGCAGCAGCAGCCTGTAAAGAAGCAGCAGCTGTATGTGAGTCCGAG 1069
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QY 77 aggtatctgggctgaagtgggtccatgaacctaaaggcttactatgccaaacttctgctcag 136
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Db 1070 ACCTGGGCTGGCAGACTGGATCATCGCGCCTGAAGGCTACCGCGCCTACTACTGTGAGG 1129
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QY 137 gcccttggccat-----acctcccgagtgagacacacacccacagcacggtgtctgg 187
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Db 1130 GGGAGTGTGCTTCCTCTGAACTCTACATCAAGCCACCAACACGCGCATCTGTGCAGA 1189
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QY 188 gactgtacaacacttgaaacctgaacctgaagcatctgcctctgctgtgctgccccaggacc 247
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Db 1190 CGCTGGTCCACTTCATCAACCCGGAACGGTGCCCAAGCCCTGCTGTGCGCCACACGCAGC 1249
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 248 tggggccctgacatcctgtactatgtttgggagagacccccaaaagtggagagagctctcca 307
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QY 308 acatgggtggtg 318
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Db 1310 GAAACATGGTG 1320
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RESULT 83
US-08-155-343A-16
; Sequence 16, Application US/08155343A
; Patent No. 5658593
; GENERAL INFORMATION:
; APPLICANT: KUBERASAMPATH, THANGAVEL
; APPLICANT: RUEGER, DAVID C.
; APPLICANT: OPPERMANN, HERMAN
; APPLICANT: COHEN, CHARLES M.
; APPLICANT: PANG, ROY H.L.
; TITLE OF INVENTION: MORPHOGENIC-INDUCED PERIODONTAL TISSUE
; TITLE OF INVENTION: REGENERATION.
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES
; STREET: 45 SOUTH STREET
; CITY: HOPKINTON
; STATE: MA
; COUNTRY: USA
; ZIP: 01748
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/155,343A
; APPLICATION NUMBER: US/08/155,343A
; FILING DATE: 15-NOV-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: FENTON ESQ., GILLIAN M.
; REGISTRATION NUMBER: 36,508
; REFERENCE/DOCKET NUMBER: CRP-067FW
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7560
; TELEFAX: (617) 248-7100

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; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1822 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 49..1341
; OTHER INFORMATION: /product= "HOP-1"
US-08-155-343A-16

Query Match          15.0%; Score 51; DB 1; Length 1822;
Best Local Similarity 50.5%; Pred. No. 1.2e-05;
Matches 157; Conservative 0; Mismatches 145; Indels 9; Gaps 1;

QY 17 actgttcgcgaacttggagggaactgtgtgtgccccctctacattgacttcgcac 76
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QY 77 aggatctgggtggaagtgggtccatgaacctaaagggctactatgccaaactctgtctcag 136
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Db 1070 ACCTGGGCTGGCAGGACTGGATCATCGCGCCTGAAGGCTACGCGCCTACTACTGTGAGG 1129

QY 137 gcccttgcccat-----acctccgcagtcgagacacacacacacacacaggtgctgg 187
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QY 188 gactgtacaacactctgaacctgaacctgaacctgaacctgaacctgaacctgaacctgaacct 247
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Db 1190 CGCTGGTCCACTTCATCAACCCGGAACCGTGCCCAAGCCCTGCTGTGCGCCACCGCAGC 1249

QY 248 tggagccccctgaccatctactgtatgttgggagagaccccccaaaagtggagcagctctcca 307
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Db 1250 TCNATGCCATCTCCGTCCCTCTACTTCGATGACAGCTCCAACGTCATCTCTGAAGAAATACA 1309

QY 308 acatggtggtg 318
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Db 1310 GAAACATGGTG 1320

RESULT 85
US-08-643-563A-16
; Sequence 16, Application US/08643563A
; Patent No. 5707810
; GENERAL INFORMATION:
; APPLICANT: SMART, JOHN
; APPLICANT: OPPERMAN, HERMAN
; APPLICANT: OZKAYNAK, ENGIN
; APPLICANT: KUBERASAMPATH, THANGAVEL
; APPLICANT: RUEGER, DAVID C.
; APPLICANT: PANG, ROY H.L.
; APPLICANT: COHEN, CHARLES M.
; TITLE OF INVENTION: MORPHOGENIC PROTEIN SCREENING METHOD
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES
; STREET: 45 SOUTH STREET
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 752,857
; FILING DATE: 30-AUG-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 667,274
; FILING DATE: 11-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: FENTON ESQ., GILLIAN M.
; REGISTRATION NUMBER: 36,508
; REFERENCE/DOCKET NUMBER: CRP-060CN
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7560
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1822 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 49..1341
; OTHER INFORMATION: /product= "HOP-1"
US-08-406-672-16

Query Match          15.0%; Score 51; DB 1; Length 1822;
Best Local Similarity 50.5%; Pred. No. 1.2e-05;
Matches 157; Conservative 0; Mismatches 145; Indels 9; Gaps 1;

QY 17 actgttcgcgaacttggagggaactgtgtgtgccccctctacattgacttcgcac 76
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QY 77 aggatctgggtggaagtgggtccatgaacctgaacctgaacctgaacctgaacctgaacctgaacct 136
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QY 188 gactgtacaacactctgaacctgaacctgaacctgaacctgaacctgaacctgaacctgaacct 247
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QY 308 acatggtggtg 318
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Db 1310 GAAACATGGTG 1320

RESULT 85
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; Sequence 16, Application US/08643563A
; Patent No. 5707810
; GENERAL INFORMATION:
; APPLICANT: SMART, JOHN
; APPLICANT: OPPERMAN, HERMAN
; APPLICANT: OZKAYNAK, ENGIN
; APPLICANT: KUBERASAMPATH, THANGAVEL
; APPLICANT: RUEGER, DAVID C.
; APPLICANT: PANG, ROY H.L.
; APPLICANT: COHEN, CHARLES M.
; TITLE OF INVENTION: MORPHOGENIC PROTEIN SCREENING METHOD
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES
; STREET: 45 SOUTH STREET
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; CITY: HOPKINTON
; STATE: MA
; COUNTRY: USA
; ZIP: 01748
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/643,563A
; FILING DATE: 06-MAY-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: TWOMEY ESQ., MICHAEL J.
; REGISTRATION NUMBER: 38,349
; REFERENCE/DOCKET NUMBER: CRP-058CN2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (508) 435-9001
; TELEFAX: (508) 435-6951
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1822 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 49..1341
; OTHER INFORMATION: /product= "HOP-1"
;
US-08-643-563A-16

Query Match 15.0%; Score 51; DB 1; Length 1822;
Best Local Similarity 50.5%; Pred. No. 1.2e-05;
Matches 157; Conservative 0; Mismatches 145; Indels 9; Gaps 1;

QY 17 acgtctccgaactggaggaaactgtgtgcgccccctctacattgacttcgac 76
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QY 77 aggatgggctggagtggtggtccatgaacctaaagggtactactatgcacacttctgtcag 136
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Db 1070 ACCTGGGCTGGCAGGACTGATCATCGCGCTGAAGCCTACGCGCTACTACTGTGAGG 1129
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QY 137 gcccttgcccat-----acctccgagtgagacacacacacacagcagcgtgtg 187
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Db 1130 GGGAGTGTGCTTCCCTCTGAACTCTACATGAACGCCACCAACCGCCATCGTGCAGA 1189
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QY 188 gactgtacaacactgtgaacctgaagcattcgtcgtcgttctggtgccccaggacc 247
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Db 1190 CGCTGTCCACTTCATCAACCCGGAACGGTGCACCAAGCCCTGCTGTGCGCCACGCGAGC 1249
   ||| || || || || || || || || || || || || || || || || || ||

QY 248 tggagccctcgaccatctgactatgttggaggagcccccaaaaggaggagcagctctcca 307
   ||| || || || || || || || || || || || || || || || || || ||
Db 1250 TCNATGCCATCTCCGCTCTACTTTCGATGACAGCTCCACGTCATCTCTGAAGAAATACA 1309
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QY 308 acatggtggtg 318
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Db 1310 GAAACATGGTG 1320

RESULT 86
US-08-447-570-1
; Sequence 1, Application US/08447570
; Patent No. 5714589
; GENERAL INFORMATION:
; APPLICANT: OPPERMANN, HERMANN
; APPLICANT: OZKAYNAK, ENGIN
; APPLICANT: KUBERASAMPATH, THANGAVEL
; APPLICANT: RUEGER, DAVID C.
; APPLICANT: PANG, ROY H.L.
```

```
; TITLE OF INVENTION: OSTEOGENIC DEVICES
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TESTA, HURWITZ & THIBEAULT
; STREET: 53 STATE STREET
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: U.S.A.
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/447,570
; FILING DATE: 21-FEB-1992
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 810,560
; FILING DATE: 20-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 827,052
; FILING DATE: 28-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 660,162
; FILING DATE: 22-FEB-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 621,988
; FILING DATE: 04-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 621,849
; FILING DATE: 04-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 616,374
; FILING DATE: 21-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 600,024
; FILING DATE: 18-OCT-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 599,543
; FILING DATE: 18-OCT-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 579,865
; FILING DATE: 07-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 569,920
; FILING DATE: 20-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 483,913
; FILING DATE: 22-FEB-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 422,613
; FILING DATE: 17-OCT-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 315,342
; FILING DATE: 23-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 232,630
; FILING DATE: 15-AUG-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 179,460
; FILING DATE: 08-APR-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: PITCHER, EDMUND R.
; REGISTRATION NUMBER: 27,829
; REFERENCE/DOCKET NUMBER: CRP-001CP6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/248-7000
; TELEFAX: 617/248-7100
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1822 base pairs
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; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: HOMO SAPIENS
; TISSUE TYPE: HIPPOCAMPUS
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 49..1341
; IDENTIFICATION METHOD: experimental
; OTHER INFORMATION: /function="OSTEOGENIC PROTEIN"
; OTHER INFORMATION: /product="Op1"
; OTHER INFORMATION: /evidence= EXPERIMENTAL
; OTHER INFORMATION: /standard_name= "Op1"
US-08-447-570-1

Query Match 15.0%; Score 51; DB 1; Length 1822;
Best Local Similarity 50.5%; Pred. No. 1.2e-05;
Matches 157; Conservative 0; Mismatches 145; Indels 9; Gaps 1;

QY 17 actgtctccgaacttgaggagaaactgtgtgtgccccctctacattgacttccgac 76
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Db 1010 ACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1069

QY 77 aggatctggctggagtgagtgagtgagtgagtgagtgagtgagtgagtgagtg 136
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1070 ACCTGGGCTGGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1129

QY 137 gcccttgcccat-----acctccgcagtgccagacacacacacacacacac 187
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Db 1130 GGGAGTGTGCCTTCCCTCTGAACCTCTGAACTCTACATGAACGCCACCAACCG 1189

QY 188 gactgtacacactctgaacctgaagcatctgcctgcctgcctgcctgcctgcct 247
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Db 1190 CGCTGGTCCACTTCATCAACCCGGAAGCGTGCCCAAGCCCTGCTGTGCCCCAG 1249

QY 248 tggagccctgacctctgtactatgttggaggagaccccccaagtgagcagctcca 307
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Db 1250 TCAATGCCATCTCCGTCCTCTACTTCGATGACAGCTCCAACGTCATCTCTGA 1309

QY 308 acatggtggtg 318
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Db 1310 GAAACATGGTG 1320

RESULT 87
US-08-643-763A-16
; Sequence 16, Application US/08643763A
; Patent No. 5733878
; GENERAL INFORMATION:
; APPLICANT: KUBERASAMPATH, THANGAVEL
; APPLICANT: RUEGER, DAVID C.
; APPLICANT: OPPERMANN, HERMAN
; APPLICANT: COHEN, CHARLES M.
; APPLICANT: PANG, ROY H.L.
; TITLE OF INVENTION: MORPHOGENIC-INDUCED PERIODONTAL TISSUE
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES
; STREET: 45 SOUTH STREET
; CITY: HOPKINTON
; STATE: MA
; COUNTRY: USA
; ZIP: 01748
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

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; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/643,763A
; FILING DATE: 06-MAY-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: FENTON ESQ., GILLIAN M.
; REGISTRATION NUMBER: 36,508
; REFERENCE/DOCKET NUMBER: CRP-067CN
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7560
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1822 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 49..1341
; OTHER INFORMATION: /product="HOP-1"
US-08-643-763A-16

Query Match 15.0%; Score 51; DB 1; Length 1822;
Best Local Similarity 50.5%; Pred. No. 1.2e-05;
Matches 157; Conservative 0; Mismatches 145; Indels 9; Gaps 1;

QY 17 actgtctccgaacttgaggagaaactgtgtgtgccccctctacattgacttccgac 76
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Db 1010 ACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1069

QY 77 aggatctggctggagtgagtgagtgagtgagtgagtgagtgagtgagtgagtg 136
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1070 ACCTGGGCTGGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1129

QY 137 gcccttgcccat-----acctccgcagtgccagacacacacacacacacac 187
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Db 1130 GGGAGTGTGCCTTCCCTCTGAACCTCTGAACTCTACATGAACGCCACCAACCG 1189

QY 188 gactgtacacactctgaacctgaagcatctgcctgcctgcctgcctgcctgcct 247
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1190 CGCTGGTCCACTTCATCAACCCGGAAGCGTGCCCAAGCCCTGCTGTGCCCCAG 1249

QY 248 tggagccctgacctctgtactatgttggaggagaccccccaagtgagcagctcca 307
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1250 TCAATGCCATCTCCGTCCTCTACTTCGATGACAGCTCCAACGTCATCTCTGA 1309

QY 308 acatggtggtg 318
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Db 1310 GAAACATGGTG 1320

RESULT 88
US-08-462-623-16
; Sequence 16, Application US/08462623
; Patent No. 5739107
; GENERAL INFORMATION:
; APPLICANT: COHEN, CHARLES M.
; APPLICANT: CHARETTE, MARC F.
; APPLICANT: KUBERASAMPATH, THANGAVEL
; APPLICANT: RUEGER, DAVID C.
; APPLICANT: OPPERMANN, HERMAN
; APPLICANT: PANG, ROY H.L.
; APPLICANT: OZKAYNAK, ENGIN
; APPLICANT: SMART, JOHN E.
; TITLE OF INVENTION: MORPHOGEN TREATMENT OF GASTROINTESTINAL
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES

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; LENGTH: 1822 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 49..1341
; OTHER INFORMATION: /function= "OSTEOGENIC PROTEIN"
; OTHER INFORMATION: /product= "hOpl-pp"
; OTHER INFORMATION: /note= "hOpl cDNA"
;
US-08-901-200A-3

Query Match 15.0%; Score 51; DB 2; Length 1822;
Best Local Similarity 50.5%; Pred. No. 1.2e-05;
Matches 157; Conservative 0; Mismatches 145; Indels 9; Gaps

QY 17 actgtcttcgcgaacttggagggaactgtgtgtgcgccccctctacattgacttcgcag 76
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Db 1010 ACAGCAGCAGCAGCAGCAGCGGCTGTGAAGAAGCAGCAGGTGTATGTCACTTCCGAG 1059
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QY 77 aggatctgggtgaagtgggtccatgaacctaaaggtgtactatgtccaactctgctcag 136
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Db 1070 ACCTGGGCTGGCAGGACTGGATCATCGCGCCCTGAAGGCTACGCCGCCCTACTACTGTGAGG 1129
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QY 137 gcccttgcocat-----acctccgcagtgccagacacacccacagcacggtgctgg 187
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1130 GCGAGTGTGCCCTTCCTCTGAACTCTCATGAACGCCACCAACGCCCATCTGTGCGAGA 1189
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 188 gactgtacaacactctgaacctgaagcatctgcctgcctctgtgtgctgcctcaggacc 247
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Db 1190 CGCTGGTCCACTTCATCAACCCGGAAACGGTGCCTCAAGCCCTGTGTGCGCCACGCGAGC 1249
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 248 tggagccctgaccatcctgtactatgttgggagagacccccaaagtggagcagctctcca 307
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1250 TCAATGCCATCCCGCTCTACTTCGATGACAGCTCCAACGTCATCTGAAGAAATACA 1309
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QY 308 acatggtggtg 318
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1310 GAAACATGGTG 1320
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RESULT 93
US-08-481-337A-9
; Sequence 9, Application US/08481337A
; Patent No. 5863738
;
GENERAL INFORMATION:
; APPLICANT: TEN DIJKE, Peter
; APPLICANT: HELDIN, Carl-Henrik
; APPLICANT: MIVAZONO, Kohei
; APPLICANT: SAMPATH, Kuber T.
;
TITLE OF INVENTION: Morphogenic Protein-Specific Cell
;
TITLE OF INVENTION: Surface Receptors and Uses Therefor
;
NUMBER OF SEQUENCES: 18
;
CORRESPONDENCE ADDRESS:
; ADDRESSEE: Testa, Hurwitz & Thibault
; STREET: 125 High St.
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
;
COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
;
CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/481,337A
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MEYERS, Thomas C.

```

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;
;
; REGISTRATION NUMBER: 36,989
; REFERENCE/DOCKET NUMBER: CRP-097CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7000
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1822 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 49..1341
; IDENTIFICATION METHOD: experimental
; OTHER INFORMATION: /function= "OSTEOGENIC PROTEIN"
; OTHER INFORMATION: /product= "Opl"
; OTHER INFORMATION: /evidence= EXPERIMENTAL
; OTHER INFORMATION: /standard_name= "Opl"
;
US-08-481-337A-9

Query Match 15.0%; Score 51; DB 2; Length 1822;
Best Local Similarity 50.5%; Pred. No. 1.2e-05;
Matches 157; Conservative 0; Mismatches 145; Indels 9; Gaps 1;

QY 17 actgttcgcgaacttgaggagaaactgtgtgtgcgccccctctacattgacttcgcac 76
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DB 1010 ACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1069
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 77 aggatctgggtggaagtgggtccatgaacctaaagggtactatgccaaacttctgtctcag 136
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DB 1070 ACCTGGCTGGCAGGACTGGATCATCGCGCCTGAAGCTACGCGCCTACTACTGTGAGG 1129
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QY 137 gcccttgccat-----acctcgcagtgycagacacaaacccacagcagggtgctgg 187
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DB 1130 GGGAGTGTGCCTTCCTCTCTGAACCTCTCATGAACGCCCAACCAACGCGCATCGTGCAG 1189
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 188 gactgtacaaactctgaacctgaagcatctgcctcgccctgctgctgcgtgccccaggacc 247
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DB 1190 CGCTGGTCCACTTCATCAACCCGGAACCGTGCCCAAGCCCTGCTGTGCGCCGCCAGCAGC 1249
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 248 tggagcccttgaccatctctgtactattgtggaggagccccccaaagtggagcagctctcca 307
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DB 1250 TCAATGCCATCTCCGTCCTCTACTTCGATGACAGCTCCAACGCTCATCTCTGAAGAAATACA 1309
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QY 308 acatggtggtg 318
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DB 1310 GAAACATGGTG 1320

RESULT 94
US-08-449-700-1
; Sequence 1, Application US/08449700
; Patent No. 5863758
; GENERAL INFORMATION:
; APPLICANT: OPPERMANN, HERMANN
; APPLICANT: OZKANAK, ENGIN
; APPLICANT: KUBERASAMPATH, THANGAVEL
; APPLICANT: RUEGER, DAVID C.
; APPLICANT: PANG, ROY H.L.
; TITLE OF INVENTION: OSTEOGENIC DEVICES
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TESTA, HURWITZ & THIBEAULT
; STREET: 53 STATE STREET
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: U.S.A.
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/449,700
; FILING DATE: 21-FEB-1992
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 810,560
; FILING DATE: 20-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 827,052
; FILING DATE: 28-JAN-1992
; APPLICATION NUMBER: US 660,162
; FILING DATE: 22-FEB-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 621,988
; FILING DATE: 04-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 621,849
; FILING DATE: 04-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 616,374
; FILING DATE: 21-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 600,024
; FILING DATE: 18-OCT-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 599,543
; FILING DATE: 18-OCT-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 579,865
; FILING DATE: 07-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 569,920
; FILING DATE: 20-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 483,913
; FILING DATE: 22-FEB-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 422,613
; FILING DATE: 17-OCT-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 315,342
; FILING DATE: 23-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 232,630
; FILING DATE: 15-AUG-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 179,460
; FILING DATE: 08-APR-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: PITCHER, EDMUND R.
; REGISTRATION NUMBER: 27,829
; REFERENCE/DOCKET NUMBER: CRP-001CP6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/248-7000
; TELEFAX: 617/248-7100
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1822 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: HOMO SAPIENS
; TISSUE TYPE: HIPPOCAMPUS
; FEATURE:
; NAME/KEY: CDS
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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/696,268B
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MEYERS, Thomas C.
; REGISTRATION NUMBER: 36,989
; REFERENCE/DOCKET NUMBER: CRP-117
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7000
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1822 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 49..1341
; OTHER INFORMATION: /function= "Osteogenic Protein"
; OTHER INFORMATION: /product= "Op1"
; OTHER INFORMATION: /standard_name= "Op1"
;
US-08-696-268B-3

Query Match 15.0%; Score 51; DB 2; Length 1822;
Best Local Similarity 50.5%; Pred. No. 1.2e-05;
Matches 157; Conservative 0; Mismatches 145; Indels 9; Gaps 1;

QY 17 actgtctccgaacttgaggagaactgtgtgtgccccctctacattgacttccgac 76
   || || || || || || || || || || || || || || || || || || || ||
Db 1010 ACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1069

QY 77 aggatctggctgggaagtgggtccatgaacctaaaggctactatgccaacttctgctcag 136
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1070 ACCTGGGCTGGCAGGACTGGATCATCGCGCTGAAGGCTACGCGCTACTACTGTGAGG 1129

QY 137 gcccttgcccat-----acctccgagtgagacacacacacacacagcagtgctgg 187
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Db 1130 GGGAGTGTGCTTCCCTCTGAACCTCTACATGAACGCCACCAACACCATCGTCGAGA 1189

QY 188 gactgtacacactctgaacctgaagcatctgctgccttctgctgctgctgctgctgac 247
   || | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1190 CGCTGGTCCACTTCATCAACCCGGAACGGTGCCCAAGCCCTGCTGTGCGCCACGAGC 1249

QY 248 tggagccctgaccatctgtactatgttggaggagcccccaaaagtggagcagctctcca 307
   || | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1250 TCAATGCCATCTCCGCTCTACTTCGATGACAGCTCCAAAGCTCCTCTCTGAAGAAATACA 1309

QY 308 acatggtggtg 318
   | | | | |
Db 1310 GAAACATGGTG 1320

RESULT 97
US-08-461-397A-16
; Sequence 16, Application US/08461397A
; Patent No. 5972884
; GENERAL INFORMATION:
; APPLICANT: COHEN, CHARLES M.
; APPLICANT: CHARETTE, MARC F.
; APPLICANT: KUBERASAMPATH, THANGAVEL
; APPLICANT: RUEGER, DAVID C.
; APPLICANT: OPPERMANN, HERMANN
; APPLICANT: PANG, ROY H.L.
; APPLICANT: OZKAYNAK, ENGIN

```

```

; APPLICANT: SMART, JOHN E.
; TITLE OF INVENTION: MORPHOGEN TREATMENT FOR LIMITING
; TITLE OF INVENTION: PROLIFERATION OF EPITHELIAL CELLS.
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES
; STREET: 45 SOUTH STREET
; CITY: HOPKINTON
; STATE: MA
; COUNTRY: USA
; ZIP: 01748
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,397A
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: PITCHER ESQ, EDMUND R.
; REGISTRATION NUMBER: 27,829
; REFERENCE/DOCKET NUMBER: CRP-074FW2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/248-7000
; TELEFAX: 617/248-7100
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1822 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 49..1341
; OTHER INFORMATION: /product= "HOP-1"
;
US-08-461-397A-16

Query Match 15.0%; Score 51; DB 2; Length 1822;
Best Local Similarity 50.5%; Pred. No. 1.2e-05;
Matches 157; Conservative 0; Mismatches 145; Indels 9; Gaps 1;

QY 17 actgtctccgaacttgaggagaactgtgtgtgccccctctacattgacttccgac 76
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QY 77 aggatctggctgggaagtgggtccatgaacctaaaggctactatgccaacttctgctcag 136
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Db 1070 ACCTGGGCTGGCAGGACTGGATCATCGCGCTGAAGGCTACGCGCTACTACTGTGAGG 1129

QY 137 gcccttgcccat-----acctccgagtgagacacacacacacacagcagtgctgg 187
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QY 188 gactgtacacactctgaacctgaagcatctgctgccttctgctgctgctgctgctgac 247
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Db 1190 CGCTGGTCCACTTCATCAACCCGGAACGGTGCCCAAGCCCTGCTGTGCGCCACGAGC 1249

QY 248 tggagccctgaccatctgtactatgttggaggagcccccaaaagtggagcagctctcca 307
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Db 1250 TCAATGCCATCTCCGCTCTACTTCGATGACAGCTCCAAAGCTCCTCTCTGAAGAAATACA 1309

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RESULT 98
US-08-912-088-16
; Sequence 16, Application US/08912088

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Db 1310 GAAACATGGTG 1320

RESULT 100
US-08-458-811-1
; Sequence 1, Application US/08458811
; Patent No. 6027743
; GENERAL INFORMATION:
; APPLICANT: KHOURI, ROGER K.
; APPLICANT: SAMPURH, KUBER T.
; APPLICANT: RUEGER, DAVID C.
; TITLE OF INVENTION: MANUFACTURE OF AUTOGENOUS REPLACEMENT
; TITLE OF INVENTION: BODY PARTS
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TESTA, HURWITZ & THIBEAULT
; STREET: 53 STATE STREET
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: U.S.A.
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/458,811
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: KELLEY, ROBIN D.
; REGISTRATION NUMBER: 34,637
; REFERENCE/DOCKET NUMBER: CRP-108
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/248-7000
; TELEFAX: 617/248-7100
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1822 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: HOMO SAPIENS
; TISSUE TYPE: HIPPOCAMPUS
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 49..1341
; IDENTIFICATION METHOD: experimental
; OTHER INFORMATION: /function= "OSTEOGENIC PROTEIN"
; OTHER INFORMATION: /product= "Opl"
; OTHER INFORMATION: /evidence= EXPERIMENTAL
; OTHER INFORMATION: /standard_name= "Opl"
US-08-458-811-1

Query Match 15.08; Score 51; DB 3; Length 1822;

Best Local Similarity 50.5%; Pred. No. 1.2e-05;
Matches 157; Conservative 0; Mismatches 145; Indels 9; Gaps 1;
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Qy 77 aggatctgggctggaaagtgggtcccatgaacctaaagggtctactatgccaaacttctgctcag 136
Db 1070 ACCTGGGCTGGCAGGACTGGATCATCGCGCTGAAGGCTACGCCGCTACTACTGTGAGG 1129
Qy 137 gcccttgcccat-----acctccgcaagtgcagacacaaacccacagcagcgtgtg 187
Db 1130 GGGAGTGTGCTTCCCTCTGAACCTCTTACATGAACGCCACCAACGCCATCTGTCAGA 1189
Qy 188 gactgtacaacactctgaacccctgaagcatctgctgccttctgtcgtgccccagacc 247
Db 1190 CGCTGGTCCACTTCATCAACCCGGAAACGGTGCCTCAAGCCCTGTGTGCGGCCACGAGC 1249
Qy 248 tggagccctgaccatccctgactatgttggaggagcccccagaagtggagcagctctcca 307
Db 1250 TCAATGCCATCTCCGTCCTCTACTTCGTGATGACAGCTCCAACGTCATCCTGAAGAAATACA 1309
Qy 308 acatggtggtg 318
Db 1310 GAAACATGGTG 1320

Search completed: October 30, 2001, 11:50:43
Job time: 4305 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 30, 2001, 09:12:22 ; Search time 1009.83 Seconds
 (without alignments)
 3173.324 Million cell updates/sec

Title: TGFB3N
Perfect score: 339
Sequence: 1 gctttgacaccaattactg.....agtttgttaaatgtagctga 339

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 10228115 seqs, 4726426750 residues

Total number of hits satisfying chosen parameters: 20456230

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Technologies, a division of Invitrogen 9800 Medical Center
Drive Rockville, Maryland 20850, USA Fax : (1) 301 610
8371 Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com" 2 others

BASE COUNT 245 a 248 c 269 g 200 t
ORIGIN

Query Match 100.0%; Score 339; DB 106; Length 964;
Best Local Similarity 100.0%; Pred. No. 8.1e-86;
Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 121 gccaaacttctgcagggcccttgccataacctccgcagtgagacacaaacccacagca 180
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QY 181 gtgctggagactgtacaacactctgaacctgaacctccgcagtgagacacaaacccacagca 180
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QY 241 caggacctggagcccttgaccacccctgtactatgttggaggagcccccacaaagtggagcag 300
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QY 301 ctctcaacatggtgtgaagtctgttgaatgtactga 339
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RESULT 2

AW412139 645 bp mRNA EST 08-FEB-2000
LOCUS uq46g03.y1 NCI_CGAP_Mam5 Mus musculus cDNA clone IMAGE:2812468 5'
DEFINITION similar to gb:M32745 mouse transforming growth factor beta-3 mRNA,
complete (MOUSE);, mRNA sequence.

ACCESSION AW412139
VERSION AW412139.1 GI:6937994

KEYWORDS EST.

SOURCE house mouse.

ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 645)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Washington University Genome Sequencing Center

Clone Distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

MGI:1045080

Seq primer: -40RP from Gibco

High quality sequence stop: 446.

FEATURES

source

1. 645

/organism="Mus musculus"

/strain="C57/B6"

/db_xref="taxon:10090"

↑

/clone="IMAGE:2812468"
/tissue_type="tumor, gross tissue"
/dev_stage="7 months"
/lab_host="DH10B"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sali;
Site_2: Noti; Cloned unidirectionally. Primer: Oligo dt.
Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Robin Humphreys,
NIH"

BASE COUNT 159 a 196 c 175 g 115 t
ORIGIN

Query Match 85.8%; Score 291; DB 115; Length 645;
Best Local Similarity 91.2%; Pred. No. 3.2e-72;
Matches 309; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

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QY 61 tacattgaacttcgacaggaatctgggtggaagtgggtccatgaacctaaaggctactat 120
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Db 349 CAGGACCTGGAGCCCTTGACCCTTGTACTATGTGGCAGACACCCCAAGTGGAGCAG 408
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QY 301 ctctcaacatggtgtgaagtctgttgaatgtactga 339
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Db 409 CTCTCAACATGTTGTTGAAGTCTGTTAAGTGCAGCTGA 447
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RESULT 3

BG175423 812 bp mRNA EST 06-FEB-2001
LOCUS 602337778F1 NCI_CGAP_Mam1 Mus musculus cDNA clone IMAGE:4460706 5'
DEFINITION mRNA sequence.

ACCESSION BG175423

VERSION BG175423.1 GI:12682126

KEYWORDS EST.

SOURCE house mouse.

ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 812)

AUTHORS NIH-MGC http://mgc.nci.nih.gov/.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Gilbert Smith, Ph.D.

cDNA Library Preparation: Life Technologies, Inc.

DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)

Clone Distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLNL0262 row: 1 column: 19

High quality sequence stop: 735.

1. 812

/organism="Mus musculus"

Location/Qualifiers

source

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/strain="FVB/N"
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/lab_host="DH10B"
/organism="Rattus norvegicus"
/strain="Sprague-Dawley"
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/clone="UI-R-C3-sm-a-12-0-UI"
/clone_lib="UI-R-C3"
/dev_stage="adult"
/lab_host="DH10B (Life Technologies)"
/notes="Vector: pMT3D-pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-C3
library is a subtracted library of a series, ultimately
derived from a mixture of individually tagged normalized
libraries from rat placenta, adult lung, brain, liver,
kidney, heart, spleen, ovary, muscle, and 8, 12 and 18-day
embryos, after a series of subtractions to reduce the
representation of cDNAs from which ESTs had already been
generated. The following serially subtracted libraries
were generated in this process: UI-R-C3, UI-R-C2p, UI-R-C1
, UI-R-C0, UI-R-A1, UI-R-E1. The tag is a string of 3-5
nucleotides present between the Not I site and the
oligo-dT track which allows identification of the library
of origin of a clone within the mixture. The subtracted
library (UI-R-C3) was constructed as follows: PCR amplified
cDNA inserts from UI-R-C2p clones from which 3' ESTs had
been derived was used as a driver in a hybridization with
the UI-R-C2p library in the form of single-stranded
circles. The remaining single-stranded circles (subtracted
library) was purified by hydroxyapatite column
chromatography, converted to double-stranded circles and
electroporated into DH10B bacteria (Life Technologies) to
generate the UI-R-C3 library. This procedure has been
previously described (Bonaldo, Lennon and Soares, Genome
Research 6:791-806, 1996)."

```

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BASE COUNT      197 a      210 c      245 g      160 t
ORIGIN
Query Match      85.8%; Score 291; DB 174; Length 812;
Best Local Similarity 91.2%; Pred. No. 3.4e-72;
Matches 309; Conservative 0; Mismatches 30; Indels 0; Gaps 0;
QY 1 gcttgacacacattactgctccgcaactggaggagaactgctgtgcccctc 60
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Db 59 GCCCTGGACCAATTTACTGCTTCCGCAACCTGGAGGAGAACTGCTGTGACGCCCTT 118
QY 61 tacattgactccgacagagatggctggagtgagtggtccatgaacctaaaggctactat 120
|| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 119 TATATTGACTTCGGCAGGATAGGCTGGAATGGGTCCACGAACCTAAGGGTTACTAT 178
QY 121 gcaactctctcagggcctggccatacctccgagtcagagacacacacacagcag 180
|| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 179 GCCAATCTTGCTAGGCCCTTGCCCATACCTCCGCGGCGAGACACACCATAGCAGC 238
QY 181 gtgctgggactgtacaactctgaacctgaagcatctgctcgcctgctgctgccc 240
|| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 239 GTGCTGGACTATACACACCTGACACAGAGCGCTGCTGCCATGCTGCGTCCCTC 298
QY 241 caggacctggagccctgacactctctgtactatgttggaggagcccccaagtggagcag 300
|| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 299 CAGGACCTGGAGCCCTGACCATCTTGTACTATGTGGCGAGAACCCCAAGGTGGAGCAG 358
QY 301 ctctccaaactggtgagtgagcttgtaaatgagtga 339
Db 359 CTGTCAACATGGTGGTGAAGTCGTGTAAGTCAGCTGA 397

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RESULT 4
BF542567 503 bp mRNA EST 11-DEC-2000
LOCUS BF542567
DEFINITION UI-R-C3-sm-a-12-0-UI.r1 UI-R-C3 Rattus norvegicus cDNA clone
ACCESSION BF542567
VERSION BF542567.1 GI:11633674
KEYWORDS EST.
SOURCE Norway rat.
ORGANISM Rattus norvegicus
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 503)
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene
discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 9704477
COMMENT Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: msoares@blue.weeg.uiowa.edu
cDNA Library Preparation: M.B. Soares Lab Clone distribution:
clones will be available through Research Genetics (www.resgen.com)
This clone is also available through the I.M.A.G.E. Consortium at

```

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LLNL (info@image.llnl.gov). IMAGE ID= 1768868
Seq primer: M13 Forward.
Location/Qualifiers
source
1. .503
/organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-C3-sm-a-12-0-UI"
/clone_lib="UI-R-C3"
/dev_stage="adult"
/lab_host="DH10B (Life Technologies)"
/notes="Vector: pMT3D-pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-C3
library is a subtracted library of a series, ultimately
derived from a mixture of individually tagged normalized
libraries from rat placenta, adult lung, brain, liver,
kidney, heart, spleen, ovary, muscle, and 8, 12 and 18-day
embryos, after a series of subtractions to reduce the
representation of cDNAs from which ESTs had already been
generated. The following serially subtracted libraries
were generated in this process: UI-R-C3, UI-R-C2p, UI-R-C1
, UI-R-C0, UI-R-A1, UI-R-E1. The tag is a string of 3-5
nucleotides present between the Not I site and the
oligo-dT track which allows identification of the library
of origin of a clone within the mixture. The subtracted
library (UI-R-C3) was constructed as follows: PCR amplified
cDNA inserts from UI-R-C2p clones from which 3' ESTs had
been derived was used as a driver in a hybridization with
the UI-R-C2p library in the form of single-stranded
circles. The remaining single-stranded circles (subtracted
library) was purified by hydroxyapatite column
chromatography, converted to double-stranded circles and
electroporated into DH10B bacteria (Life Technologies) to
generate the UI-R-C3 library. This procedure has been
previously described (Bonaldo, Lennon and Soares, Genome
Research 6:791-806, 1996)."

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BASE COUNT      106 a      151 c      133 g      112 t      1 others
ORIGIN
Query Match      84.4%; Score 286.2; DB 150; Length 503;
Best Local Similarity 91.5%; Pred. No. 7.1e-71;
Matches 303; Conservative 0; Mismatches 28; Indels 0; Gaps 0;
QY 9 cccaattactgctccgcaactggaggagaactgctgtgccccctctacattga 68
|| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 CACCGACTACTGCTTCCGCAACCTGGAGGAGAACTGCTGTGCGCCCTCTACATTGA 120
QY 69 ctccgacagagatctggctggaagtgggtccatgaacctaaaggctactatgccaaact 128
|| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 121 CTTCCGGCAGGATCTAGGCTGGAATGGTCCACCAACCTAAGGTTACTATGCCAAT 180
QY 129 ctgctcaggcccttgcccatacctccgagtcagagacacacacacacagcagctgctg 188
|| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 181 CTGCTCAGGCTTGGCCCTTACCTCCGAGCTCAGACACACACACAGCAGCGTGTCTGG 240
QY 189 actctacaacctgaacctgaacctgacctgctcgccttgcctgctgctgctgctgct 248
|| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 241 ACTATACAACACCTTGAACCCGGAGGCATCGCCCTCGGCATCTGCTGTGCCCCCAAG 300
QY 249 ggagccctgaccatcctgtactatgttggaggagcccccaagtggagcagctctccaa 308
|| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 301 GGACCTCTGACCATCTTGTACTATGTTGGCAGAACCCCAAGGTGGAGCAGCTGTCCAA 360
QY 309 catggtggtgaagtcttctgtaaatgtagctga 339
|| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 361 CATGGTGGTGAAGTCGTGTAAGTCAGCTGA 391

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RESULT 5
BF101203
LOCUS BF101203 1820 bp mRNA EST
DEFINITION 601754782F1 NCI_CGAP_Mam1 Mus musculus cDNA clone IMAGE:398358 5',

```

DEFINITION	Accession	Version	Keywords	Source	Organism
REFERENCE	Authors				
TITLE					
JOURNAL					
COMMENT					
FEATURES	Source				
BASE COUNT					
ORIGIN					
Query Match					
Best Local					
Matches					
QY	1	g	g	g	g
Db	195	G	G	G	G
QY	61	t	t	t	t
Db	255	T	T	T	T
QY	121	g	g	g	g
Db	315	G	G	G	G
QY	181	g	g	g	g
Db	375	G	G	G	G
QY	241	c	c	c	c
Db	435	C	C	C	C
RESULT	7				
AA915041					
LOCUS					
DEFINITION					

RESULT	7
AA915041	
LOCUS	
DEFINITION	

[illegible]


```
Db 416 TACATTGACTTCGCAAGACCTCGGCTGGAAGTGGATCCACGAGCCCAAGGCTACCAT 357
QY 121 gcaactctgtcagcccttgcocatacctccgcagtcgagacacacacacacagcag 180
Db 356 GCCAACTTCTGCTGGGCGCTGCCCTACATTTGGAGCGTGGACACGAGTACAGCAAG 297
QY 181 gtgcgggactacaacactgaacctgaacctgaagcatctgctcgcctgtcgtgcgcc 240
Db 296 GTCCCTGGCCCTGTACAACCAAGCATACCCGGCGGCGCTCGGCGCGCGCTGCTGCGTGGCG 237
QY 241 caggacctgagccctgacctctgtactatgttggaggagaccccccaaaagtggagcag 300
Db 236 CAGGCGCTGGAGCCCTGCCCTGCTGCTACTACGTGGCGCGCAAGCCCAAGGTGGAGCAG 177
QY 301 ctctcaacatggtggtgaagtcttgaatgtagctga 339
Db 176 CTGTCCAACATGATCGTGGCTCCTGCAAGTGCAGCTGA 138

RESULT 13
LOCUS BF726995 600 bp mRNA EST 05-JAN-2001
DEFINITION sapiens cDNA clone by15c03 5', mRNA sequence.
ACCESSION BF726995
VERSION BF726995.1 GI:12042906
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
TITLE Wislow,G.J., Bernstein,S., Behal,A. and Smith,D.
JOURNAL NEIBANK: EST analysis and bioinformatics for ocular genomics
COMMENT Invest. Ophthalmol. Vis. Sci. 41 (2000) In press
Contact: Wislow G
Section on Molecular Structure and Function
National Eye Institute
6/331, NIH, Bethesda, MD 20892-2740, USA
Tel: 301 402 3452
Fax: 301 496 0078
Email: graeme@helix.nih.gov
Plate: 15 row: c column: 03
Seq primer: M13RP1 reverse primer (ABI).
FEATURES
Location/Qualifiers
1..600
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="by15c03"
/clone_lib="Human Lens cDNA (Un-normalized, unamplified);
By"
/tissue_type="Lens"
/dev_stage="Adult"
/lab_host="EMDH10B"
/Note="Organ: Eye; Vector: pCMVSPORT6; Two human lenses
from different adults (both approximately 40 years old)
together yielded 20ug of total RNA and 150ng mRNA for cDNA
library synthesis. A directionally cloned cDNA library in
the pCMVSPORT6 vector was constructed at Life Technologies
, essentially following the protocols of the Superscript
plasmid system full details of which are contained in the
manufacturer's instruction manual
(http://www.lifetech.com/). First strand synthesis was
carried out using a Not I primer-adaptor
[5',-pGAGTAGTCTAGATCGAGCGCGCC(T)15-3']. Not I/blunt
end inserts were cloned into the Not I/EcoR V sites in the
vector. EST analysis was performed on the unamplified
library at the NIH Intramural Sequencing Center (NISC)."
BASE COUNT 91 a 170 c 216 g 122 t
ORIGIN

Query Match , 60.4%; Score 204.6; DB 168; Length 600;
```

```
Best Local Similarity 75.2%; Pred. No. 1.1e-47;
Matches 255; Conservative 0; Mismatches 84; Indels 0; Gaps 0;
QY 1 gcttggacacaaactactctccgcaacttggagagaactgctgtgtgccccctc 60
Db 512 GCCTGGACACCAACTATTGCTTCAGCTCCACGGAGAGAACTGCTGCGTGGCGAGGTG 453
QY 61 tacattgacttcgacagagatctgggctggaagtgggtccatgaacctaaaggtactat 120
Db 452 TACATTGACTTCGCAAGACCTCGGCTGGAAGTGGATCCACGAGCCCAAGGCTACCAT 393
QY 121 gcaactctgtcagcccttgcocatacctccgcagtcgagacacacacacacagcag 180
Db 392 GCCAACTTCTGCTGGGCGCTGCCCTACATTTGGAGCGTGGACACGAGTACAGCAAG 333
QY 181 gtgcgggactacaacactctgaacctgaacctgaagcatctgctcgcctgtcgtgcgcc 240
Db 332 GTCTGGCCCTGTACAACCAAGCATACCCGGCGGCGCTGCGCGCGCGCTGCTGCGTGGCG 273
QY 241 caggacctgagccctgacctctgtactatgttggaggagaccccccaaaagtggagcag 300
Db 272 CAGGCGCTGGAGCCCTGCCCTGCTGCTACTACGTGGCGCGCAAGCCCAAGGTGGAGCAG 213
QY 301 ctctcaacatggtggtgaagtcttgaatgtagctga 339
Db 212 CTGTCCAACATGATCGTGGCTCCTGCAAGTGCAGCTGA 174

RESULT 14
LOCUS AI131171/c 727 bp mRNA EST 27-OCT-1998
DEFINITION q15c11.x1 Soares fetal heart_NBHH19W Homo sapiens cDNA clone
IMAGE:1709684 3' similar to gb:X02812.cds1 TRANSFORMING GROWTH
FACTOR BETA 1 PRECURSOR (HUMAN); contains element TARI TARI
repetitive element ;, mRNA sequence.
ACCESSION AI131171
VERSION AI131171.1 GI:3601187
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
TITLE NCI-CCGAP http://www.ncbi.nlm.nih.gov/ncicgap.
JOURNAL National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
COMMENT Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 782 Std Error: 0.00
Seq primer: -40ml3 fwd. Et from Amersham
High quality sequence stop: 390.
FEATURES
Location/Qualifiers
1..727
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1709684"
/clone_lib="Soares_fetal_heart_NBHH19W"
/sex="unknown"
/dev_stage="19 weeks"
/lab_host="DHI0B (ampicillin resistant)"
/Note="Organ: heart; Vector: pT73D (Pharmacia) with a
modified polylinker; Site.1: Not I; Site.2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5',
TGTTACCATCTCAAGTGGAGCGCGCATCTTTTTTT 3'], RI
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT73 vector
(Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by
M.Fatima Bonaldo. This library was constructed from the
```

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same fetus as the fetal lung library, Soares fetal lung
NHLL19W."
BASE COUNT      126 a      210 c      251 g      140 t
ORIGIN

Query Match      59.9%; Score 203; DB 16; Length 727;
Best Local Similarity 74.9%; Pred. No. 3.2e-47;
Matches 254; Conservative 0; Mismatches 85; Indels 0; Gaps 0;

QY 1 gcttgacacaaattactctcccaacttgagagaaactgtgtgccccctc 60
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 483 GCCTCGACCAACATATTGCTTCAGCTCCACGGAGAAAGTCTGCTGGCGACATG 424
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 61 tacattgacttcgcagcaggaactgggtggaagtgcattgaacccaagggctactat 120
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 423 TACATTGACTTCGCAAGGACCTCGCTGGAAGTGGATCCACGAGCCCAAGGGCTACCAT 364
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 121 gcaaatctgtcagggcccttgcccatcactccgcagtgacacacacccacagcacy 180
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 363 GCCAAGCTTTGCTCGGGCCCTGCCCTACATTTGGAGCCTGGACACGCGATGACGCAAG 304
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 181 gtctggagactgtacacactctgaacctgaagcatctgcctgcctgtggtgccc 240
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 303 GTCCTGGCCCTGTACACACAGCATAACCCGGCGCCTCGCGCGCGCTGCTGCGTGCCG 244
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 241 caggacctggagccctcgacctctgtactatgttgaggagaccccaagtgagcag 300
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 243 CAGGCGCTGGAGCGCTGCGCCATCGTACTAGTGTGGCGCGCAGCCCAAGGTGGAGCAG 184
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 301 ctctcaacatggtggtgaagtctgttaaatgtagctga 339
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 183 CTGTCCACATGATGCTGCGCTCCTCGAAGTGCAGCTGA 145

RESULT 15
AI089904/c
LOCUS
DEFINITION
  gal6a08.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:1686902 3'
  similar to gb:X02812.cdsl TRANSFORMING GROWTH FACTOR BETA 1
  PRECURSOR (HUMAN); contains element MER22 repetitive element ;, mRNA
  sequence.
ACCESSION
  AI089904
VERSION
  AI089904.1 GI:3428963
KEYWORDS
  EST.
SOURCE
  human.
ORGANISM
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1 (bases 1 to 480)
  NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  National Cancer Institute / National Institute of Neurological
  Disorders and Stroke, Brain Tumor Genome Anatomy Project
  (CGAP/BTGP), Tumor Gene Index
  Unpublished (1998)
  Contact: Robert Strausberg, Ph.D.
  Email: cgabbs-r@mail.nih.gov
  Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
  Ph.D.
  cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
  Bonaldo, Ph.D.
  CDNA Library Arrayed by: Greg Lennon, Ph.D.
  DNA Sequencing by: Washington University Genome Sequencing Center
  Clone Distribution: NCI-CGAP clone distribution information can be
  found through the I.M.A.G.E. Consortium/LLNL at:
  www-bio.llnl.gov/dbrr/image/image.html
  Insert Length: 895 Std Error: 0.00
  Seq primer: -40ml3 fwd. Et from Amersham
  High quality sequence stop: 414.
  Location/Qualifiers
  1. .480
  /organism="Homo sapiens"
  /db_xref="taxon:9606"

FEATURES
  source
```

```
/clone="IMAGE:1686902"
/clone_lib="NCI_CGAP_Brn23"
/tissue_type="glicoblastoma (pooled)"
/lab_host="DH10B"
/note="Organ: brain; Vector: pT73D-Pac (Pharmacia) with a
modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5',
TGTACCAATCTGAAGTGGAGCGCGCATATCTTTTTTTTTTTTTTTTTTTT
T 3']; double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pT73 vector.
Library is normalized, and was constructed by Bento
Soares and M.Fatima Bonaldo."
BASE COUNT      74 a      140 c      179 g      87 t
ORIGIN

Query Match      59.5%; Score 201.8; DB 16; Length 480;
Best Local Similarity 75.4%; Pred. No. 6.5e-47;
Matches 251; Conservative 0; Mismatches 82; Indels 0; Gaps 0;

QY 7 gacacaaattactctccgaacttgagagaaactgtgtgccccctctacatt 66
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 471 GACACCAACTATTGCTTCAGCTCCACGGAGAAGAACTGCTGCTGGCGAGCTGTACATT 412
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 67 gacttcgcagcaggaactgtggtggaagtgggtccatgaacctaaaggctactatgccaac 126
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 411 GACTTCCGCAAGGACCTCGGCTGGAGTGGATCCACGAGCCCAAGGCTACCATGCCAAC 352
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 127 ttctgctcagggcccttgcctacacctccgcagtgacacacacacagcagcgtgctg 186
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 351 TTCTGCCCTCGGGCCCTGCGCCCTACATTTGGAGCCTGGACACAGTACAGCAAGGTCCTG 292
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 187 ggactgtacaacactctgaacctgaagcatctgctgcgtgctgtgctgccccaggac 246
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 291 GCCCTGTACAAACAGCATAAACCCGGCGCCTCGGGCGCGCTGCTGCTGCGCGAGCGG 232
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 247 ctgagagcccttgaccactctgactatgttgaggagaccccccaagtggagcagctctcc 306
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 231 CTGGAGCGCTGCGCCATCGTACTAGTGTGGCGCGCAAGCCCAAGGTGGAGCAGCTGTCC 172
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 307 aacatggtggtgaagtctttaaattagctga 339
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 171 AACATGATCGTGGCGCTCCTGCAAGTGCAGCTGA 139

RESULT 16
AI073988/c
LOCUS
DEFINITION
  xb06a06.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2575474 3'
  similar to gb:X02812.cdsl TRANSFORMING GROWTH FACTOR BETA 1
  PRECURSOR (HUMAN); contains element TAR1 repetitive element ;, mRNA
  sequence.
ACCESSION
  AI073988
VERSION
  AI073988.1 GI:6028986
KEYWORDS
  EST.
SOURCE
  human.
ORGANISM
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1 (bases 1 to 572)
  NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
  Tumor Gene Index
  Unpublished (1997)
  Contact: Robert Strausberg, Ph.D.
  Email: cgabbs-r@mail.nih.gov
  Tissue Procurement: Chris Moskaluk, M.D., Ph.D., Michael R.
  Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Life
  Technologies, Inc. cDNA Library Arrayed by: Christa Prange, The
  I.M.A.G.E. Consortium DNA Sequencing by: Washington University
  Genome Sequencing Center
  Clone distribution: NCI-CGAP clone distribution information can be
```

found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -40UP from Gibco
High quality sequence stop: 396.

FEATURES

source
Location/Qualifiers
1..572
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2575474"
/clone_lib="NCI_CGAP_GUL"
/tissue_type="2 pooled high-grade transitional cell tumors"
/lab_host="DH10B"
/note="Organ: genitourinary tract; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dt. Library constructed by Life Technologies."
93 a 159 c 206 g 114 t

BASE COUNT

ORIGIN
93 a 159 c 206 g 114 t

Query Match 59.4%; Score 201.4; DB 111; Length 572;
Best Local Similarity 74.6%; Pred. No. 8.8e-47;
Matches 253; Conservative 0; Mismatches 86; Indels 0; Gaps 0;

Qy 1 gctttggacacaaattactgtctccgaacttggaggagaactgtgtgtgccccctc 60
Db 488 GCCCTGGACACCACTATTGCTTCAGCTCCACGGAGAAACTGCTGCTGGCGAGCTG 429
Qy 61 tacattgacttcgcagagatcgtggtggaagtgggtccatgaacctaaaggctactat 120
Db 428 TACATTGACTTCGCGAAGGACCTCGCGTGGAAAGTGGATCCAGAGCCCAAGGGCTACCAT 369
Qy 121 gccaaacttctgcagggcccttgccatccctccgcagtcgagacacacacacagcacg 180
Db 368 GCCAACTTTTGGCTCGGGCCCTGCCCTTACATTTGGAGCGTCGACACGCGAGTACAGCAAG 309
Qy 181 gtgtggagactgtacaaactctgaacctgaagcatctgctgccttgcgtgctgccc 240
Db 308 GTCTCGGCCCTGTACAAACGAGATAACCGGGCGCTCGCGCGCGCTGCTGCGTGGCGG 249
Qy 241 caggacctggagccctgaacctctgtactctgttggagagaccccaaaagtggagcag 300
Db 248 CAGGCGCTGGAGCCGCTGCCCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 189
Qy 301 ctctccaaatggtggtgaagtcttgaatgtactgtgaaatgtactga 339
Db 188 CTGTCCAACATGATGCTGGCTCCTGCAAGTGCACTGA 150

RESULT 17

BF543086/c
LOCUS
DEFINITION
UI-R-AFL1-aaq-f-07-0-UI-r1 UI-R-AFL1 Rattus norvegicus cDNA clone
UI-R-AFL1-aaq-f-07-0-UI 5', mRNA sequence.
BF543086
VERSION
BF543086.1 GI:11634193
KEYWORDS
EST.
SOURCE
Norway rat.
ORGANISM
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE

1 (bases 1 to 471)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
AUTHORS
Normalization and subtraction: two approaches to facilitate gene
TITLE
discovery
JOURNAL
Genome Res. 6 (9), 791-806 (1996)
MEDLINE
97044477
COMMENT
Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA

Tel: 319 335 8250
Fax: 319 335 9565
Email: msoares@blue.weeg.uiowa.edu
cDNA Library Preparation: M.B. Soares Lab Clone Distribution:
clones will be available through Research Genetics (www.resgen.com)
This clone is also available through the I.M.A.G.E. Consortium at
LLNL (info@image.llnl.gov). IMAGE ID= 1790668
Seq primer: M13 Forward.

FEATURES

source
Location/Qualifiers
1..471
/organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-AFL1-aaq-f-07-0-UI"
/clone_lib="UI-R-AFL1"
/dev_stage="adult"
/lab_host="DH10B (Life Technologies)"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-AFL1
library is a normalized library constructed from 15 dpc
rat atrioventricular (AV) canal. The tag is a string of 5
nucleotides present between the Not I site and the
oligo-dT track. The library was constructed as described
by Bonaldo, Lennon and Soares, Genome Research 6: 791-806
, 1996. Tissue provided by Jim Lin, Department of Biology,
University of Iowa."
118 a 105 c 110 g 137 t 1 others

BASE COUNT

ORIGIN
118 a 105 c 110 g 137 t 1 others

Query Match 59.1%; Score 200.4; DB 150; Length 471;
Best Local Similarity 74.3%; Pred. No. 1.6e-46;
Matches 252; Conservative 0; Mismatches 87; Indels 0; Gaps 0;

Qy 1 gctttggacacaaattactgtctccgaacttggaggagaactgtgtgccccctc 60
Db 464 GCTTTGGATGCCCTTATTGCTTTAGGAATGTGCAGGATAATTGCTGCTTCCGCTCTT 405
Qy 61 tacattgacttcgcagagatcgtgctggaagtgggtccatgaacctaaaggctactat 120
Db 404 TACATTGATTTTAAAGAGGATCTTGGATGGAAATGGATCCATGAACCAAGGATACAAT 345
Qy 121 gccaaacttctgcagggcccttgccatccctccagtcgagacacacacacacagcacg 180
Db 344 GCTAACTTCTGCTGGGCGATGCCCTTATCTCTGGAGTTTACACACACACACACAAA 285
Qy 181 gtgtgggagactgtacaaactctgaacctgaagcatctgctgcctgtgctgctgccc 240
Db 284 GTCTCAGCCTGTACAAACACACATAAACCCCGAAGCTTCTGCTTCCCTTGTGTGCTCC 225
Qy 241 caggacctggagccctgacctctgtactatgttggaggagaccccccaagtggagcag 300
Db 224 CAGGATCTGGAGACCCTGACCATCTTACTACATTGGCAATACGCCCAAGATCGAACA 165
Qy 301 ctctccaaatggtggtgaagtcttgaatgtactgtgaaatgtactga 339
Db 164 CTTTCCAACATGATGCTCAAGTCTTGTGAATGCAAGCTAA 126

RESULT 18

BE645704/c
LOCUS
DEFINITION
7e74h10.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:3288259 3'
similar to gb:X02812.cds1 TRANSFORMING GROWTH FACTOR BETA 1
PRECUSOR (HUMAN); contains element TAR1 repetitive element ;, mRNA
sequence.
BE645704
VERSION
BE645704.1 GI:9970015
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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REFERENCE
AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
          Tumor Gene Index
JOURNAL   Unpublished (1997)
COMMENT   Contact: Robert Strausberg, Ph.D.
          Email: cgapbs-r@mail.nih.gov
          Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.
          Emmert-Buck, M.D., Ph.D.
          cDNA Library Preparation: M. Bento Soares, Ph.D.
          cDNA Library Arrayed by: Greg Lennon, Ph.D.
          DNA Sequencing by: Washington University Genome Sequencing Center
          Clone distribution: NCI-CGAP clone distribution information can be
          found through the I.M.A.G.E. Consortium/LLNL, send email to:
          info@image.llnl.gov
          Seq primer: -40UP from Gibco.
          Location/Qualifiers
            1..474
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /clone="IMAGE:3288259"
            /clone_lib="NCI_CGAP_Pr28"
            /sex="male"
            /dev_stage="adult"
            /lab_host="DH10B"
            /note="Organ: prostate; Vector: pT7T3D-Pac (Pharmacia)
            with a modified polylinker; Plasmid DNA from the
            normalized library NCI_CGAP_Pr22 was prepared, and ss
            circles were made in vitro. Following HAP purification,
            this DNA was used as tracer in a subtractive hybridization
            reaction. The driver was PCR-amplified cDNAs from a pool
            of 5,000 clones made from the same library (clonesIDs
            985608-986759, 1101192-1101959, and 1217928-1220615)."
            Subtraction by Bento Soares and M. Fatima Bonaldo.
          BASE COUNT      75 a 138 c 176 g 85 t
          ORIGIN

          Query Match      58.5%; Score 198.2; DB 138; Length 474;
          Best Local Similarity 74.9%; Pred. No. 6.9e-46;
          Mismatches 83; Indels 0; Gaps 0;

          QY 9 caccattactgttcgcgaacttgaggagagaaactgtgtgtgccccctctacattga 68
          ||||| ||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
          Db 474 CACCAACTATTGCTTCAGCTCCACGGAGAGAACTGCTCGTGGCGCAGGTGACATTTGA 415

          QY 69 cttccgacagatctg9ggtcgaagtggccatgaacctaaagggtctactatgccaactt 128
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
          Db 414 CTTCCGCAAGGACCTCGGCTGGAAGTGGATCCACGAGCCCAAGGGCTACCATGCCCACTT 355

          QY 129 ctgctcaggcccttgccatactccgcaagtgcagacacacacacacacagcggtgctggg 188
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
          Db 354 TTGCTTCGGGGCCTGCCCTTACATTTGGAGCCTGGACACGCGAGTACAGAAAGGTCTCTGGC 295

          QY 189 actgtacaacactctgaacccctgaagcatctgcctgcctctgtcgtgctgccccagacact 248
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
          Db 294 CTGTGTACACACAGCATACACCGGGCGCTCGGGGGCGCGTCTGCTGCCCGCAGCGCT 235

          QY 249 ggaagccctgaccatctgtactatgtgtggaggacccccaaagtggagcagctctccaa 308
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
          Db 234 GGAGCGCGTCCCATCTGTACTACTGTGGCGCGCAAGCCCAAGGTGGAGCAGCTGTCCAA 175

          QY 309 catgtgtggaagtcttttaaatgtagctga 339
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
          Db 174 CATGATCGTGGCTCTCTGCAAGTGCAGCTGA 144

          RESULT 19
          LOCUS BE464068 568 bp mRNA EST 27-JUL-2000
          DEFINITION hx84h02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3194547 3'
          similar to gb:X02812.cds1 TRANSFORMING GROWTH FACTOR BETA 1
          PRECURSOR (HUMAN); contains element TAR1 TAR1 repetitive element ;,

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mRNA sequence.
BE464068
VERSION BE464068.1 GI:9509843
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
          1 (bases 1 to 568)
REFERENCE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
TITLE Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
          Email: cgapbs-r@mail.nih.gov
          Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
          Emmert-Buck, M.D., Ph.D.
          cDNA Library Preparation: M. Bento Soares, Ph.D.
          cDNA Library Arrayed by: Greg Lennon, Ph.D.
          DNA Sequencing by: Washington University Genome Sequencing Center
          Clone distribution: NCI-CGAP clone distribution information can be
          found through the I.M.A.G.E. Consortium/LLNL, send email to:
          info@image.llnl.gov
          Seq primer: -40UP from Gibco
          High quality sequence stop: 395.
          Location/Qualifiers
            1..568
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /clone="IMAGE:3194547"
            /clone_lib="NCI_CGAP_Kid11"
            /lab_host="DH10B"
            /note="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with
            a modified polylinker; Site 1: Not I; Site 2: Eco RI;
            Plasmid DNA from the normalized library NCI_CGAP_Kid3 was
            prepared, and ss circles were made in vitro. Following HAP
            purification, this DNA was used as tracer in a subtractive
            hybridization reaction. The driver was PCR-amplified cDNAs
            from a pool of 5,000 clones made from the same library
            (clonesIDs 1322376-1323911, 1456007-1456775, and
            1500552-1502855). Subtraction by Bento Soares and M.
            Fatima Bonaldo.
          BASE COUNT      96 a 159 c 203 g 110 t
          ORIGIN

          Query Match      58.5%; Score 198.2; DB 136; Length 568;
          Best Local Similarity 74.0%; Pred. No. 7.1e-46;
          Mismatches 88; Indels 0; Gaps 0;

          QY 1 gctttggaaccaattactgcttcgcgaacttgaggagagaactgctgtgtgccccctc 60
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
          Db 479 GCCTTGACACCACTATTGCTTCAGCTCCACGGAGAGAAATTGCTGCTGGGAAGCTG 420

          QY 61 tacattgaactccgacaggaatctgtggaagtgggtcccatgaacctaaaggctactat 120
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
          Db 419 TACATTGACTTCCGACAGGACCTCGGTTGGAAGTGGATCCACGAGCCCAAGGGCTACCAT 360

          QY 121 gcaaaccttctgctcaggcccttgccatactccgcagctgcagacacacacacagcagc 180
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
          Db 359 GCCAACTTTTGCCTCGGGCCTGCCCTTACATTTTGGAGCCTGGACACGACGATACAGCAAG 300

          QY 181 gtgctgggaactgtacaacactctgaacctgaacctgaacatctgctcgtcgtgtgctgcc 240
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
          Db 299 GTCTTGCCCTGTACAACACAGCATAAACCGGGCGCTCGGGGGCGCGCTGTGCTGCTGCCG 240

          QY 241 caggacctggagccctgaccatctactatattggaggagcccccaagtgagcag 300
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
          Db 239 CAGCGCTGGAGCGCTGCCCCATCTGTACTACTGTGGGCCCGCCCAAGCCCAAGTGGAGCAG 180

          QY 301 ctctcccaactggtgggtgaagctcttgaatgttagctga 339
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
          Db 179 CTGTCCAACATGATCGTGGCTTCTCTGCAAGTGCAGCTGA 141

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RESULT 20
A1148173/c
LOCUS      785 bp      mRNA      EST      26-OCT-1998
DEFINITION q56d01.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:1704097 3'
            similar to gb:X02812.cds1 TRANSFORMING GROWTH FACTOR BETA 1
            PRECURSOR (HUMAN); contains PTR5.b3 TAR1 repetitive element ;, mRNA
            sequence.
ACCESSION  A1148173
VERSION    A1148173.1
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE  1 (bases 1 to 785)
            NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
            National Cancer Institute / National Institute of Neurological
            Disorders and Stroke, Brain Tumor Genome Anatomy Project
            (CGAP/BTGP), Tumor Gene Index
            Unpublished (1998)
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
            Ph.D.
            cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
            Bonaldo, Ph.D.
            cDNA Library Arrayed by: Greg Lennon, Ph.D.
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www.bio.lni.gov/bbrp/image/image.html
            Insert length: 953 Std Error: 0.00
            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 356.
FEATURES   Location/Qualifiers
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            /db_xref="taxon:9606"
            /clone="IMAGE:1704097"
            /clone_lib="NCI_CGAP_Brn23"
            /tissue_type="glioblastoma (pooled)"
            /lab_host="DH10B"
            /note="Organ: brain; Vector: pT73D-Pac (Pharmacia) with a
            modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
            strand cDNA was primed with a Not I - oligo(dT) primer [5'
            TGTACCAATCTGAAGTGGAGCGCGGCATATCTTTTCTTTTCTTTTCTTTTCTTTT
            T 3']; double-stranded cDNA was ligated to Eco RI
            adaptors (Pharmacia), digested with Not I and cloned into
            the Not I and Eco RI sites of the modified pT7T3 vector.
            Library is normalized, and was constructed by Bento
            Soares and M.Fatima Bonaldo."
BASE COUNT 137 a 217 c 267 g 164 t
ORIGIN

Query Match 58.5%; Score 198.2; DB 16; Length 785;
Best Local Similarity 74.0%; Pred. No. 7.6e-46;
Matches 251; Conservative 0; Mismatches 88; Indels 0; Gaps 0;

QY 1 gcttggacaccattactgttcgcgaacttgagagagaactgtgtgtgcgccccctc 60
Db 497 GCCCTGGACACCAATATTGCTTCAGCTCCACGGAGAAGAACTGCTGGCTGGCGAGCTG 438

QY 61 tacattactccgacaggaactgtggaagtgggtccatgaactaaaggtactat 120
Db 437 TACATTGACTTCCGACAGGACTCGGTGGAACTGGATCCACGAGCCCAAGGGGTACCAT 378

QY 121 gccaaactctgctcaggcccttgcatactccagtcgagacacacacacagcagc 180
Db 377 GCCAACTTTTGCTCGGGCCCTGCCCCCTACATTTGGAGCCCTGGACACGCGATACAGCAAG 318

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QY 181 gtgctggagactgtacaacacttgaacacctgaagcatctgcctgcctgtgctggtgccc 240
Db 317 GTCCTGGCCCTGTACAAACAGCATAACCCGGCGCCCTCGCGCGCGTGTGCTGCTGCC 258

QY 241 caggacctggagcccttgaccatcctgtactatgttgggagagaccccccaagttagcag 300
Db 257 CAGGCCCTGGAGGACCTGCGCCATCGTGTACTAGTGGGCGCAAGCCCAAGGTGGAGCAG 198

QY 301 ctctcaacatggtggtgaagctctttaaagttagctga 339
Db 197 CTGTCCAACATGATCGTGGCGCTCTCGAAGTGCACCTTA 159

RESULT 21
A512491/c
LOCUS      646 bp      mRNA      EST      03-MAR-2000
DEFINITION xx75d02.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2849475 3'
            similar to gb:X02812.cds1 TRANSFORMING GROWTH FACTOR BETA 1
            PRECURSOR (HUMAN); contains element TAR1 repetitive element ;, mRNA
            sequence.
ACCESSION  A512491
VERSION    A512491.1
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE  1 (bases 1 to 646)
            NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
            National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
            Unpublished (1997)
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Life Technologies catalog #: 11547-015
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            image.llnl.gov/image/html/iresources.shtml
            Seq primer: -40UP from Gibco
            High quality sequence stop: 396.
FEATURES   Location/Qualifiers
            source
            1..646
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /clone="IMAGE:2849475"
            /clone_lib="NCI_CGAP_Lym12"
            /tissue_type="lymphoma, follicular mixed small and large
            cell"
            /lab_host="DH10B"
            /note="Organ: lymph node; Vector: pCMV-SPORT6; Site_1:
            SalI; Site_2: NotI; Cloned unidirectionally. Primer:
            Oligo df. Average insert size 1.25 kb. Life Technologies
            catalog #: 11547-015"
BASE COUNT 115 a 178 c 208 g 144 t 1 others
ORIGIN

Query Match 58.3%; Score 197.8; DB 117; Length 646;
Best Local Similarity 74.0%; Pred. No. 9.5e-46;
Matches 250; Conservative 0; Mismatches 88; Indels 0; Gaps 0;

QY 2 ctttggacacaattactgtcttcgcaacttgagagagaactgtgtgccccctct 61
Db 495 CCTTGGACACAATATTGCTTCAGCTCCACGGAGAAGAACTGCTGGCTGGCGAGCTGT 436

QY 62 acattgactccgacaggaactgggtggaagtgggtccatgaacctaaagggtactatg 121
Db 435 ACATTGACTTCGCAAGGACCTCGCTGGAGTGGATCCACGAGCCCAAGGGGTACCATG 376

QY 122 ccaactctgtcagggcccttgcatactccgagtcgagacacacacacacagcagc 181
Db 375 CCAACTTTTGCTCGGGCCCTGCCCTACATTTGGAGCCCTGGACACGCGATACAGCAAG 316

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/lab_host="DH10B"
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and Eco RI sites of the modified pT7T3 vector. Library

visit <http://lgsun.grc.nia.nih.gov/cDNA/15k.html> for details.
 Plate: H3055 row: G column: 07
 Seq primer: -21M13 Forward
 High quality sequence stop: 608
 POLYA=Yes.

FEATURES

source location/Qualifiers
 1..608
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="H3055G07"
 /clone_lib="NIA Mouse 15k cDNA Clone Set"
 /sex="Clones arrayed from a variety of cDNA libraries"
 /dev_stage="Clones arrayed from a variety of cDNA libraries"
 /lab_host="DH10B"
 /note="Vector: pSPORT1; Site_1: SalI; Site_2: NotI; This clone is among a rearayed set of 15,247 clones from 11 embryo cDNA libraries (including preimplantation stage embryos from unfertilized egg to blastocyst, embryonic part of E7.5 embryos, extraembryonic part of E7.5 embryos, and E12.5 female mesonephros/gonad) and one newborn ovary cDNA library. Average insert size 1.5 kb. All source libraries are cloned unidirectionally with Oligo(dT)-Not primers. References include: (1) Genome-wide expression profiling of mid-gestation placenta and embryo using a 15,000 mouse developmental cDNA microarray, 2000, Proc. Natl. Acad. Sci. U S A, 97: 9127-9132; (2) Large-scale cDNA analysis reveals phased gene expression patterns during preimplantation mouse development, 2000, Development, 127: 1737-1749; (3) Genome-wide mapping of unselected transcripts from extraembryonic tissue of 7.5-day mouse embryos reveals enrichment in the t-complex and under-representation on the X chromosome, 1998, Hum Mol Genet 7: 1967-1978."

BASE COUNT 151 a 137 c 145 g 174 t 1 others

Query Match 57.1%; Score 193.4; DB 173; Length 608;
 Best Local Similarity 73.2%; Pred. No. 1.7e-44;
 Matches 248; Conservative 0; Mismatches 91; Indels 0; Gaps 0;

QY 1 gctttgacacaaattactgttcgcaactggaggagaactgctgtggtgccccctc 60
 Db 452 GCTTTGGATGCTGCTACTGCTTTAGAAATGTCAGGATAATTGCTTGCCTTCTT 393

QY 61 tacattgacttcgacaggtatcgtggtggaagtgggtccatgaacctaaaggctactat 120

Db 392 TACATTGATTTTAAGAGGGATCTTGGATGGAAATGGATCCATGAACCCAAAGGGTACAAAT 333

QY 121 gccaaattctcagggcccttgccataacctccgagtcgagacacacacccacagcag 180

Db 332 GCTAACTTCTGTGTGGGGCATGCCATATCTATGGAGTTTACAGACATCAACACACAAA 273

QY 181 gtgctggagactgtacacacactctgaacctgaagcatctgcctgccttgcgtgctgcc 240

Db 272 GTCTCAGCTGTACACACACATAAATCCCGAAGCTTCCGCTTCCCTTGTGTGTGTC 213

QY 241 cagacactggagccctgacacactctgtactatctgttgggagagacccccaaagtggagc 300

Db 212 CAGGATCTGGAAACCACTGACCATTTCTATTACATTTGGAATACGCCCAAGATCGAACAG 153

QY 301 ctctcccaatggtggtggaagtctgttaaatgtagctga 339

Db 152 CTTTCCCAATATGATGTCAAGTCTGTAAATGCAGCTAA 114

RESULT

28
 AI323791/c 681 bp mRNA EST 23-DEC-1998
 LOCUS mm47e08.x1 Stratagene mouse melanoma (#937312) Mus musculus cDNA
 DEFINITION clone IMAGE:524678 3', similar to gb:x57413 Mouse mRNA for

ACCESSION

AI323791 GI:4058220

VERSION

EST.

KEYWORDS

house mouse.

SOURCE

Mus musculus

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 681)

Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,

Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,

Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,

Theising, B., Wyllie, I., Lennon, G., Soares, B., Wilson, R. and

Waterston, R.

The WashU-HMI Mouse EST Project

Unpublished (1996)

Contact: Marra M/Mouse EST Project

WashU-HMI Mouse EST Project

Washington University School of MedicineP

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: mouseest@watson.wustl.edu

This clone is available royalty-free through LML; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

MGI:318526

This clone was previously sequenced on the 5' end only, this new

data is from the 3' end

High quality sequence stop: 366.

Location/Qualifiers

1..681

/organism="Mus musculus"

/db_xref="taxon:10090"

/clone="IMAGE:524678"

/clone_lib="Stratagene mouse melanoma (#937312)"

/dev_stage="M2 cells"

/dev_host="SOLR (kanamycin resistant)"

/note="Organ: skin; Vector: pBluescript SK-; Site_1: EcoRI

; Site_2: XhoI; Cloned unidirectionally, primer: Oligo

dt. From M2 cells, a highly metastatic derivative of the

K-1735 (mouse) melanoma. Average insert size: 1.0 kb;

Uni-ZAP XR Vector; -5' adaptor sequence: 5' GAATTCGGCAGGAG

3' -3' adaptor sequence: 5' CTCAGTGTGTGTGTGTGTGTGTGT 3'

BASE COUNT 164 a 151 c 163 g 200 t

ORIGIN

Query Match 57.1%; Score 193.4; DB 18; Length 681;

Best Local Similarity 73.2%; Pred. No. 1.7e-44;

Matches 248; Conservative 0; Mismatches 91; Indels 0; Gaps 0;

QY 1 gctttgacacaaattactgttcgcaactggaggagaactgctgtggtgccccctc 60

Db 461 GCTTTGGATGCTGCTGCTTTAGAAATGTCAGGATAATTGCTTGCCTTCTT 402

QY 61 tacattgacttcgacaggtatcgtggtggaagtgggtccatgaacctaaaggctactat 120

Db 401 TACATTGATTTTAAGAGGGATCTTGGATGGAAATGGATCCATGAACCCAAAGGTACAAT 342

QY 121 gccaaattctcagggcccttgccataacctccgagtcgagacacacccacagcag 180

Db 341 GCTAACTTCTGTGTGGGGCATGCCATATCTATGGAGTTTACAGACATCAACACACAAA 282

QY 181 gtgctggagactgtacacacactctgaacctgaagcatctgcctgccttgcgtgctgcc 240

Db 281 GTCCCTCAGCCTGTACACACACATAAATCCCGAAGCTTCCGCTTCCCTTGTGTGTGTC 222

QY 241 caggaacctggagccctgacacactctgtactatctgttgggagagacccccaaagtggagcag 300

Db 221 CAGGATCTGGAAACCACTGACCATTTCTATTACATTTGGAATACGCCCAAGATCGAACAG 162

QY 301 ctctcccaatggtggtggaagtctgttaaatgtagctga 339

LOCUS	BF287476	529 bp	mRNA	EST	28-NOV-2000
DEFINITION	EST452067 Rat Gene Index, normalized rat, Rattus norvegicus cDNA Rattus norvegicus cDNA clone RGIG52 3' sequence, mRNA sequence.				
ACCESSION	BF287476				
VERSION	BF287476.1	GI:11218546			
KEYWORDS	EST.				
SOURCE	Norway rat. Rattus norvegicus				
ORGANISM	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.				
REFERENCE	1 (bases 1 to 529)				
AUTHORS	Malek,R.L., Cho,J., Lee,Y., Karamycheva,S., Parvizi,B., Pertea,G., Sultana,R., Tsai,J., White,J., Quackenbush,J. and Lee,N.H.				
TITLE	Generation of ESTs from Normalized Rat Embryo, Bento Soares				
JOURNAL	Unpublished (2000)				
COMMENT	Other_ESTs: EST351042 Contact: Lee, NH The Institute for Genomic Research 9712, Medical Center Drive, Rockville, MD 20850, USA Tel: (301)-838-3529 Fax: (301)-838-0208 Email: nhlee@tigr.org This clone is available through the ATCC, contact the ATCC tel#703-365-2700 for further information.				
FEATURES	Location/Qualifiers				
source	1..529	/organism="Rattus norvegicus"			
		/db_xref="taxon:10116"			
		/clone="RGIG52"			
		/clone_lib="Rat Gene Index, normalized rat, Rattus norvegicus cDNA"			
		/tissue_type="mixed tissue"			
		/lab_host="DH5-alpha"			
		/note="vector: pT37/pac; Site_1: EcoRI; Site_2: NotI; Combination of ROV, RBR, RKI, RLI, RPL, REM, RMU, ' RHE, RPC, RPN"			
BASE COORD	91 a 141 c 190 g 107 t				
ORIGIN					
Query Match	56.6%; Score 191.8; DB 146; Length 529;				
Best Local Similarity	72.9%; Pred. No. 4.6e-44;				
Matches	247; Conservative 0; Mismatches 92; Indels 0; Gaps 0;				
QY	1	gctttggacaccacttgcttcgcgaacttgaggagaaactgtgtgtgcgccctc 60			
Dd	477	GCCCTGGATACCAATTACTGCTTCAGCTCCACAGAGAAGAACTGCTGTGTACGCAGCGTG 418			
QY	61	tacattgactccgcacaggactgtggctggaagtgggtccactgaacctaaagggtactact 120			
Dd	417	TACATTGACTTTAGAAGGACCTGGGTGGGAAGTGGATTCACAGAGCCCAAGGGCTACCAT 358			
QY	121	gccaaactctgctcaggcccttggccatatccctcgcaagtgcagacacaaccaacagcacg 180			
Dd	357	GCCAACCTCTCTCTGGGGCCCTGCCCTACATTTTGGAGCCTGGACACACACAGTACAGCAAG 298			
QY	181	gtgctggagactgtacaacactctgaacctgaagcatctgctcgtcgtgctgctgcccc 240			
Dd	297	GTCCTTGCCCTTTACAACCAACAACCCGGGTGCTTCCGCATCACCGTGTATGGTGGTGGCG 238			
QY	241	caggacctggagcccctgacctcctgactatgttactatgtggagacccccaaagttagacag 300			
Dd	237	CAGCCTTTGGAGACCACATGCCCATCGTTTACCTGGGTGCGAAGCCCAAGGTGGAGCAG 178			
QY	301	ctctccaacatggtggtggaagctctttaaattagctga 339			
Dd	177	TTGTCCAACATGATCGTCGCGCTCTCTGCAAGTGCAGCTGA 139			
RESULT	32				
AI323392/c					
LOCUS	AI323392	573 bp	mRNA	EST	23-DEC-1998

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Db 359 GCCAACTTCTGTGGGACCCCTGCCCTATATTTTGGAGCCTGGACACACAGTACAGCAAG 300
QY 181 gtctgggactgtacaacactctgaaccctgaagcattctgcctgcctgtgctgctgccc 240
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 299 GTCTTGGCCCTTACAAACACAAACCCGGCGCTTCGGCGTCAACCGTGTGCGTGGCG 240
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 241 caggacctggagccctgaccatctgtactatgtttgggaggaccccccaagtgagcag 300
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 239 CAGGCTTTGGAGCCACTGCCCATCGTCTACTACGTGGGTGCGAAGCCCAAGTGGAGCAG 180
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 301 ctctcaacatgtgtggaagctcttgaatgtagctga 339
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 179 TTGTCCAACATGATTTGCGCTCTCTGCAAGTGCAGCTGA 141

RESULT 33
BG518882
LOCUS 602578182F1 NCI_CGAP_Mam5 Mus musculus cDNA clone IMAGE:3481700 5',
DEFINITION mRNA sequence.
ACCESSION BG518882
VERSION BG518882.1 GI:13514180
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 721)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM8510 row: d column: 21
High quality sequence stop: 640.
FEATURES
source
1..721
Location/Qualifiers
/organism="Mus musculus"
/strain="C57/B6"
/db_xref="taxon:10090"
/clone_lib="NCI_CGAP_Mam5"
/tissue_type="tumor, gross tissue"
/dev_stage="7 months"
/lab_host="DH10B"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Robin Humphreys,
NIH"
BASE COUNT 164 a 232 c 187 g 138 t
ORIGIN

Query Match 56.1%; Score 190.2; DB 154; Length 721;
Best Local Similarity 72.6%; Pred. No. 1.4e-43;
Matches 246; Conservative 0; Mismatches 93; Indels 0; Gaps 0;

QY 1 gctttgacaccaatctactctccgaacttgagagagactgtgtgcccctc 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 296 GCCTTGATACCAACATTTGCTTACGCTCCACAGAGAAGAACTCTGTGCGGCACGTG 355
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 61 tacattgacttcgcagacgatctgggtggaagtgggtccatgaacctaaagggctactat 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 356 TACATTGACTTTAGGAGGACCTGGGTGGAGTGGATCCAGGCCCAAGGGGTACCAT 415

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QY 121 gccaaacttctgctcaggcccttgcccataccctcccgagtcgagacacacacacacgacg 180
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 416 GCCAACTTCTGTCTGGGACCCCTGCCCTATATTTTGGAGCCTGGACACACAGTACAGCAAG 475
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 181 gtctgggactgtacaacactctgaaccctgaagcattctgcctgccttgccttgcctgcgcc 240
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 476 GTCTTGGCCCTTACAAACACAAACCCGGCGCTTCGGCGTCAACCGTGTGCGTGGCG 535
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 241 caggacctggagccctgaccatctgtactatgtttgggaggaccccccaagtgagcag 300
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 536 CAGGCTTTGGAGCCACTGCCCATCGTCTACTACGTGGGTGCGAAGCCCAAGTGGAGCAG 595
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 301 ctctcaacatgtgtggaagctcttgaatgtagctga 339
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 596 TTGTCCAACATGATTTGCGCTCTCTGCAAGTGCAGCTGA 634

RESULT 34
AI323037
LOCUS 477 bp mRNA EST 23-DEC-1998
DEFINITION mJ35f01.Y1 Soares mouse embryo NDME13.5 14.5 Mus musculus cDNA
clone IMAGE:478105 5' similar to gb:X02812.cds1 TRANSFORMING GROWTH
FACTOR BETA 1 PRECURSOR (HUMAN); gb:M32745 mouse transforming
growth factor beta-3 mRNA, complete (MOUSE);, mRNA sequence.
ACCESSION AI323037
VERSION AI323037.1 GI:4057466
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 477)
AUTHORS Marra M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisler, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
Waterston, R.
TITLE The WashU-HHMI Mouse EST Project
JOURNAL Unpublished (1996)
COMMENT Contact: Marra M/Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:288849
This read is a RESEQUENCE of a previously sequenced mouse clone
correct orientation)
Seq primer: -40RP from Gibco
High quality sequence stop: 415.
FEATURES
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1..477
Location/Qualifiers
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone_lib="IMAGE:478105"
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/sex="unknown"
/tissue_type="embryo"
/dev_stage="13.5-14.5dpc total fetus"
/lab_host="DH10B"
/note="Vector: p7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5',
TGTTACCAATCTGAAGTGGGCGCGCGCGGAAATTTTTTTTTTTTTTTTTTTT
T 3'], on equal amounts of mRNA from 2 13.5dpc and 2
14.5dpc embryos [total RNA provided by Minoru Ko, Wayne
State Univ., from 2]; double-stranded cDNA was ligated to
Eco RI adaptors (Pharmacia), digested with Not I and

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VERSION	AT1434956.1										GI:4299804									
KEYWORDS	EST.																			
SOURCE	human.																			
ORGANISM	Homo sapiens																			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;																			
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.																			
TITLE	1 (bases 1 to 567)																			
JOURNAL	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap .																			
COMMENT	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index																			
	Unpublished (1997)																			
	Contact: Robert Strausberg, Ph.D.																			
	Email: cgapsb-r@mail.nih.gov																			
	Life Technologies catalog #: 11547-015																			
	DNA Sequencing by: Washington University Genome Sequencing Center																			
	Clone distribution: NCI-CGAP clone distribution information can be																			
	found through the I.M.A.G.E.E. Consortium/LLNL at:																			
	www-bio.llnl.gov/bbrp/image/image.html																			
	Insert length: 873 Std Error: 0.00																			
	Seq primer: -400p from Gibco																			
	High quality sequence stop: 380.																			
FEATURES	Location/Qualifiers																			
source	1..567																			
	/organism="Homo sapiens"																			
	/db_xref="taxon:9606"																			
	/clone="IMAGE:2133535"																			
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	/tissue_type="lymphoma, follicular mixed small and large																			
	cell"																			
	/lab_host="DH10B"																			
	/note="Organ: lymph node; Vector: pCMV-SPORT6; Site_1:																			
	Sal1; Site_2: NotI; Cloned unidirectionally. Primer:																			
	Oligo dt. Average insert size 1.25 kb. Life Technologies																			
	catalog #: 11547-015"																			
BASE COUNT	87 a 163 c 209 g 107 t 1 others																			
ORIGIN																				
Query Match	54.0%; Score 183; DB 20; Length 567;																			
Best Local Similarity	72.3%; Pred. No. 1.5e-41;																			
Matches 237; Conservative	0; Mismatches 91; Indels 0; Gaps 0;																			
Qy 12	caattactgttcgcgaacttggaggagaactgtgtgtgcgccctctacattgactt 71																			
Db 471	CAACTATTGCTTACGTCACGAGAGAGACTGCTGCCGTGGCGGCTGTACATTGACTT 412																			
Qy 72	ccgacagagatcggctggagtggtgcctatgaacctaaagggtactatgccaaactctg 131																			
Db 411	CGCAAGGACCTCGGCTGNAAGTGGATCCAGGCCCAAGGGCTACCATGCCAACTCTG 352																			
Qy 132	ctcaggcccttgccatctccgcagtcgagacacacccacagacagtgctggagact 191																			
Db 351	CCTCGGGCCCTTGCCTCCATTTGAGCCCTGGACACGACGATCAGCAAGGTCTCTGGCCCT 292																			
Qy 192	gtacaacactctgaacctgaagcatctgcctgccttgcgtgcgtgccagagacctgga 251																			
Db 291	GTACAACGACGATAACCGGGCGGCTCGGGCGGCGCGTGTGCTGCCGAGCGGCTGGA 232																			
Qy 252	gccctgaccatcctgtactatgttggaggagaccccccaagtggagcagctctccaacat 311																			
Db 231	GCCCTGCCATCTGTGTACTGTACGTGGGCGCGCAAGCCCAAGGTGGAGCAGCTGTCCAACAT 172																			
Qy 312	ggtggtgaagtcttgaatgtagctga 339																			
Db 171	GATCGTGGCTCTCTGCAAGTGCAGCTGA 144																			
RESULT 39																				
BF042894/c																				
LOCUS	BF042894 515 bp mRNA										EST 10-OCT-2000									
DEFINITION	BP250019B10B3 Soares normalized bovine placenta										Bos taurus cDNA									
ACCESSION	clone BP250019B10B3 5', mRNA sequence.																			
	BF042894																			

JOURNAL
MEDLINE
COMMENT

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?ti=st2-QV3-BT0571-030
200-078-d08st3-2000-02-03&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 9
High quality sequence stop: 516.
Location/Qualifiers
1..517
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="BT0571"
/dev_stage="Adult"
/note="Organ: breast; Vector: puc18; Site_1: SmaI; Site_2:
SmaI; A mini-library was made by cloning products derived
from ORESTES PCR (U.S. Letters Patent application No. 196
,716 - Ludwig Institute for Cancer Research) profiles
into the puc 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."
BASE COUNT 130 a 131 c 150 g 106 t
ORIGIN

Query Match 51.9%; Score 176; DB 163; Length 517;
Best Local Similarity 100.0%; Pred. No. 1.4e-39;
Matches 176; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 164 acacaaccacacgacggtgctgggactgtacacactctgaacctgaagcatctgcct 223
|||||
Db 9 ACACACCCACACGACGGTGGGACTGTACAACTCTGAACCCCTGAAGCATCTGCCT 68
|||||

QY 224 cgcttgcgtgcgtgccccaggacctggagccctgacctcctgtactatgttggaggga 283
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Db 69 CGCCTTGTCTGCGTCCCGAGGACCTGGAGCCCTGACCTCCTGTACTATGTTGGGAGGA 128
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QY 284 ccccaaatggagcagctctcccaacatggtggtgaagtcttgaatagtactga 339
|||||
Db 129 CCCCCAAGTGGAGCAGCTCTCCACATGGTGGTGAAGTCTTTGTAATGTAGCTGA 184
|||||

RESULT 46
AW600944 AW600944 336 bp mRNA EST 23-MAR-2000
LOCUS RC1-BN0014-210100-012-e01 BN0014 Homo sapiens cDNA, mRNA sequence.
DEFINITION
ACCESSION AW600944
VERSION AW600944.1 GI:7305683
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 336)
REFERENCE HCGP http://www.ludwig.org.br/ORESTES.
AUTHORS The FAPESP/LICR Human Cancer Genome Project
JOURNAL Unpublished (1999)
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001

Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?ti=RC1st2=RC1-BN0014-
210100-012-e01st3-2000-01-21&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 20
High quality sequence stop: 336.
Location/Qualifiers
1..336
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="BN0014"
/dev_stage="Adult"
/note="Organ: breast_normal; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the puc 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
BASE COUNT 101 a 77 c 67 g 91 t
ORIGIN

Query Match 51.8%; Score 175.6; DB 118; Length 336;
Best Local Similarity 71.3%; Pred. No. 1.7e-39;
Matches 232; Conservative 0; Mismatches 94; Indels 0; Gaps 0;

QY 14 attactgttcgcgaacttgaggagaaactgtgtgccccctctacattgacttcc 73
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Db 7 ACTATTGCTTTGAAAATGTGCAGGATAATTGCTGCTACGTCCACTTTACATTGATTCA 66
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QY 74 gacaggatctgggctggaagtgggtccatgaacctaaaggctactatgccaacttcgct 133
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Db 67 AGAGGGACCTTAGGTGGAAATGGATACACGAAACCCAAAGGTTACAAATGCCAACTTCTGTG 126
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QY 134 caggcccttcccatcctccgagtcagacacacacccacagcagcgtgctgggactgt 193
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Db 127 CTGGAGCATCCCGTATTATGGAGTTTCAGACACTCAGCAGCAGGCGTCTGAGCTTAT 186
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QY 194 acaacactctgaacctgaagcatctgcctgccttgcgtgccccagacctggagc 253
|||||
Db 187 ATAATACATAAACCAGAGAGCATCTCTCTCTCTGCTGCGTGTCCCAAGATTAGAAC 246
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QY 254 ccttgacctctgtactatgttggggagcccccccaagtggagcagctctcccaatgg 313
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Db 247 CTCTAACCATCTCTACTACATTGGCAAAACACCCAAAGATTGAACAGCTTTCTAATATGA 306
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QY 314 tggtagactctgtataatagtactga 339
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Db 307 TTGTAAAGTCTTGCATAATGCAGCTAA 332
|||||

RESULT 47
BG058796/c BG058796 403 bp mRNA EST 25-JAN-2001
LOCUS naf10f12.x1 Soares_NPBMC Homo sapiens cDNA clone IMAGE:4140814 3'
DEFINITION similar to SW:TFGFI_CERAE P09533 TRANSFORMING GROWTH FACTOR BETA 1
PRECUSOR ; contains element PTR5 repetitive element ; , mRNA
sequence.
ACCESSION BG058796
VERSION BG058796.1 GI:12525613
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 403)
REFERENCE NCI-CCGAP http://www.ncbi.nlm.nih.gov/ncicgap.
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)

Qy	275	ttggaggagccccc	aaaggagcagctctccaaacatggtggtgaagctcttgaatgta	334
Db	241	TGGGTGCGAAGCCCAAGGTGGAGCAGTTGCTCCACATGATTGTGGCTCCTGCAAGTGCA	300	
Qy	335	gctga	339	
Db	301	GCTGA	305	
RESULT	49			
AI421250/c				
LOCUS		AI421250	540 bp	mrna
DEFINITION		tf14d02.x1 NCI_CGAP_Brn23 Homo sapiens CDNA clone IMAGE:2096163 3' similar to gb:X02812.cds1 TRANSFORMING GROWTH FACTOR BETA 1 PRECURSOR (HUMAN); contains element TAR1 repetitive element ;, mRNA sequence.	EST	28-MAR-1999
ACCESSION		AI421250		
VERSION		AI421250		
KEYWORDS		AI421250.1	GI:4267181	
SOURCE		EST.		
ORGANISM		human.		
REFERENCE		Homo sapiens		
AUTHORS		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
TITLE		1 (bases 1 to 540)		
JOURNAL		NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap .		
COMMENT		National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGP), Tumor Gene Index Unpublished (1998)		
		Contact: Robert Strausberg, Ph.D.		
		Email: cgapbs-re@mail.nih.gov		
		Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D., Ph.D.		
		CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.		
		CDNA Library Arrayed by: Greg Lennon, Ph.D.		
		DNA Sequencing by: Washington University Genome Sequencing Center		
		Clone Distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.lnl.gov/bbrp/image/image.html		
		Insert Length: 874 Std Error: 0.00		
		Seq primer: -40UP from Gibco		
		High quality sequence stop: 373.		
FEATURES		Location/Qualifiers		
source		1..540		
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		/db_xref="taxon:9606"		
		/clone="IMAGE:2096163"		
		/clone_lib="NCI_CGAP_Brn23"		
		/tissue_type="glioblastoma (pooled)"		
		/lab_host="DH10B"		
		/note="Organ: brain; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker: Site1: Not I; Site2: Eco RI; 1st strand CDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAAGTGGAGCGGCATATCTTTTTTTTTTTTTTTTTTTTTTTTTTTT 3']; Double-stranded CDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized, and was constructed by Bento Soares and M.Fatima Bonaldo."		
BASE COUNT		85 a	156 c	201 g
ORIGIN				98 t
Query Match		51.28;	Score 173.6;	DB 20; Length 540;
Best Local Similarity		72.66;	Prod. No. 6.8e-39;	
Matches		238; Conservative	0; Mismatches	89; Indels 1; Gaps 1;
Qy	12	caattactgcttcgcgaacttggaggagaactcgtgtgtgcgccccctctacattgactt	71	
Db	464	CAACTATGGCTCAGCTCCAGCGAGAAACTTCGCGTGGCGAGCTGTACATTGACTT	405	


```

BASE COUNT      97 a      148 c      206 g      108 t
ORIGIN

Query Match      50.4%; Score 171; DB 173; Length 559;
Best Local Similarity 71.1%; Pred. No. 3.8e-38;
Matches 241; Conservative 0; Mismatches 95; Indels 3; Gaps 1;

QY 1 gcttggacacaaattactgctccgcaacttgagagagaactgctgtgtgccccctc 60
  || || || || || || || || || || || || || || || || || || || ||
Db 481 GCCCTGGACACCAACTATTGCTTCAGCTCCACGGAGAGAACTTCTGCGTACGCAACTG 422

QY 61 tacattgacttcgacagagatctgggctggaagtgggtccatgaaacctaaaggtactat 120
  || || || || || || || || || || || || || || || || || || || ||
Db 421 TACATTGACTTCA---AGGACCTCGGCTGTAAGTGGATCCTTAGCCCAAGGGCTTCCAT 365

QY 121 gcaactctctcaggccctggccatactccgcagctccgcagtcgacacaaacacagcag 180
  || || || || || || || || || || || || || || || || || || || ||
Db 364 GCCAATTCTTGCTCGGGCCCTGCCCTTACATTTGGAGCTGGACAGCAGTACAGCAAG 305

QY 181 gtgctgggactgtacaaactctgaacctgaagcatctgccttgcctgtgctgctgccc 240
  || || || || || || || || || || || || || || || || || || || ||
Db 304 GTCTGGCCCTGTACACACAGCATACCCGGCGCTCGCGGCCCTGCTGCTGCTCGG 245

QY 241 caggacctggagccctgacctctgtactatgttgggagagaccccccaagtggagcag 300
  || || || || || || || || || || || || || || || || || || || ||
Db 244 CAGGCGCTGGAACCGCTGCCATCGTGTACTACGTGGCGCGCAAGCCCAAGGTGGAGCAG 185

QY 301 ctctcaacatggtggtgaagctctgtataatgtagctga 339
  || || || || || || || || || || || || || || || || || || || ||
Db 184 CTGTCCAACATGATCGTGGCTCTCTGCAAGTGCAGTTTA 146

RESULT 53
AL530080/c      AL530080      798 bp      mRNA      EST      13-FEB-2001
LOCUS
DEFINITION      AL530080 LTI_NFL001_NBC4 Homo sapiens cDNA clone CS0DD009YM06 3
prime, mRNA sequence.
ACCESSION      AL530080
VERSION        AL530080.1 GI:12793573
KEYWORDS       EST.
SOURCE         human.
ORGANISM       Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 798)
Li.W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
1. .798
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0DD009YM06"
/clone_lib="LTI_NFL001_NBC4"
/sex="male"
/tissue_type="neuroblastoma cells"
/lab_host="DH10B"
/Note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed
by Life Technologies. Contact : Feng Liang Life
Technologies, a division of Invitrogen 9800 Medical Center
Drive Rockville, Maryland 20850, USA Fax : (1) 301 610
8371 Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com"

BASE COUNT      97 a      148 c      206 g      108 t
ORIGIN

Query Match      50.4%; Score 170.8; DB 106; Length 798;
Best Local Similarity 72.8%; Pred. No. 4.6e-38;
Matches 246; Conservative 1; Mismatches 88; Indels 3; Gaps 2;

QY 1 gcttggacacaaattactgctccgcaacttgagagagaactgctgtgtgccccctc 60
  || || || || || || || || || || || || || || || || || || || ||
Db 402 GCCCTGGACACCAACTATTGCTTCAGCTCCACGGAGAGAACTGCTGCTGCGCAGCTG 343

QY 61 tacattgacttcgacagagatctgggctggaagtgggtccatgaaacctaaaggtactat 120
  || || || || || || || || || || || || || || || || || || || ||
Db 342 TACATTAACTTCGCAAGGACCTCGGCTGGAGTGGATCCACGAGCCCAAGGGTCCAT 283

QY 121 gcaactctctcaggccctggccatactccgcagctccgcagtcgacacaaacacagcag 180
  || || || || || || || || || || || || || || || || || || || ||
Db 282 GCCAACTTCTTGCTCGGGCCCTGCCCTTACATTTGGAGCTGGACAGCAGGACGAAG 223

QY 181 gtgctgggactgtacaaactctgaacctgaagcatctgccttgcctgtgctgctgccc 240
  || || || || || || || || || || || || || || || || || || || ||
Db 222 GTCTGGCCCTGTACACACAGCATACCCGG--GCCTCGGGCGCGCTGC-GGCTGCCG 166

QY 241 caggacctggagccctgacctctgtactatgttgggagagaccccccaagtggagcag 300
  || || || || || || || || || || || || || || || || || || || ||
Db 165 CAGGCGCTGGAGCGCTGCGCTTGTCTGTACTACGTGGCGCGCAAGCCCAAGGTGGGCGG 106

QY 301 ctctcaacatggtggtgaagctctgtataatgtagctg 338
  || || || || || || || || || || || || || || || || || || || ||
Db 105 CTGTCCAACATGCTGCTGCTCTCTGCAAGGCGCGCTG 68

RESULT 54
AL304490/c      AI304490      449 bp      mRNA      EST      01-FEB-1999
LOCUS
DEFINITION      q054e06.x1 NCI_CGAP_Co8 Homo sapiens cDNA clone IMAGE:1912354 3'
similar to gb:X02812.cdsl TRANSFORMING GROWTH FACTOR BETA 1
PRECURSOR (HUMAN); contains PTRS.t3 TARI repetitive element ;, mRNA
sequence.
ACCESSION      AI304490
VERSION        AI304490.1 GI:3988179
KEYWORDS       EST.
SOURCE         human.
ORGANISM       Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 449)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgaps@remail.nih.gov
Tissue Procurement: Christopher Moskaiuk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 933 Std Error: 0.00
Seq primer: -400P from Gibco
High quality sequence stop: 385.
Location/Qualifiers
1. .449
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1912354"
/clone_lib="NCI_CGAP_Co8"
/tissue_type="adenocarcinoma"
/lab_host="DH10B"

```

BASE COUNT		66 a		128 c		163 g		92 t	
ORIGIN									
/note="Organ: colon; Vector: pF7T3D-Pac (Pharmacia) with modified polylinker; 1st strand cDNA was prepared from colon adenocarcinoma, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pF7T3 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo."									
Query Match		49.7%		Score 168.6;		DB 18;		Length 449;	
Best Local Similarity		74.2%		Pred. No. 1.7e-37;					
Matches 213;		Conservative 0;		Mismatches 74;		Indels 0;		Gaps 3;	
Qy	53	gccccctcattgacttcgacagagatctggctggaagtgggtccatgaacctaaag	112						
Db	449	GGCAGCTGTACATTGCTTCGCAAGGACCTTCGCTGGAAGTGGATCCACGAGCCCAAGG	390						
Qy	113	gctactatgccaactcttctgcagggcccttgcccatcctccgcagtcgacagacacacc	172						
Db	389	GCTACCATGCCAACTTTTGCTCGGGCCCTGCCCTACATTTGGAGCCTGGACACGCAGT	330						
Qy	173	acagcacggtgctgggactgtacaacactctgaacctgaagcatctgcctgccttgcct	232						
Db	329	ACAGCAAGGTCTGGCCCTGTACAAACGACGATAACCGGGCGCTCGGGCGCGCGTCT	270						
Qy	233	gcgtgccccaggaacctgagccctcgacctctgtactatgttggaggagaccctcaaaag	292						
Db	269	CGTGTCCGACAGGCGCTGGAGCGCTGCGCATCGTGTACTAGTGGCGCGCAAGCCCAAG	210						
Qy	293	tggagcagctctccaaatggtggtgaagtcttgaatgtagtctga	339						
Db	209	TGGAGCAGCTGTCCAATGATCGTGGCTCCTGCCAAGTGCAGCTGA	163						
RESULT 55									
AI360877/c									
LOCUS	AI360877	328 bp	mRNA	EST	15-FEB-1999				
DEFINITION	qy01c06.x1 NCI-CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2010730 3' similar to gb:X02812_cds1 TRANSFORMING GROWTH FACTOR BETA 1								
PRECUSOR (HUMAN);	mRNA sequence.								
ACCESSION	AI360877								
VERSION	AI360877.1								
KEYWORDS	GI:4112498								
SOURCE	EST.								
ORGANISM	human.								
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.								
AUTHORS	NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.								
TITLE	National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGP), Tumor Gene Index								
JOURNAL	Unpublished (1998)								
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D., Ph.D. cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html								
Trace considered overall poor quality									
Insert Length: 628 Std Error: 0.00									
Seq primer: -400p from Gibco									
High quality sequence stop: 1.									
Location/Qualifiers									

KEYWORDS	EST.	AUTHORS	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap .
SOURCE	house mouse.	TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
ORGANISM	Mus musculus	JOURNAL	Unpublished (1997)
REFERENCE	Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 576)	COMMENT	Contact: Robert Strausberg, ph.D. Email: cgapbs-r@mail.nih.gov Life Technologies catalog #: 11548-013 DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html Insert Length: 614 Std Error: 0.00 Seq primer: -400P from Gibco.
AUTHORS	Ko, M.S.H., Kitchen, J.R., Wang, X., Threat, T.A., Sun, T., DePalma, G.E., Liang, Y., Kargul, G.J., Sharara, R. and Doi, H.	FEATURES	Location/Qualifiers
TITLE	Systematic analyses of genes expressed in 2-cell stage mouse embryos (The ERAFO/Doi Project at Wayne State University) (Ko, M.S.H. et al.)	Source	1..408
JOURNAL	Unpublished (1998)		/organism="Homo sapiens"
COMMENT	Contact: Hirofumi Doi		/db_xref="taxon:9606"
	Doi Biosymmetry Project, ERAFO		/clone="IMAGE:2294345"
	Japan Science and Technology Corporation (JST)		/clone_lib="NCI-CGAP_Pan1"
	WBG Marine East 12F, 2-6 Nakase, Mihama-ku, Chiba 261-71, Japan		/tissue_type="adenocarcinoma"
	Email: hd@bioa.jst.go.jp .		/lab_host="DH10B"
FEATURES	Location/Qualifiers		/note="Organ: pancreas; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.72 kb. Life Technologies catalog #:
Source	1..576		11548-013"
	/organism="Mus musculus"	BASE COUNT	58 a 118 c 154 g 78 t
	/strain="C57BL/6J"	ORIGIN	
	/db_xref="taxon:10090"		
	/clone="J0728H08"		
	/clone_lib="Mouse two-cell stage embryo cDNA"		
	/dev_stage="two-cell stage embryo"		
	144 a 123 c 134 g 164 t 11 others		
BASE COUNT	144 a 123 c 134 g 164 t 11 others		
ORIGIN			
Query Match	45.1%; Score 152.8; DB 107; Length 576;	Query Match	45.0%; Score 152.4; DB 22; Length 408;
Best Local Similarity	73.0%; Pred. No. 5.6e-33;	Best Local Similarity	74.4%; Pred. No. 6.8e-33;
Matches	249; Conservative 0; Mismatches 88; Indels 4; Gaps 4;	Matches	192; Conservative 0; Mismatches 66; Indels 0; Gaps 0;
QY 1	gcttggacacaaattactgtccgaacttggagg-agaactgtgtgtcgcccccct 59	QY 82	ctgggctggaagtgggtccatgaacctaaagggctactatgccaaattctctcagggccct 141
DB 452	gcttggagtgccgtactgcgtttgaaatgtgcaggaaataatgctgcttcgcccctt 393	DB 407	ctcggttggaagtggatccacgagcccgagggctaccatgccaaacttctgctcgggccc 348
QY 60	ctacattgactccgaca-ggactctgggtggaagtgggtccatgaacctaaagggctact 118	QY 142	tgccatactccgcagtcgagacacacacccagcacgctgtggtggtgactgtacacact 201
DB 392	ttacattgaatttttagaggatcttggaatggaatggatccatgacccaggg-taca 334	DB 347	tgccctctacattttggagccctggacacgcagctacagcagaggtcttggccctgtacacac 288
QY 119	atgccaaactctgtcagggcccttgccataacctccgcagtcgagacacacacccacaga 178	QY 202	ctgaaccctggaagcatctgctgctgctgctgctgctgctgctgctgctgctgctgctgctg 261
DB 333	atgctaactctctgtgtggtgggagatcccatatctatgagatgttgcagacactcaacac 274	DB 287	catacccgccgcccctcgccggcgccgctgctgctgctgctgctgctgctgctgctgctgct 228
QY 179	cggtactgggactgtacaacactggaacctggaagcatctcctcgctgctgctgctgctg 238	QY 262	atcctgtactatgttgggagaccccccaagtgagcagctctctccaaactggtggtgaag 321
DB 273	aagtcctcagcctgtac 215	DB 227	atcgtgtactacgttggggccgcaagcccgagcagctgtcccaacatgatctgctgctg 168
QY 239	ccaggacccgtgagccctgac 298	QY 322	tctgtaaatgtagctga 339
DB 214	cccagatctggaac 155	DB 167	tcctgcaagtgcagctga 150
QY 299	agctctcaacatggtgtggaagtcttgaatgtagctga 339		
DB 154	agctttccaatatgattgtgcaagctgtgtaaatgcagctaa 114	RESULT 62	
LOCUS	AI634937/c	W98872	
DEFINITION	tz74f09.x1 NCI-CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2294345 3' similar to gb:X02812.cds1 TRANSFORMING GROWTH FACTOR BETA 1 PRECURSOR (HUMAN); contains element MER22 repetitive element ;, mRNA sequence.	LOCUS	W98872 431 bp mRNA EST 16-JUL-1996
ACCESSION	AI634937		mi89e01.r1 Soares mouse embryo NbM13.5 14.5 Mus musculus cDNA clone IMAGE:421464 5' similar to gb:X02812.cds1 TRANSFORMING GROWTH FACTOR BETA 1 PRECURSOR (HUMAN);, mRNA sequence.
VERSION	AI634937.1 GI:4686267	ACCESSION	W98872
KEYWORDS	EST.	VERSION	W98872.1 GI:1428996
SOURCE	human.	KEYWORDS	EST.
ORGANISM	Homo sapiens	SOURCE	house mouse.
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 408)	ORGANISM	Mus musculus
REFERENCE	1		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 431)
		REFERENCE	1
		AUTHORS	Marta, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisler, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.

Best Local Similarity 71.0%; Pred. No. 1.1e-30;									
Matches 218; Conservative 0; Mismatches 86; Indels 3; Gaps 2;									
QY	1	gctttgacacaaattactcttcgcgaacttgcgagagaactgctgtgctgcgccctc	60						
Db	222	GCCTGGATACCAACTATTGCTTCAGCTCCACAGAAGAAGTGTGTGTGCGCAGTNG	281						
QY	61	tacattgactctccgacaggatctgggtcgaagtgggtccatgaacctaaagggctactat	120						
Db	282	TACATTGACTTTAGGAAGGACCTGGGTTGGAAGTGGATCCACGAGCCCAAGGGCTACCAT	341						
QY	121	gcaactctgtctcagggcccttgcccatactctccgcagtgcgacacacacccacgacg	180						
Db	342	GCCAACTTCTGTCTGGGACCTGCCCTATATTATTGGAGCGCTGGACACACACAGTACAGCAAG	401						
QY	181	gtctgggactgtacaacactctgaacctctgaacctctgaacctctgctcgtctgctggtgcc	240						
Db	402	GTCTTGGCCCTCTACAAACCAACACACCCGGGGCTTCGGGCTCACCGTGTGGTGCCG	461						
QY	241	caggacctggagcccttgacctctgactctgtactatgttgggaggacccccaaagtggagcag	300						
Db	462	ACG-ITTTGGAGCACTGCCCATCGTCTACTACG-TGGGTCCGAACCCCAAGTGGAGCAG	518						
QY	301	ctctcca 307							
Db	519	TTGTCCA 525							
RESULT 67									
BG540633									
LOCUS									
DEFINITION									
ACCESSION									
VERSION									
KEYWORDS									
SOURCE									
ORGANISM									
REFERENCE									
AUTHORS									
TITLE									
JOURNAL									
COMMENT									
<p>NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: CLONTECH Laboratories, Inc. cDNA Library Preparation: CLONTECH Laboratories, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLM1519 row: h column: 05 High quality sequence stop: 562. Location/Qualifiers</p>									
FEATURES									
source									
<p>1..889 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:4694836" /clone_lib="NIH_MGC_77" /lab_host="DH10B (T1 phage-resistant)" /note="Organ: lung; Vector: pDNR-LIB (Clontech); Site:1. SfiI (ggcgccctcgccc); Site_2: SfiI (ggcattatggcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGGCTATTGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCGCGGCGCGCATG-dt(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.9 kb (range 0.5-4.0 kb). 12/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."</p>									
BASE COUNT 260 a 230 c 190 g 209 t									

CA). NOTE: THIS IS A NIH-MGC LIBRARY.

BASE COUNT	260 a	230 c	190 g	209 t
------------	-------	-------	-------	-------

ORIGIN
 Query Match 42.4%; Score 143.6; DB 155; Length 889;
 Best Local Similarity 68.2%; Pred. No. 2.5e-30;
 Matches 214; Conservative 0; Mismatches 99; Indels 1; Gaps 1;
 QY 1 gcttggacacaaattactgtccgcgaacttgaggagaactgctgtgtgcgccctc 60
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 274 GCTTTGGATCGGGCTATTGCTTTAGAAATGTGCAGGATAATTGCTGCTACGTCACATT 333
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 61 tacattgaactcc-gacaggatctcgggtggaagtgggtcccatgaacctaaagggtacta 119
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 334 TACATTGATTTCAAGAGGGCATCTAGGGTGGAAATGGATACGCAACCAAGGGTACAA 393
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 120 tgcaactctgtcaggcccttgcacatacctcgcagtgtagagtcagacacacacccacgac 179
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 394 TGCCAACTTCTGCTGGAGCATGCCGTATTTATGGAGTTTCAGACATCAGCAGCAG 453
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 QY 180 ggtgctggagctgtacaaactctgaacccctgaagcatctgcctgcctgtcgtcggtgcc 239
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 454 GGTCTGAGCTTATATAATACATAAAATCCAGAAGCATCTGCTTCTCCTTCTGCTGCTGTC 513
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 240 ccaggacctggagccctgaacatcctgtactatgtttggaggagcccccaagtggagca 299
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 Db 514 CCAAGATTGAACCCCTTAAACATTTCTACTACATTGGAAACACCAAGATGGAACAG 573
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 300 gctctcaacatgg 313
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 574 CTTTCTTAATTTG 587
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 RESULT 68
 AW295761/c
 LOCUS
 DEFINITION
 UI-H-B11-afh-a-02-0-UI.s1 NCL_CGAP_Sub3 Homo sapiens cDNA clone
 IMAGE:2721675 3', mRNA sequence.
 ACCESSION
 AW295761
 VERSION
 AW295761.1 GI:6702397
 KEYWORDS
 EST.
 SOURCE
 human.
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE
 1 (bases 1 to 409)
 AUTHORS
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 TITLE
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL
 Unpublished (1997)
 COMMENT
 Contact: Robert Strausberg, Ph.D.
 Email: cgaps-r@mail.nih.gov
 The sequence contained an oligo-dT track that was present in the
 oligonucleotide that was used to prime the synthesis of first
 strand cDNA and therefore this may represent a bonafide poly A
 tail. cDNA library Preparation: M.B. Soares Lab Clone Distribution:
 NCI-CGAP clone distribution information can be found through the
 I.M.A.G.E. Consortium/LLNL at:
 www.bio.llnl.gov/bbrp/image/image.html The following repetitive
 elements were found in this cDNA sequence: 102-157,
 >GC-rich#Low_complexity
 Seq primer: M13 Forward
 POLYA=Yes.
 FEATURES
 Location/Qualifiers
 1..409
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:2721675"
 /clone_lib="NCI_CGAP_Sub3"
 /lab_host="DH10B (Life Technologies)"
 /note="Vector: p7f3D-pac (Pharmacia) with a modified
 polylinker; Site_1: Not I; Site_2: Eco RI; The
 NCI_CGAP_Sub3 library is a subtracted library derived from
 the NCI_CGAP_Sub1 library, which is a subtracted library

derived from BI. BI constitutes a mixture of 21 normalized or subtracted NCI_CGAP libraries: NCI_CGAP_Co1, NCI_CGAP_Pr22, NCI_CGAP_Pr28, NCI_CGAP_Co10, NCI_CGAP_Co16, NCI_CGAP_Kid5, NCI_CGAP_Kid12, NCI_CGAP_Kid3, NCI_CGAP_Kid11, NCI_CGAP_Lym2, NCI_CGAP_Br2, NCI_CGAP_Co8, NCI_CGAP_CLL1, NCI_CGAP_Le12, NCI_CGAP_Brn23, NCI_CGAP_Lu5, NCI_CGAP_Lu24, NCI_CGAP_Lu19, NCI_CGAP_G4, NCI_CGAP_G6, NCI_CGAP_Brn25. These 21 libraries were pooled and a single-stranded DNA preparation of the resulting mixture was used as a tracer in a subtractive hybridization with a driver whose composition is detailed below:

NCI_CGAP_Kid3 pool 1 LLAM 3334-3337, 3682-3683.
 3798-3803 (IMAGE Clonoids 1322376-1323911, 1456008-1456777, 1500552-1502855); NCI_CGAP_Kid5 pool 1 LLAM 3338-3344, 3722-3725, 3776-3778 (IMAGE Clonoids 1323912-1325831, 1471368-1472903, 1492104-1493255); NCI_CGAP_Lu5 pool 1 LLAM 3575-3582, 3851-3854 (IMAGE Clonoids 1414920-1417991, 1520904-1522439); NCI_CGAP_G4 pool 1 LLAM 3164-3167, 3716-3720, 3733-3735 (IMAGE Clonoids 1257096-1258631, 1468064-1470983, 1475592-1476743); NCI_CGAP_Pr22 pool 1 LLAM 2457-2459, 2758-2759, 3062-3068 (IMAGE Clonoids 985608-986759, 1101192-1101959, 1217928-1220615); NCI_CGAP_Co10 pool 1 LLAM 2644-2653, 2871-2872 (IMAGE Clonoids 1057416-1061255, 1144584-1145351). Subtraction was performed as previously described [Bonaldi, Lennon & Soares (1996): Normalization and Subtraction: Two Approaches To Facilitate Gene Discovery. Genome Research 6, 791-806.

TAG_LIB=NCI_CGAP_Pr22
 TAG_TISSUE=prostate
 TAG_SEQ=AAAGTG"

BASE COUNT	57 a	115 c	153 g	84 t
ORIGIN				
Query Match	42.3%	Score 143.4;	DB 114;	Length 409;
Best Local Similarity	73.5%;	Pred. No. 2.4e-30;		
Matches 183;	Conservative	0;	Mismatches 66;	Indels 0;
Gaps	0;			
Qy	91	aagtggtgcctgaacctaaagggtctactatgcacaaacttctgtcagggcccttgcccatc	150	
Db	409	AAGTGGATCCACGAGCCCAAGGGCTACCATCCCAACTTCTGCCTCGGGCCCTGCCCTAC	350	
Qy	151	ctcgcagtcagacacacacacagcagtgctgggagctgtacacaaactctgaacct	210	
Db	349	ATTGGAGCCCTGGACACGACGATACGAAGGTCCTGGCCCTGTACACACGATACACCG	290	
Qy	211	gaagcatgtcctgcctgtgcgtgccagagacctggagccctgacacatctgtac	270	
Db	289	GGCGCTCGGGCGCGCGTGTGCTGCGCGGAGGGCTGGAGCCCGCTGCCCATGTGTAC	230	
Qy	271	tatgttgggagaccccccacaaagtggagcagctctccacatgtgtggaagcttctgtaa	330	
Db	229	TACGTGGGCCGCAAGCCCAAGGTGGAGCAGCTGTCCAACATGATCGTGGCTCTGCAAG	170	
Qy	331	tgtagtcta	339	
Db	169	TGCAGCTGA	161	
RESULT 69				
AI192407/c				
LOCUS	AI192407	348 bp	mRNA	EST
DEFINITION	q98cc09.x1 Soares_pregnant_uterus_NDHPU Homo sapiens cDNA clone IMAGE:1722256 3', similar to gb:Y00083 TRANSFORMING GROWTH FACTOR BETA 2 PRECURSOR (HUMAN);, mRNA sequence.			28-OCT-1998
ACCESSION	AI192407			
VERSION	AI192407.1	GI:3743616		
KEYWORDS	EST.			
SOURCE	human.			
ORGANISM	Homo sapiens			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			

Db	352	AATGCTGAAACAAATATCTCAGATTTTGGCCCTTGACAAAGCATCACAAACCCAGGAGCC	411
Qy	217	tctgctcgccttgctgctgcccaggacctggagccctgaccactcctgtactatgtt	276
Db	412	TTGCCACCCCTGCTGTGTCCTCCAGGACTGGACCCACTGCCAATCTCTACTACGTG	471
Qy	277	ggaggagcccccagaagtgcagcagctcccaacatgctgtaagtctgtgtaaatagc	336
Db	472	GCAGCAACACAAGGTGGAGCAGCTGTCCAATATGATCGTGAAGTCTCTGCAAGTAGC	531
Qy	337	tga 339	
Db	532	TAA 534	
RESULT	76		
LOCUS	AI918883	392 bp mRNA EST	28-JUL-1999
DEFINITION	tu13b10.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2250907 3' similar to gb:X02812.cds1 TRANSFORMING GROWTH FACTOR BETA 1 PRECURSOR (HUMAN);contains element TAR1 MER22 repetitive element ;, mRNA sequence.		
ACCESSION	AI918883		
VERSION	AI918883.1	GI:5638738	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 392)		
AUTHORS	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.		
TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index		
JOURNAL	Unpublished (1997)		
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgabps-r@mail.nih.gov Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D. CDNA Library Preparation: M. Bento Soares, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/dbp/image/image.html Seq primer: -40UP from Gibco High quality sequence stop: 335.		
FEATURES	Location/Qualifiers		
source	1..392		
	/organism="Homo sapiens"		
	/db_xref="taxon:9606"		
	/clone="IMAGE:2250907"		
	/clone_lib="NCI_CGAP_Pr28"		
	/sex="male"		
	/dev_stage="adult"		
	/lab_host="DH10B"		
	/note="Organ: prostate; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Plasmid DNA from the normalized library NCI_CGAP_Pr22 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIds 985608-986759, 1101192-1101959, and 1217528-122615). Subtraction by Bento Soares and M. Fatima Bonaldo."		
BASE COUNT	57 a	117 c	150 g
ORIGIN	67 t 1 others		
Query Match	39.7%;	Score 134.6;	DB 103; Length 392;
Best Local Similarity	73.6%;	Pred. No. 7.7e-28;	
Matches 184;	Conservative 0;	Mismatches 65;	Indels 1; Gaps 1;

Qy	90	gaagtgggtccatgaacctaaagggctactatgccaactcttctgctcagcccttgcccata	149
Db	388	GAAAGTGATCCAGAGCC-AAGGGCTACCATCTGCTCGGCTCGGGCCCTGCCCTTA	330
Qy	150	ctcccgagctgcagacacacacacagcacgctgctgctggactgtacaacacttgaaccc	209
Db	329	CATTGGAGCCTGGACACGAGTACACAGAGTCTGGCCCTGTACAAACGACATACCC	270
Qy	210	tgaagcatctgctcgccttgccttgcctgctgctgccccagacctggagcccttgacctctgta	269
Db	269	GGGCGCCTCGCGCGCGCTGCTGCTGCTGCGCGAGCTGGAGCGCTGGCCCATCGTGTGA	210
Qy	270	ctatgttgaggagaccccccaaaagtggagcagctctcaacatgctgctggaagtctttaa	329
Db	209	CTAGTGGGCCGCAAGCCCAAGGTGGAGCAGCTGTCCAACATGATCGTGGCTCTCTGCAA	150
Qy	330	atgtagctga 339	
Db	149	GTGACGTGA 140	
RESULT	77		
LOCUS	AA533093/c	542 bp mRNA EST	21-AUG-1997
DEFINITION	nj19g04.s1 NCI_CGAP_AAL Homo sapiens cDNA clone IMAGE:992982 3' similar to gb:X02812.cds1 TRANSFORMING GROWTH FACTOR BETA 1 PRECURSOR (HUMAN);contains element MER22 repetitive element ;, mRNA sequence.		
ACCESSION	AA533093		
VERSION	AA533093.1	GI:2277189	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 542)		
AUTHORS	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.		
TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index		
JOURNAL	Unpublished (1997)		
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgabps-r@mail.nih.gov Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael R. Emmert-Buck, M.D., Ph.D. CDNA Library Preparation: Stratagene, Inc., David B. Krizman, Ph.D. CDNA Library Arraying: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html Insert length: 1687 Std Error: 0.00 Seq primer: -40ml3 fwd. ET from Amersham High quality sequence stop: 142.		
FEATURES	Location/Qualifiers		
source	1..542		
	/organism="Homo sapiens"		
	/db_xref="taxon:9606"		
	/clone="IMAGE:992982"		
	/clone_lib="NCI_CGAP_AAL"		
	/tissue_type="adrenal adenoma"		
	/lab_host="SOLR (kanamycin resistant)"		
	/note="Organ: adrenal gland; Vector: Bluescript SK-; Site_1: EcoRI; Site_2: XhoI; Cloned unidirectionally. Primer: Oligo dt. Two pooled bulk adrenal adenomas. 5' adaptor sequence: 5' GAATTCGGCAGAG 3' 3' adaptor sequence: 5' CTCAGTCTTTTTTTTTTTTTTTT 3' Average insert size: 1.6 kb."		
BASE COUNT	92 a	152 c	196 g
ORIGIN	102 t		
Query Match	39.6%;	Score 134.2;	DB 8; Length 542;

[illegible][illegible]

QY 120 tggcaacttctgtctcaggcccttg-ccatatactctcgagtcgagacacacccacagca 178

[illegible]

QY 239 ccaggacactggagccctgaccatcctgtactatgttgggagagacccccaaagtgcagc 298
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
db 214 CCCAGGATCTGGAAACCACTGACCATTCTTATTACATTTGGGAATACGCCCAAGATCGAAC 155

QY 299 agcttccaaacatggtggtagtccttgtaaattgagctga 339
||||| ||||| ||||| ||||| ||||| ||||| |||||
db 154 AGCATTCCAAATGATGTTGCAGCTTGTAAATGCCAGCTAA 114

RESULT 81
AU016439/C

LOCUS	AU016439	465 bp	MRNA	EST	15-OCT-1998
DEFINITION	AU016439	Mouse two-cell stage embryo	cdna	Mus musculus	CDNA clone
ACCESSION	AU016439	J0725B08	3', mRNA sequence.		

VERSION	A0016439.1	GI:3371443
KEYWORDS	EST.	
SOURCE	house mouse.	
ORGANISM	Mus musculus	

REFERENCE

1 (bases 1 to 465)

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Craniata; Depalma

AUTHORS

CO, M. S. H., Kitchin, J. R., Wang, X., Threat, T. A., Sun, T., Depalma

TITLE
Liang, Y., Kargul, G.J., Sharara, R. and Doi, H.
Systematic analyses of genes expressed in 2-cell stage mouse
embryos (The ERATO/Doi Project at Wayne State University) (Ko
M.S.H. et al.)

**JOURNAL
COMMENT**
Unpublished (1998)
Contact: Hirofumi Doi
Doi Biosymmetry Project, ERATO
Japan Science and Technology Corporation (JST)

FEATURES
source 1.465
Location/Qualifiers
Email: hd@bloa.jst.go.jp.
WBG Marine East 12F, 2-6 Nakase, Mihama-ku, Chiba 261-71, Japan

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/organism="Mus musculus"  
/strain="C57BL/6J"  
/db_xref="taxon:10090"  
/clone="J0725B08"
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BASE COUNT	123 a	97 c	112 g	127 t	6 others
ORIGIN					

Query Match 38.5%; Score 130.4; DB 107; Length 465;
Best Local Similarity 70.7%; pred. NO. 1.2e-26;

	Matches	212;	Conservative	0;	Mismatches	85;	Indels	3;	Gaps	
QY	42	ctgctgtgtgcgccccctctacattgacttcggacaggaatctaggcctggaagtgggtcca	101							

Accession	Sequence	Position
D8	412 CTGNCCTTCGCCCCCTCTCTTTTACATTGATTTTANGNGGGGATCTGGNATGGAAATGGATCCC	353
QY	102 tgaacctaaagggtactatgccaac-ttctgtcaggcccttgcccataccctccgagtg	160

352 ATGACCCCAAGGGTACAATGCTAACTTTCTGTGCTGGGCGATGCCCATATCTATGGAGTT 293

Db

161 cagacacaa-cacagcacggtgctgggacigtacaacactctgaacccctgaagcatct 219

Qy

Db 292 CAGACACTTCAACACACACCAAGTCCTCAGCCTGTACACACACCA/ANATCCCGAA -CTTCC 233

Qy	220	gcctcgcttgctgctgccccaggagcaactggagccccctgaccatcctgttactatgttggg	279
Db	233	gcttcccccttgctgctgctgccccaggagctctggagccaccctgaccattctctattacattgga	174
Qy	280	aggacccccaaagtggagcagctctccaacatggtggtgaagctctgtaaatagctga	339
Db	173	aatagccccaagatcgcaacagctttccaatatgattgctcaagtcttgtaaatgagcgtaa	114
RESULT	82		
BE737006			
LOCUS			
DEFINITION	BE737006	915 bp mRNA EST	15-SEP-2000
	601306787F1 NIH_MGC_39	Homo sapiens cDNA clone IMAGE:3641081	5',
ACCESSION		mRNA sequence.	
VERSION	BE737006		
KEYWORDS	BE737006.1	GI:10150998	
SOURCE	EST.		
ORGANISM	human.		
REFERENCE	Homo sapiens		
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi.		
TITLE	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
JOURNAL	1 (bases 1 to 915)		
COMMENT	NIH-MGC http://mgc.nci.nih.gov/.		
	National Institutes of Health, Mammalian Gene Collection (MGC)		
	Unpublished (1999)		
	Contact: Robert Strausberg, Ph.D.		
	Email: cgapbs-r@mail.nih.gov		
	Tissue Procurement: ARCC		
	cDNA Library Preparation: Ling Hong/Rubin Laboratory		
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)		
	DNA Sequencing by: Incyte Genomics, Inc.		
	Clone distribution: MGC clone distribution information can be		
	found through the I.M.A.G.E. Consortium/LLNL at:		
	http://image.llnl.gov		
	Plate: LLCM346 row: e column: 18		
	High quality sequence stop: 424.		
FEATURES	Location/Qualifiers		
source	1..915		
	/organism="Homo sapiens"		
	/db_xref="taxon:9606"		
	/clone="IMAGE:3641081"		
	/clone_lib="NIH_MGC_39"		
	/tissue_type="adenocarcinoma"		
	/lab_host="DH10B (phage-resistant)"		
	/note="Organ: pancreas; Vector: pOTB7; Site: 1: XhoI;		
	Site: 2: EcoRI; cDNA made by oligo-dT priming.		
	Directionally cloned into EcoRI/XhoI sites using the		
	following 5' adaptor: GGCACGAG(C). Library constructed		
	by Ling Hong in the laboratory of Gerald M. Rubin		
	(University of California, Berkeley) using ZAP-cDNA		
	synthesis kit (Stratagene) and Superscript II RT (Life		
	Technologies)."		
BASE COUNT	229 a	279 c	276 g
ORIGIN	131 t		
Query Match	38.1%	Score 129.2;	DB 139; Length 915;
Best Local Similarity	73.4%	Pred. No. 3.1e-26;	
Matches	179; Conservative	0; Mismatches	63; Indels 2; Gaps
Qy	1	gccttgacaccattactgtctccgaacttggagagaaactgtgtgcgccccctc	60
Db	189	GCCTTGGACACCAACTATTGCTTCAGCTCCACGGAGAAAGACTGCTGCTGCGGACAGCTG	248
Qy	61	tacattgacttcgcagcaggtatggctggaaagtgggtccatgaacctaaagggtactat	120
Db	249	TACATTGACTTCCGCAAGGACCTCGCTGGAGTGGATCCACGAGCCCAAGGCTACCAT	308
Qy	121	gccaaactctgtcaggcccttgccccatacctccgcagtgcagacacaacccacagcaog	180
Db	309	GCCAACTCTGCTCGGGCCCTGCCCTACATTGTGGAGCTGGACACGAGTACAGCAAG	368

Insert Length: 860 Std Error: 0.00
 Seq primer: Promega -21ml3
 High quality sequence stop: 281.

FEATURES

source

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Location/Qualifiers
1. .398
/organism="Homo sapiens"
/db_xref="GDB:543039"
/db_xref="taxon:9606"
/clone="IMAGE:136821"
/clone_lib="Soares placenta Nb2HP"
/sex="Female"
/dev_stage="Placenta obtained at birth (full term)"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: placenta; Vector: pT73D (Pharmacia) with a
modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
AACTGGAGAATCGCGCCGCGAGGAATTTTCTTTTCTTTT 3'],
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT73 vector. Library
went through one round of normalization. Library
constructed by Bento Soares and M.Patima Bonaldo. "
```

BASE COUNT
 ORIGIN

```

61 a 112 c 147 g 64 t 14 others
Query Match 36.1%; Score 122.4; DB 187; Length 398;
Best Local Similarity 65.9%; Pred. No. 2.2e-24;
Matches 182; Conservative 0; Mismatches 93; Indels 1; Gaps 1;

QY 64 attgacttcgacagatctggctggaagtgggtccatgaacctaaagggctactatgcc 123
|||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 398 ATTGACTTCGNAAGNACCTGGCTGGAGTGATCCACGCCAACCGGCTACNATGCC 339

QY 124 aacttctgcagcccttgccatccctcgcagtgacagacacacccacagcacgtg 183
|||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 338 ACTCTGCGTCCGCTGGCCCTGATTTGGAGCCTGGACACGCGAGTAGNAGCAAGTC 279

QY 184 ctgggactgtacaacactctgaacctgaacctctgctcgcctgtcgtcggtgccccag 243
|||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 278 CTGGCCCTGTACACACGAGCATCAACNCGCNGTGGCGGCGCGTGTCTGCGCGAG 219

QY 244 gacctggagccctgacctctgtactatgttggaggaccacccacaaagtggagcagctc 303
|||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 218 GCCTGGAGCGCTGCCATCGTGTACTAG-TGGCGCGAAGCCCAAGGTGGACACCTG 160

QY 304 tccaacatggtggaagtgtttgtaaatgtagtga 339
|||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 159 TCAACATGATCGTGGCTCCTGCAAGTGCAGCTGA 124
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RESULT 90
 LOCUS

AW600942 259 bp mRNA EST 23-MAR-2000
 RC1-BN0014-210100-012-d10_1 BN0014 Homo sapiens cDNA, mRNA

DEFINITION

sequence.

ACCESSION

AW600942

VERSION

AW600942.1 GI:7305681

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 259)
 HCGP http://www.ludwig.org.br/ORESTES.
 The FAPESP/LICR Human Cancer Genome Project
 Unpublished (1999)
 Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC1&t2=RC1-BN0014-
 210100-012-d10_1&t3=2000-01-21&t4=1)

Seq primer: puc 18 forward

High quality sequence stop: 258.

FEATURES

source

```

Location/Qualifiers
1. .259
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="BN0014"
/dev_stage="Adult"
/note="Organ: breast_normal; Vector: puc18; Site_1: SmaI;  

Site_2: SmaI; A mini-library was made by cloning products  

derived from ORESTES PCR (U.S. Letters Patent application  

No. 196,716 - Ludwig Institute for Cancer Research)  

profiles into the puc 18 vector. Reverse transcription of  

tissue mRNA and cDNA amplification were performed under  

low stringency conditions."
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BASE COUNT
 ORIGIN

```

69 a 48 c 62 g 80 t
Query Match 36.0%; Score 122; DB 118; Length 259;
Best Local Similarity 72.5%; Pred. No. 2.7e-24;
Matches 158; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 122 ccaacttctgcagcccttgccatccctcgcagtcgacacacacccacagcacg 181
|||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 222 CCAACTTCTGCTGGAGCATGCCGCTATTATTGGAGTTCAGACACTCAGACAGCAGGG 163

QY 182 tgcgtggactgtacaacactctgaacctctgtactatgttggaggaccacccacaaagtggagcagc 301
|||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 162 TCCTGAGCTTATATAATACCAATAATCCAGAACGATCTGCTTCTCCTTCTGCTGCC 103

QY 242 aggacctggagccctgaccctctgtactatgttggaggaccacccacaaagtggagcagc 301
|||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 102 AAGATTAGAACCTCTAACCATCTCTACTACTATTGGCAAAACACCCACAGATTGAACAGC 43

QY 302 tctcaacatggtggaagtgtttgtaaatgtagtga 339
|||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 42 TTCTAATATGTTGTTAAAGTCTTGCAAAATGCAGCTAA 5
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RESULT 91
 LOCUS

AI689283 288 bp mRNA EST 16-DEC-1999
 tx93b05.x1 NCI-CGAP_Ut4 Homo sapiens cDNA clone IMAGE:2277105 3'

DEFINITION
 similar to gb:X02812_cds1 TRANSFORMING GROWTH FACTOR BETA 1
 PRECURSOR (HUMAN); contains PTRS.t3 PTR5 repetitive element ;, mRNA

sequence.

ACCESSION

AI689283

VERSION

AI689283.1 GI:4900577

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 288)
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Email: csapbs-r@mail.nih.gov
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
 Emmert-Buck, M.D., Ph.D.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be

derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

```

BASE COUNT      36 a   53 c   45 g   41 t
ORIGIN

Query Match      33.0%; Score 112; DB 164; Length 175;
Best Local Similarity 100.0%; Pred. No. 1.7e-21;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gcttggacacaaattactctccgaacttggagagaaactgtgtgccccctc 60
|||||
Db 136 GCTTTGGACACCAATTACTTCTCCCACTTGGAGGAGAACTGCTGTGGCCGCCCTC 77
|||||

QY 61 tacattgactccgacagatctggctggaagtgggtccatgaacctaaag 112
|||||
Db 76 TACATTGACTCCGACAGGATCTGGCTGGAGTGGGTCCATGACCTAAGG 25
|||||

RESULT 96
BF901708      255 bp      mRNA      EST      18-JAN-2001
LOCUS      CM2-MT0190-091200-585-a10 MT0190 Homo sapiens cDNA, mRNA sequence.
DEFINITION      BF901708
ACCESSION      BF901708
VERSION      BF901708.1 GI:12293167
KEYWORDS      EST.
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
,M.J., Soares,F., Brenclani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?ti=CM2&t2=CM2-MT0190-
091200-585-a10&t3=2000-12-09&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 7
High quality sequence stop: 234.
FEATURES
Location/Qualifiers
1..255
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="MT0190"
/dev_stage="Adult"
/Note="Organ: marrow; Vector: puc18; Site_1: SmaI; Site_2:
SmaI; A mini-library was made by cloning products derived
from ORESTES PCR (U.S. Letters Patent application No. 196
,716 - Ludwig Institute for Cancer Research) profiles
into the pUC 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."
BASE COUNT      47 a   72 c   85 g   51 t
ORIGIN

```

ORIGIN

Query Match 33.0%; Score 112; DB 171; Length 255;
Best Local Similarity 72.1%; Pred. No. 1.8e-21;
Matches 173; Conservative 0; Mismatches 65; Indels 2; Gaps 2;

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QY 1 gcttggacacaaattactctccgaacttggagagaaactgtgtgccccctc 60
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Db 239 GCATTGGACACCAACTATTCTTCAGTTCCACGGAGAAAGAACTGCTGCTGCGCAGCTG 180
|||||

QY 61 tacattgactccgacagatctggctggaagtgggtccatgaacctaaagggctactat 120
|||||
Db 179 TACATTGACTTCCGCAAGGACCCCGCTGGAGTGGATCCACGAGCCCAAGGGCTACCAT 120
|||||

QY 121 gccaaactcttg-ctcagggcccttgcctacatccctccgagtcgagacacacacacagcac 179
|||||
Db 119 GCCAACTTCTGCTCGGGCCCTGCCCATACATTTTGAGCGCTGTACACGAGTACAG-AA 61
|||||

QY 180 ggtgtgggactgtacacactctgaacctctgaagcatctgcctcgtctgtgctgctgccc 239
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Db 60 GGTCTTGGGCTGTACAACACGACCAACCCGGCGCTACGGCGCGCTGCTCGCGGCC 1
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RESULT 97

AA927529/c
LOCUS AA927529 428 bp mRNA EST 17-JUN-1998
DEFINITION om71a11.s1 NCI-CGAP.GC4 Homo sapiens cDNA clone IMAGE:1552604 3' similar to gb:X02812_cds1 TRANSFORMING GROWTH FACTOR BETA 1
PRECUSOR (HUMAN);, mRNA sequence.

ACCESSION

AA927529
VERSION AA927529.1 GI:3076426
KEYWORDS EST.
SOURCE human.

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 428)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

JOURNAL

Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael Emmert-Buck, M.D., Ph.D.

COMMENT

cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Sequencing by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 501 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 141.

FEATURES

Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1552604"
/clone_lib="NCI-CGAP.GC4"
/tissue_type="pooled germ cell tumors"
/lab_host="DH10B"
/Note="Vector: pT73D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from 3 pooled germ cell tumors, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo."
74 a 118 c 154 g 82 t

BASE COUNT

ORIGIN

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Query Match          32.7%; Score 111; DB 13; Length 428;
Best Local Similarity 66.8%; Pred. No. 3.9e-21;
Matches 189; Conservative 0; Mismatches 90; Indels 4; Gaps 2;

QY 58 ctctacattgacttcgcacagatctggctggaagtgg-gtccatgaacctaaaggcta 116
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 424 CTGTACATTGACTTCGCAAGGACCTCGGCTGGAAGTGGATTCCAGCTAGCCAAGGGTA 365
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 117 ctatgcacacttctgcagccctgcccatacctccagtcagacagacacacacag 176
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 364 CCATGCCCAACTCTTGCTTCGCGCGTCCCTTACATTTGGAGCCTGGACAGCAGTACAT 305
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 177 cagcgtgctgggactgtacaaactctgaacctgaagcatctgcctcgcttgcgtg 236
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 304 CAAGGTCTTGCCCTGTACAACAGCATATTACCCGCGCTCGCGCGCGTGTGCGTG- 244
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 237 gcccaggacctggagccctgacctctgtactatgtttgggagaccccccaagtgg 296
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 245 --CGAGGCGCTGGAGCGCTGCCATCGTACTACGTGTGCGGAGCCCAAGGTGGA 188
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 297 gcagctctccaacatggtgtgaagtctgtgaaatgactga 339
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 187 GCAGCTGTCCAACATGATCGTGGCTCTCTGCAAGTGCAGCTGA 145

RESULT 98
AW579188/c
LOCUS          AW579188      248 bp      mRNA      EST      16-MAR-2000
DEFINITION    RC1-DT0028-130100-011-h01_1 DT0028 Homo sapiens cDNA, mRNA
sequence.
ACCESSION     AW579188
VERSION       AW579188.1 GI:7254237
KEYWORDS      EST.
SOURCE        human.
ORGANISM      Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE     1 (bases 1 to 248)
AUTHORS       HCGP http://www.ludwig.org.br/ORESTES.
TITLE         The FAPESP/LICR Human Cancer Genome Project
JOURNAL       Unpublished (1999)
COMMENT       Contact: Simpson A.J.G.
               Laboratory of Cancer Genetics
               Ludwig Institute for Cancer Research
               Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
               Brazil
               Tel: +55-11-2704922
               Fax: +55-11-2707001
               Email: asimpson@ludwig.org.br
               This sequence was derived from the FAPESP/LICR Human Cancer Genome
               Project. This entry can be seen in the following URL
               (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC1&t2=RC1-DT0028-
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               Seq primer: puc 18 forward
               High quality sequence stop: 206.
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                   /organism="Homo sapiens"
                   /db_xref="taxon:9606"
                   /clone_lib="DT0028"
                   /dev_stage="Adult"
                   /note="Organ: denis_drash; Vector: puc18; Site_1: SmaI;
                   Site_2: SmaI; A mini-library was made by cloning products
                   derived from ORESTES PCR (U.S. Letters Patent application
                   No. 196,716 - Ludwig Institute for Cancer Research)
                   profiles into the pUC 18 vector. Reverse transcription of
                   tissue mRNA and cDNA amplification were performed under
                   low stringency conditions."
BASE COUNT    65 a 49 c 58 g 76 t
ORIGIN
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Query Match          32.6%; Score 110.4; DB 118; Length 248;
Best Local Similarity 69.4%; Pred. No. 5.2e-21;
Matches 150; Conservative 0; Mismatches 66; Indels 0; Gaps 0;

QY 124 aacttctgctcagcccttgcccatacctgcgcagtcgacacacacacacacagcggtg 183
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DB 220 AACATCAGAGCTGGAGCATGCCGTATTATTATGGAGTTCAGACACTCAGCACAGGGTTC 161
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 184 ctgggactgtacaacactctgaacctgaacatctgcctgccttgcctgctgcctgcag 243
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 160 CTGAGCTTTATTATTACCATTAAGTCTCTGAAGCACTGCTTCTCTCTGCTGCGGGTCCCAA 101
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 244 gacctgagccctgagccatctgactatgttgggagagaccccccaagtgagcagctc 303
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 100 GATTTAGAACCTCTAACCATTTCTTACTACATTGGCATTACACCAAGATTGAACAGCTT 41
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 304 tccaacatggtggtggaagctctgttaaatgtagctga 339
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DB 40 TCTTATATGATTGTAAAGTCTTGTCAAATGCAGCTAA 5

RESULT 99
AW600960/c
LOCUS          AW600960      266 bp      mRNA      EST      23-MAR-2000
DEFINITION    RC1-BN0014-210100-012-h01_1 BN0014 Homo sapiens cDNA, mRNA
sequence.
ACCESSION     AW600960
VERSION       AW600960.1 GI:7305699
KEYWORDS      EST.
SOURCE        human.
ORGANISM      Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE     1 (bases 1 to 266)
AUTHORS       HCGP http://www.ludwig.org.br/ORESTES.
TITLE         The FAPESP/LICR Human Cancer Genome Project
JOURNAL       Unpublished (1999)
COMMENT       Contact: Simpson A.J.G.
               Laboratory of Cancer Genetics
               Ludwig Institute for Cancer Research
               Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
               Brazil
               Tel: +55-11-2704922
               Fax: +55-11-2707001
               Email: asimpson@ludwig.org.br
               This sequence was derived from the FAPESP/LICR Human Cancer Genome
               Project. This entry can be seen in the following URL
               (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC1&t2=RC1-BN0014-
               210100-012-h01_1&t3=2000-01-21&t4=1)
               Seq primer: puc 18 forward
               High quality sequence stop: 218.
               Location/Qualifiers
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                   /db_xref="taxon:9606"
                   /clone_lib="BN0014"
                   /dev_stage="Adult"
                   /note="Organ: breast_normal; Vector: puc18; Site_1: SmaI;
                   Site_2: SmaI; A mini-library was made by cloning products
                   derived from ORESTES PCR (U.S. Letters Patent application
                   No. 196,716 - Ludwig Institute for Cancer Research)
                   profiles into the pUC 18 vector. Reverse transcription of
                   tissue mRNA and cDNA amplification were performed under
                   low stringency conditions."
BASE COUNT    72 a 51 c 59 g 84 t
ORIGIN
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Query Match          32.4%; Score 110; DB 118; Length 266;
Best Local Similarity 72.2%; Pred. No. 6.9e-21;
Matches 143; Conservative 0; Mismatches 55; Indels 0; Gaps 0;
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GenCore version 4.5
 Copyright (c) 1993 - 2000 CompuGen Ltd.
 OM protein - protein search, using sw model
 Run on: October 30, 2001, 08:48:51 ; Search time 17.46 Seconds
 (without alignments)
 392.355 Million cell updates/sec

Title: TGFB3P
 Perfect score: 634
 Sequence: 1 ALDNYCFRNLNCCVRPL.....RTPKVEQLSNVMVKCKCSX 113

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000
 Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	ID	Description
1	633	99.8	112 12 AAR12404	Transforming Growth
2	633	99.8	112 14 AAR39640	Mature human Trans
3	633	99.8	112 17 AAR92772	Human TGF-beta 3.
4	633	99.8	112 17 AAR91958	Human transforming
5	633	99.8	112 18 AAW26173	Mature transformin
6	633	99.8	112 18 AAW08175	TGF active fragmen
7	633	99.8	112 20 AAY08301	Human growth facto
8	633	99.8	112 20 AAW97093	The mature form of
9	633	99.8	112 20 AAW84209	Transforming growt
10	633	99.8	112 21 AAY92012	Human transforming
11	633	99.8	112 22 AAB35939	TGF-beta 3 amino a

12	633	99.8	115	22	AAB73206	TGF-beta3 C-termin
13	633	99.8	202	11	AAR06548	Protein with tumou
14	633	99.8	412	13	AAR20621	Transforming Growt
15	633	99.8	412	16	AAR73598	Human TGF-beta 3 p
16	633	99.8	412	19	AAW80417	Amino acid sequenc
17	630	99.4	112	19	AAW78782	Human transforming
18	630	99.4	204	15	AAR46229	Human TGF-beta-3.
19	630	99.4	204	19	AAW78787	Human transforming
20	630	99.4	457	11	AAR04080	Polyptide sequen
21	627	98.9	413	13	AAR22038	Mutant transformin
22	621	97.9	112	11	AAR04078	Sequence of porcin
23	621	97.9	112	19	AAW78783	Pig transforming g
24	621	97.9	456	15	AAR46228	Pig TGF-beta-3. S
25	621	97.9	456	19	AAW78786	Pig transforming g
26	620	97.8	112	17	AAR86770	Tissue-derived tum
27	620	97.8	165	17	AAR86771	Tissue-derived tum
28	617	97.3	412	11	AAR08264	Tumour growth inhi
29	612	96.5	112	11	AAR04077	Sequence of human
30	595	93.8	112	14	AAR39642	Transforming Growt
31	595	93.8	112	17	AAR92775	Hybrid TGF-beta 1-
32	595	93.8	112	17	AAR91959	Human TGF-beta-lik
33	591	93.2	112	14	AAR39644	Transforming Growt
34	591	93.2	112	17	AAR91960	Human TGF-beta-lik
35	591	93.2	112	17	AAR92776	Hybrid TGF-beta 2-
36	577	91.0	112	14	AAR39646	Transforming Growt
37	577	91.0	112	17	AAR91961	Human TGF-beta-lik
38	577	91.0	112	17	AAR92777	Hybrid TGF-beta 3-
39	555	87.5	98	12	AAR11944	Truncated TGF-beta
40	555	87.5	98	20	AAY16699	WO9914235 Seq ID N
41	555	87.5	98	21	AAB09521	Human TGF-beta 3,
42	555	87.5	98	21	AAB02787	Human TGF-beta3 am
43	555	87.5	98	21	AAY92556	TGF-beta 3 finger-
44	539	85.0	112	14	AAR39641	Transforming Growt
45	538	84.9	112	14	AAR39645	Transforming Growt
46	535	84.4	112	9	AAP80462	Sequence from whic
47	535	84.4	112	12	AAR12403	Transforming Growt
48	535	84.4	112	14	AAR39639	Mature human Trans
49	535	84.4	112	17	AAR92774	Human TGF-beta 2.
50	535	84.4	112	17	AAR91957	Human transforming
51	535	84.4	112	18	AAW08174	TGF active fragmen
52	535	84.4	112	20	AAY08300	Human growth facto
53	535	84.4	112	20	AAW97092	The mature form of
54	535	84.4	112	20	AAW84208	Transforming growt
55	535	84.4	112	21	AAY92011	Human transforming
56	535	84.4	112	22	AAB35938	TGF-beta 2 amino a
57	535	84.4	115	22	AAB73205	TGF-beta2 C-termin
58	535	84.4	390	13	AAR20126	Sequence of hybrid
59	535	84.4	414	16	AAR83055	Transforming growt
60	535	84.4	414	16	AAR73597	Human TGF-beta 2 p
61	535	84.4	442	10	AAP91899	Sequence encoded b
62	535	84.4	442	11	AAR05748	Human TGF-Beta2-44
63	535	84.4	442	13	AAR20125	Sequence of human
64	535	84.4	442	16	AAR79922	Human transforming
65	533	84.1	391	10	AAP91900	Sequence encoded b
66	532	83.9	390	11	AAR05665	Human Transforming
67	532	83.9	390	11	AAR05666	Hybrid transformin
68	532	83.9	390	11	AAR05749	Human TGF-Beta2 ex
69	513	80.9	390	13	AAR27522	TGF-beta 1/beta 2
70	507	80.0	389	16	AAR79921	Simian-human hybri
71	503	79.3	390	11	AAR05492	Chimeric simian TG
72	500	78.9	112	11	AAR04076	Sequence of mature
73	500	78.9	112	11	AAR08142	Platelet-derived h
74	500	78.9	112	13	AAR22134	PDGF subunit a. H
75	500	78.9	112	14	AAR43263	TGF-beta. Homo sa
76	500	78.9	112	14	AAR42311	Recombinant human
77	500	78.9	112	17	AAR92773	Human TGF-beta 1.
78	500	78.9	112	17	AAR91956	Human transforming
79	500	78.9	112	19	AAW08173	TGF-beta1 active f
80	500	78.9	112	19	AAW78781	Human transforming
81	500	78.9	112	20	AAY08299	Human growth facto
82	500	78.9	112	20	AAW97091	The mature form of
83	500	78.9	112	20	AAW84207	Transforming growt
84	500	78.9	112	21	AAY92010	Human transforming

85 500 78.9 112 21 AAY67950 Human transforming
 86 500 78.9 112 22 AAB35937 TGF-beta 1 amino a
 87 500 78.9 115 22 AAB73204 TGF-beta1 C-termin
 88 500 78.9 118 18 AAW08176 TGF-beta fusion pr
 89 500 78.9 122 18 AAW08181 TGF-beta fusion pr
 90 500 78.9 124 18 AAW08177 TGF-beta fusion pr
 91 500 78.9 128 18 AAW08188 TGF-beta fusion pr
 92 500 78.9 130 18 AAW08185 TGF-beta fusion pr
 93 500 78.9 131 18 AAW08182 TGF-beta fusion pr
 94 500 78.9 132 18 AAW08189 TGF-beta fusion pr
 95 500 78.9 133 18 AAW08178 TGF-beta fusion pr
 96 500 78.9 134 18 AAW08187 TGF-beta fusion pr
 97 500 78.9 134 18 AAW08190 TGF-beta fusion pr
 98 500 78.9 135 18 AAW08183 TGF-beta fusion pr
 99 500 78.9 136 18 AAW08186 TGF-beta fusion pr
 100 500 78.9 137 18 AAW08180 TGF-beta fusion pr

ALIGNMENTS

RESULT 1

AAR12404
 ID AAR12404 standard; Protein; 112 AA.

XX AC AAR12404;

DT 29-AUG-1991 (first entry)

XX DE Transforming Growth Factor beta 3.

XX KW TGF-beta3; biologically active protein production.

XX OS Homo sapiens.

XX PN EP433225-A.

XX PD 19-JUN-1991.

XX PF 27-NOV-1990; 90EP-0810922.

XX PR 06-DEC-1989; 89GB-0027546.

XX PA (CIBA) CIBA GEIGY AG.

XX PI Cerletti N, McMaster GK, Cox D, Schmitz A, Meyhack B;

XX DR WPI; 1991-180005/25.

XX DR N-PSDB; AAQ11995.

XX PT Prodn. of Transforming Growth Factor type-beta-like proteins - by
 PT subjecting denatured monomeric form to refolding conditions

XX PS Example; Page 27; 35pp; English.

XX CC The TGF-beta3 coding sequence was isolated from the CI-215 human
 CC glioma cell line. It was incorporated into an appropriate vector to
 CC transform Saccharomyces cerevisiae or E.coli. Monomeric TGF-beta1
 CC was purified, denatured and dissolved in 140ml 50mM Tris/HCl pH8. 1M
 CC NaCl, 5mM EDTA, 2mM reduced glutathione, 1mM oxidised glutathione
 CC and 33mM Chaps. After 72 hrs at 4 deg C, pH was adjusted to 2.5 and
 CC the mixture was conc. 10 times. The conc. soln was diluted to the
 CC original vol. with 10mM HCl and conc to a final vol of 10 ml. The
 CC supernatant from centrifugation at 5000g for 30 min contained
 CC disulphide-linked dimeric TGF-beta3.

XX SQ Sequence 112 AA;

Query Match 99.8%; Score 633; DB 12; Length 112;
 Best Local Similarity 100.0%; Pred. No. 1.6e-56;
 Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALDTNYCFRNLEBNCVRLYIDFRQDLGKWWHEPKGYGVANFCGPGPYLRSADTTHST 60
 Db |||||
 QY 61 VLGLYNTLNPEASASPCCVPODLEPLTILYVGRTPKVEQLSNMVKSCKCS 112
 Db |||||

RESULT 2

AAR39640
 ID AAR39640 standard; Protein; 112 AA.

XX AC AAR39640;

DT 26-AUG-1993 (first entry)

XX DE Mature human Transforming Growth Factor-beta3.

XX KW hTGF-beta3; hybrid protein; wound healing; cancer treatment;
 KW bone repair; growth regulation.

XX OS Homo sapiens.

XX PN EP542679-A.

XX PD 19-MAY-1993.

XX PF 03-NOV-1992; 92EP-0810845.

XX PR 11-NOV-1991; 91EP-0810870.

XX PA (CIBA) CIBA GEIGY AG.

XX PI McMaster GK, Cox D, Cerletti N, Kuhla J;

XX DR WPI; 1993-161126/20.

XX DR N-PSDB; AAQ41601.

XX PT New hybrid transforming growth factor-beta molecules - comprise
 PT portions of mature TGF-beta isoforms; useful as wound healants,
 PT cardioprotective, antiinflammatory and immunosuppressive agents etc.

XX PS Claim 4; Page 24; 48pp; English.

XX CC The invention covers hybrid TGF-beta molecules consisting of parts
 CC of the human isoforms TGF-beta1, TGF-beta2 and TGF-beta3 (see AAQ41599,
 CC AAQ41600 and AAQ41601, respectively). The hinge points between parts
 CC derived from different parent isoforms are pref. between amino acids
 CC 44 and 45, 56 and 57, 79 and 80, 90 and 91, or 22 and 23. The hybrid
 CC molecules promote cell migration, inhibit the growth of A375
 CC melanoma cells, accelerate the healing of partial-thickness burn
 CC wounds and full-thickness incisional wounds and increase formation
 CC of fibrous granular tissue. See e.g. AAQ41602-Q41607 for pref. hybrids.

XX SQ Sequence 112 AA;

Query Match 99.8%; Score 633; DB 14; Length 112;
 Best Local Similarity 100.0%; Pred. No. 1.6e-56;
 Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALDTNYCFRNLEBNCVRLYIDFRQDLGKWWHEPKGYGVANFCGPGPYLRSADTTHST 60
 Db |||||
 QY 61 VLGLYNTLNPEASASPCCVPODLEPLTILYVGRTPKVEQLSNMVKSCKCS 112
 Db |||||

RESULT 3

AAR92772

```

ID  AAR92772 standard; Protein; 112 AA.
XX
AC  AAR92772;
XX
DT  17-JUL-1996 (first entry)
XX
DE  Human TGF-beta 3.
XX
KW  Transforming growth factor type beta; TGF-beta 3;
KW  protein renaturation; protein folding.
XX
OS  Homo sapiens.
XX
PN  WO96034332-AL.
XX
PD  08-FEB-1996.
XX
PF  12-JUL-1995; 95WO-EP02719.
XX
PR  25-JUL-1994; 94EP-0810439.
XX
PA  (CIBA ) CIBA GEIGY AG.
XX
PI  Cerletti N;
XX
DR  N-PSDB; AAT17234.
XX
PT  Prodn. of dimeric biologically active transforming growth factor
PT  by refolding denatured monomer in detergent-free folding buffer
PT  contg. specific organic solvent to improve yield
XX
PS  Example 1B; Page 34; 54pp; English.
XX
CC  Non-soluble, monomeric transforming growth factor TGF-beta 3
CC  (AAR92772) was recovered from E. coli LC 137 (DSM 5658) transformants
CC  carrying plasmid pPLMu.TGF-beta 3, which includes the coding
CC  sequence (AAT17234) for TGF-beta 3. A biologically active, dimeric
CC  form of TGF-beta 3 was obtd. by refolding this monomer in detergent-
CC  free buffer contg. DMSO and/or DMF. Dimers of TGF-beta 1 (AAR92773)
CC  and TGF-beta 2 (AAR92774), and hybrid dimers (see also AAR92775-77),
CC  were also produced.
XX
SQ  Sequence 112 AA;

Query Match 99.8%; Score 633; DB 17; Length 112;
Best Local Similarity 100.0%; Pred. No. 1.6e-56;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 ALDTNYCFRNLENCVVRPLYIDFRQDLGWKWHPEKGYVANFCSGPCPYLRSADTTHST 60
DB  1 aldtncfrnleencvvrplyidfrqdlgwkwvhepkgyvanfcsgpcpylrsadtthst 60

QY  61 VLGLYNTLNPEASASPCCPVQDLEPLTILYVGRTPKVEQLSNMVKSCKS 112
DB  61 vlglntlnpeasaspcpcvpqdlepltilyyvgrtpkveqlsnmvkscks 112

RESULT 4
AAR91958
ID  AAR91958 standard; Protein; 112 AA.
XX
AC  AAR91958;
XX
DT  10-JUN-1996 (first entry)
XX
DE  Human transforming growth factor beta 3.
XX
KW  Transforming growth factor beta; TGF; regulator; method;
KW  proliferation; differentiation; wound healing; solvent.
XX
OS  Homo sapiens.

```

```

XX  WO96034332-AL.
XX  08-FEB-1996.
XX  12-JUL-1995; 95WO-EP02718.
XX  25-JUL-1994; 94EP-0810438.
XX  (CIBA ) CIBA GEIGY AG.
XX  Cerletti N;
XX  WPI; 1996-116999/12.
XX  N-PSDB; AAT15464.
XX  Prodn. of dimeric, biologically active transforming growth factor
XX  beta - by refolding denatured monomer in buffer contg. mild
XX  detergent and specific organic solvents to improve yields
XX  Claim 17; Page 38; 59pp; English.
XX  AAR91956-B91958 are the amino acid sequences of human transforming
XX  growth factor (TGF) beta-1, TGF beta-2 and TGF beta-3 which are used to
XX  produce TGF beta-like proteins in dimeric form. The TGF beta-like
XX  proteins produced are hybrids of 2 different types of TGF beta e.g.
XX  TGF beta-1-3, TGF beta-2-3, etc, or bone morphogenic proteins e.g.
XX  BMP-2. The TGF beta hybrids were made using a new process of producing
XX  dimeric, biologically active TGF beta-like proteins. The new process
XX  involves treating denatured TGF beta monomers with folding buffer contg.
XX  a mild detergent (CHAPS, CHAPSO or digitonin) and at least one of the
XX  solvents DMSO (dimethyl sulphoxide), DMSO2 (dimethylsulphone) and DMF
XX  (dimethyl formamide). The detergent allows folding of the monomer such
XX  that, after dimerisation, the TGF beta-like protein retains biological
XX  activity and remains in soluble form. The method allows relatively high
XX  yields of biologically active TGF beta-like proteins in their native
XX  dimeric form. TGF-beta like proteins are multifunctional regulators of
XX  cellular activity and a typical use is to stimulate wound healing.
XX  Sequence 112 AA;

Query Match 99.8%; Score 633; DB 17; Length 112;
Best Local Similarity 100.0%; Pred. No. 1.6e-56;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 ALDTNYCFRNLENCVVRPLYIDFRQDLGWKWHPEKGYVANFCSGPCPYLRSADTTHST 60
DB  1 aldtncfrnleencvvrplyidfrqdlgwkwvhepkgyvanfcsgpcpylrsadtthst 60

QY  61 VLGLYNTLNPEASASPCCPVQDLEPLTILYVGRTPKVEQLSNMVKSCKS 112
DB  61 vlglntlnpeasaspcpcvpqdlepltilyyvgrtpkveqlsnmvkscks 112

RESULT 5
AAR926173
ID  AAR926173 standard; Protein; 112 AA.
XX
AC  AAR926173;
XX
DT  28-NOV-1997 (first entry)
XX
DE  Mature transforming growth factor beta3.
XX
KW  Transforming growth factor beta3; TGF-beta3; human; mature protein;
KW  acid-stable; heat-stable; homodimer; mitogenesis; cell proliferation;
KW  cell growth; wound; oral mucositis; intestinal mucositis; osteoarthritis;
KW  bone disease; bone repair; therapy.
XX
OS  Homo sapiens.
XX
PN  WO9705166-AL.

```


PT tag and a bone morphogenetic active fragment, used for enhancing
 XX wound healing or bone growth
 XX
 PS Disclosure; Page 43-44; 64pp; English.
 XX
 CC The present sequence represents a transforming growth factor beta active
 CC fragment. The protein can be used in place of a bone morphogenetic
 CC active fragment to create the fusion proteins of the invention. When a
 CC bone morphogenetic active fragment is used, the fusion proteins are
 CC designated bone morphogenetic fusion proteins. The bone morphogenetic
 CC fusion protein may contain some or all of the following elements: a
 CC purification tag, a proteinase site, an ECM/bone binding site, a second
 CC proteinase site, and a bone morphogenetic protein active fragment.
 CC The bone morphogenetic fusion proteins can be used for enhancing wound
 CC healing or bone growth.
 XX
 SQ Sequence 112 AA;

Query Match 99.8%; Score 633; DB 20; Length 112;
 Best Local Similarity 100.0%; Pred. No. 1.6e-56;
 Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALDTNCFRNLENCVRLPYIDFRQDLGWKWHPEKGYANFCGCPYLRSADTTHT 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1 aldtncfrnleencvrrplyidfrqdlgwkwhepkgyanfcsgpcpylrsadtthst 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||

QY 61 VLGLYNTLNPEASAPCCVPQDLEPLTILYVGRTPKVEQLSNMVVKSCKS 112
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 61 vlglyntlnpeasapccvpqdleptililyvgrtpkveqlsnmvvksckscs 112
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||

RESULT 10
 AAY92012
 ID AAY92012 standard; Protein; 112 AA.
 XX
 AC AAY92012;
 XX
 DT 19-JUL-2000 (first entry)
 XX
 DE Human transforming growth factor beta 3 monomer.
 XX
 KW human transforming growth factor beta 3 monomer; CKGF; mutant;
 KW cystine knot growth factor; hairpin loop; infertility.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 1..20
 FT /note= "optionally mutated to increase electrostatic
 FT interaction between beta hairpin structure and
 FT a receptor"
 FT
 FT Domain 21..40
 FT /label= beta_hairpin_loop_1
 FT /note= "mutant optionally comprises one or more
 FT substitutions in these residues"
 FT
 FT Misc-difference 41..81
 FT /note= "optionally mutated to increase electrostatic
 FT interaction between beta hairpin structure and
 FT a receptor"
 FT
 FT Domain 82..102
 FT /label= beta_hairpin_loop_3
 FT /note= "mutant optionally comprises one or more
 FT substitutions in these residues"
 FT
 FT Misc-difference 103..112
 FT /note= "optionally mutated to increase electrostatic
 FT interaction between beta hairpin structure and
 FT a receptor"
 FT
 XX WO200017360-A1.
 XX 30-MAR-2000.
 PD
 XX

PF 19-MAR-1999; 99WO-US05908.
 XX
 PR 22-SEP-1998; 98WO-US19772.
 XX
 PA (UYMA-) UNIV MARYLAND BALTIMORE.
 XX
 PI Weintraub BD, Szkudlinski MW;
 XX
 DR WPI; 2000-283585/24.
 XX
 CC New mutant cystine knot growth factor proteins comprising one or more
 CC mutant subunits, useful for treating or preventing diseases e.g.
 CC hypothyroidism and thyroid cancer
 XX
 PS Claim 223; Page 301; 320pp; English.
 XX
 CC This is the wild type human transforming growth factor beta 3 monomer.
 CC Mutants comprise at least one electrostatic charge altering mutation in a
 CC beta hairpin loop, resulting in increased bioactivity.
 CC Mutant cystine knot growth factor (CKGF) proteins comprising one or more
 CC mutant subunits and having novel properties or improved pharmacological
 CC properties, compared to wild type CKGFs, are claimed. The CKGF
 CC superfamily comprises at least four families of growth factors: the
 CC glycoprotein hormones, the platelet-derived growth factor (PDGF) family,
 CC the neurotrophins and the transforming growth factor-beta family; the
 CC families are known to be structurally similar (especially comprising the
 CC cystine knot topology) and it was shown that mutations at certain
 CC positions in the CKGF hairpin loops of family members and other members
 CC of the CKGF superfamily could significantly alter the biological
 CC activities of the CKGF.
 CC Mutant transforming growth factor family proteins or analogues are useful
 CC for treatment of ovulatory dysfunction, luteal phase defect, unexplained
 CC infertility, time-limited conception and in assisted reproduction.
 XX
 SQ Sequence 112 AA;

Query Match 99.8%; Score 633; DB 21; Length 112;
 Best Local Similarity 100.0%; Pred. No. 1.6e-56;
 Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALDTNCFRNLENCVRLPYIDFRQDLGWKWHPEKGYANFCGCPYLRSADTTHT 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1 aldtncfrnleencvrrplyidfrqdlgwkwhepkgyanfcsgpcpylrsadtthst 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||

QY 61 VLGLYNTLNPEASAPCCVPQDLEPLTILYVGRTPKVEQLSNMVVKSCKS 112
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 61 vlglyntlnpeasapccvpqdleptililyvgrtpkveqlsnmvvksckscs 112
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||

RESULT 11
 AAB35939
 ID AAB35939 standard; protein; 112 AA.
 XX
 AC AAB35939;
 XX
 DT 26-FEB-2001 (first entry)
 XX
 DE TGF-beta 3 amino acid sequence.
 XX
 KW Heparin binding; vascular graft; matrix; cell adhesion; growth factor;
 KW wound healing; dermal wound; wound healing; TGF-beta 3.
 XX
 OS Unidentified.
 XX
 PN WO200064481-A1.
 XX
 PD 02-NOV-2000.
 XX
 PF 22-APR-1999; 99WO-IB00800.
 XX
 PR 22-APR-1999; 99WO-IB00800.
 XX

PT Tissue-derived tumour growth inhibitors - used in diagnosis and
 PT treatment of tumours and treatment of proliferative type
 XX disorders, burns and wounds

PS Disclosure; Fig 27; 81pp; English.

XX Gene product may be used to inhibit growth of tumour cells, to
 CC treat proliferative type disorders, burns and other wounds, and may
 CC also be used as an immune modulator. Detection of proteins and of
 CC TGF-alpha can indicate presence of a tumour.
 CC Proteins may be produced from a bacterial or eukaryotic expression
 CC system.

XX Sequence 202 AA;

Query Match 99.8%; Score 633; DB 11; Length 202;
 Best Local Similarity 100.0%; Pred. No. 3.1e-56;
 Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALDTNVCFRNLENCVRLYIDFRDLGKWKVHEPKGYANFCSGPCPYLRSADTTHST 60
 |||||
 Db 91 aldtncfrnleencvrrplyidfrdglgkwkwhpkgyanfcsgpcpylrsadtthst 150
 |||||
 QY 61 VLGLYNTLNPEASAPCCVPQDLEPLTILYVGRTPKVEQLSNMVKCKCS 112
 |||||
 Db 151 vlglyntlnpeasapccvpqdlepltillyvgrtpkveqlsnmvkcskcs 202
 |||||

RESULT 14

AAR20621
 ID AAR20621 standard; Protein; 412 AA.

XX AAR20621;

DT 05-MAY-1992 (first entry)

XX Transforming Growth Factor beta 3.

XX Human; TGF-beta 3; homodimer; ss.

XX Homo sapiens.

XX Key Location/Qualifiers
 FT Modified-site 74..76
 FT /label= glycosylation
 FT Modified-site 135..137
 FT /label= glycosylation
 FT Modified-site 142..144
 FT /label= glycosylation
 FT Modified-site 158..160
 FT /label= glycosylation

XX W09200318-A.

XX 09-JAN-1992.

XX 25-JUN-1991; 91WO-US04541.

XX 25-JUN-1990; 90US-0543348.

XX (ONCO-) ONCOGENE SCI INC.

XX Iwata KK, Foulkes JG, Tendijke P, Haley JD;

XX WPI: 1992-041510/05.

XX N-PSDB; AAQ20576.

XX Transforming growth factor beta 3 proteins, precursors and
 PT mutants - obtd. from polypeptide and antibodies, with optimal
 PT therapeutic use due to genetic manipulation of coding sequence
 XX Example 2; Fig 1; 107pp; English.

XX

XX

XX

CC The TGF-beta3 gene sequence was obtained from three shorter
 CC overlapping clones derived from human placental, human
 CC umbilical cord and A673 cells cDNA libraries, respectively. The
 CC predicted amino acid sequence of the gene encoding TGF-beta3 shows
 CC extensive homology to TGF-beta 1 and beta 2. Based on the
 CC functional and structural homology, it is likely that TGF-beta 3
 CC has therapeutic activity in cancer therapy, wound healing and
 CC immunosuppression. See also AAQ22229 and AAR20622.

XX Sequence 412 AA;

Query Match 99.8%; Score 633; DB 13; Length 412;
 Best Local Similarity 100.0%; Pred. No. 7e-56;
 Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALDTNVCFRNLENCVRLYIDFRDLGKWKVHEPKGYANFCSGPCPYLRSADTTHST 60
 |||||
 Db 301 aldtncfrnleencvrrplyidfrdglgkwkwhpkgyanfcsgpcpylrsadtthst 360
 |||||
 QY 61 VLGLYNTLNPEASAPCCVPQDLEPLTILYVGRTPKVEQLSNMVKCKCS 112
 |||||
 Db 361 vlglyntlnpeasapccvpqdlepltillyvgrtpkveqlsnmvkcskcs 412
 |||||

RESULT 15

AAR73598

ID AAR73598 standard; Protein; 412 AA.

XX AAR73598;

DT 21-DEC-1995 (first entry)

XX Human TGF-beta 3 protein.

XX Transforming growth factor-beta; Human TGF-beta protein; TGF-beta 1;
 KW TGF-beta 3; osteogenic cell source; OGS; bone deficiency;
 KW bone-inducing cofactor.

XX OS Homo sapiens.

XX PN US5409896-A.

XX PD 25-APR-1995.

XX PF 12-NOV-1993; 93US-0401906.

XX PR 01-SEP-1989; 89US-0401906.

XX PR 12-NOV-1991; 91US-0790856.

XX PR 18-MAY-1993; 93US-0063841.

XX PR 12-NOV-1993; 93US-0132405.

XX PA (GETH) GENENTECH INC.

XX PI Ammann AJ, Rudman CG;

XX WPI: 1995-169610/22.

XX Compsn. for treating skeletal tissue deficiency - comprising

XX transforming growth factor-beta and an osteogenic cell source in a

XX carrier

XX Claim 3; Column 19-22; 19pp; English.

XX This sequence represents human transforming growth factor-beta 3

XX (TGF-beta 1). This sequence and the sequence for human TGF-beta 1 (see

XX AAR73596) are claimed within the scope of the invention. The invention

XX is a composition consisting of a TGF-beta protein and an osteogenic cell

XX source (OCS) formulated in an acceptable carrier other than a bone

XX morphogenic cofactor. This composition can be used for the restoration

XX of bone deficiency. This provides for the generation of mature bone

XX only where it is required, without the inclusion of a specific

CC bone-inducing cofactor. This method can be used with any of the 5 human
 XX TGF-beta's or with TGF-beta from other species.

SQ Sequence 412 AA;

Query Match 99.8%; Score 633; DB 16; Length 412;
 Best Local Similarity 100.0%; Pred. No. 7e-56;
 Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALDTNYCFRNLENCVVRPLYIDFRQDLGKWKVHHPKGYIANFCSGPCPYLRSADTTHST 60
 |||||
 Db 301 aldtncfmrleencvvrplyidfrqdlgwkwhepkgyanfcsgpcpylrsadtthst 360
 |||||
 QY 61 VLGLYNTLNPEASASPCVQDLEPLTILYVGRTPKVEQLSNMVKSKCS 112
 |||||
 Db 361 vlglntlnpeasaspcvqpdleptilyvgrtpkveqlsnmrvksckcs 412
 |||||

RESULT 16

AAW80417
 ID AAW80417 standard; Protein; 412 AA.

AC AAW80417;

DT 14-JAN-1999 (first entry)

XX Amino acid sequence of human transforming growth factor-beta 3.

XX Human transforming growth factor-beta 3; TGF-beta3; oxygen tension;
 KW trophoblast invasion regulation; inhibitor; HIF-1 alpha;
 KW TGF-beta family cytokine receptor; hypoxia inducible factor 1 alpha;
 KW preeclampsia; pregnancy; choriocarcinoma.

XX Homo sapiens.

XX W09840747-A1.

XX 17-SEP-1998.

XX 05-MAR-1998; 98WO-CA00180.

XX 07-MAR-1997; 97US-0039919.

XX (HOSP-) HOSPITAL FOR SICK CHILDREN.
 XX (MOUN) MOUNT SINAI HOSPITAL CORP.

XX Caniggia I, Lye S, Post M;

XX WPI; 1998-520837/44.

XX N-PSDB; AAV63209.

XX Regulation of trophoblast invasion - by, e.g. transforming growth
 PT factor-beta3 inhibitor, useful for detecting or treating
 PT preeclampsia in pregnant women

PS Disclosure; Fig 1; 59pp; English.

XX The present sequence encodes human transforming growth factor-beta 3
 CC (TGF-beta3). The specification describes a composition for regulating
 CC trophoblast invasion which comprises an inhibitor of TGF-beta3,
 CC TGF-beta family cytokine receptors, hypoxia inducible factor 1 alpha
 CC (HIF-1 alpha) or oxygen tension. The composition is used in methods of
 CC diagnosing, monitoring, preventing or treating conditions requiring
 CC regulation of trophoblast invasion, especially preeclampsia in pregnant
 CC women or choriocarcinomas.

XX Sequence 412 AA;

Query Match 99.8%; Score 633; DB 19; Length 412;
 Best Local Similarity 100.0%; Pred. No. 7e-56;
 Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALDTNYCFRNLENCVVRPLYIDFRQDLGKWKVHHPKGYIANFCSGPCPYLRSADTTHST 60
 |||||
 Db 301 aldtncfmrleencvvrplyidfrqdlgwkwhepkgyanfcsgpcpylrsadtthst 360
 |||||
 QY 61 VLGLYNTLNPEASASPCVQDLEPLTILYVGRTPKVEQLSNMVKSKCS 112
 |||||
 Db 361 vlglntlnpeasaspcvqpdleptilyvgrtpkveqlsnmrvksckcs 412
 |||||

RESULT 17

AAW78782
 ID AAW78782 standard; Protein; 112 AA.

XX AAW78782;

XX 21-DEC-1998 (first entry)

XX Human transforming growth factor-beta 3 N-terminal sequence.

XX Transforming growth factor-beta 3; TGF-beta 3; human.

XX Homo sapiens.

XX US5801231-A.

XX 01-SEP-1998.

XX 22-MAR-1985; 85US-0715142.

XX 13-MAR-1987; 87US-0025423.

XX 22-MAR-1985; 85US-0715142.

XX 04-AUG-1989; 89US-0389929.

XX 04-MAR-1992; 92US-0845893.

XX 05-NOV-1993; 93US-0147364.

XX 30-MAY-1995; 95US-0454468.

XX (GETH) GENENTECH INC.

XX Derynck RMA, Goeddel DV;

XX WPI; 1998-494840/42.

XX DNA encoding transforming growth factor-beta precursor sequence -
 PT useful for analysis to perform manipulations to increase yield of
 PT recombinant production of the protein

XX Disclosure; Fig 3; 26pp; English.

XX This is the amino acid sequence of human transforming growth factor
 CC beta-3 (TGF-beta 3, see also AAW78787). The sequence shows homology
 CC to human TGF-beta 1 (see AAW78781), porcine TGF-beta 3 (see AAW78783)
 CC and bovine TGF-beta 2 (see AAW78784) N-terminal sequences. The
 CC invention relates to the recombinant production of TGF-beta. DNA
 CC encoding TGF-beta has been isolated and cloned into vectors which
 CC are replicated in bacteria and expressed in eukaryotic cells.
 CC TGF-beta recovered from transformed cells can be used in known
 CC therapeutic applications.

XX Sequence 112 AA;

Query Match 99.4%; Score 630; DB 19; Length 112;
 Best Local Similarity 99.1%; Pred. No. 3.2e-56;
 Matches 111; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALDTNYCFRNLENCVVRPLYIDFRQDLGKWKVHHPKGYIANFCSGPCPYLRSADTTHST 60
 |||||
 Db 1 aldtncfmrleencvvrplyidfrqdlgwkwhepkgyanfcsgpcpylrsadtthst 60
 |||||
 QY 61 VLGLYNTLNPEASASPCVQDLEPLTILYVGRTPKVEQLSNMVKSKCS 112
 |||||
 Db 61 vlglntlnpeasaspcvqpdleptilyvgrtpkveqlsnmrvksckcs 112
 |||||

Handwritten signature

XX	Human transforming growth factor-beta 3.
DE	
XX	
KW	Transforming growth factor-beta 3; TGF-beta 3; pig.
XX	
OS	Homo sapiens.
XX	
PH	Key
FT	Location/Qualifiers
FT	93..204
FT	/label= Mat_protein
FT	Misc-difference 17
FT	/note= "encoded by ATT"
XX	
PN	US5801231-A.
XX	
XX	01-SEP-1998.
PD	
XX	
XX	22-MAR-1985; 85US-0715142.
PF	
XX	
XX	13-MAR-1987; 87US-0025423.
PR	22-MAR-1985; 85US-0715142.
PR	04-AUG-1989; 89US-0389929.
PR	04-MAR-1992; 92US-0845893.
PR	05-NOV-1993; 93US-0147364.
PR	30-MAY-1995; 95US-0454468.
XX	
PA	(GETH) GENENTECH INC.
XX	
PI	Derynck RMA, Goeddel DV;
XX	
DR	WPI; 1998-494840/42.
DR	N-PSDB; AAV52935.
XX	
XX	DNA encoding transforming growth factor-beta precursor sequence -
PT	useful for analysis to perform manipulations to increase yield of
PT	recombinant production of the protein
XX	
XX	Example 6; Fig 5; 26pp; English.
PS	
XX	
CC	This is a partial amino acid sequence of the human transforming
CC	growth factor-beta 3 precursor (preTGF-beta 3); deduced from an
CC	isolated cDNA clone (see AAV52935). The invention relates to the
CC	recombinant production of TGF-beta. Biologically active TGF-beta
CC	is defined as being capable of inducing EGF-potentiated anchorage
CC	independent growth of target cell lines and/or growth inhibition of
CC	neoplastic cell lines. Nucleic acids encoding TGF-beta have been
CC	isolated and cloned into vectors which are replicated in bacteria
CC	and expressed in eukaryotic cells. TGF-beta recovered from
CC	transformed cells is used in known therapeutic applications.
XX	
SQ	Sequence 204 AA;

Query Match	99.4%	Score 630;	DB 19;	Length 204;
Best Local Similarity	99.1%;	Pred. No. 6.3e-56;		
Matches 111;	Conservative 1;	Mismatches 0;	Indels 0;	Gaps 0;

QY	1	ALDTNYCFRNLNCCVRPLYIDFRQDLGWKWKWHEPKGYIYANFCSGPCPYLRSDATHTHST	60
Db	93	altdnycfrnlneccvrplyidfrqdlgwkwkwhpkgyyanfcsgpcpylrsadtthst	152
QY	61	VLGLYNTLNPEASASPCCVQDLPLEPTILYVVGRTKVEQLSNMVKSCKCS	112
Db	153	vlglyntlnpeasaspcvcvqdlpleptilyvvgrtkveqlsnmvkscskcs	204

RESULT 20
AAR04080
ID AAR04080 standard; protein; 457 AA.
XX
AC AAR04080;
XX
DT 31-MAY-1989 (first entry)

XX Polypeptide sequence of porcine TGF-beta 3.
DE Transforming growth factor beta-3 (TGF beta 3); tumour cells; growth
KW inhibition.
XX WO8912101-A.
XX 14-DEC-1989.
PD 08-JUN-1988; 88WO-US01945.
XX 08-JUN-1988; 88WO-UO01945.
PR (GETH) GENENTECH INC.
XX Derynck RM, Goeddel DV;
XX WPI; 1990-007474/01.
DR N-PSDB; AAQ02819.
XX Nucleotide sequence encoding transforming growth factor beta-3 used as a
PT probe, or to produce TGF beta 3, for inhibiting growth of certain normal
PT and neoplastic cells, eg A549.
XX Disclosure; Fig. 5; 61pp; English.
XX This sequence represents porcine transforming growth factor-beta 3 (TGF-
CC beta 3) polypeptide. The corresponding nucleic acid sequence of this
CC subtype is useful as a probe or to produce this protein for normal and
CC neoplastic cell growth inhibition. It differs from human TGF-beta 3 at
CC several AA positions.
XX Sequence 457 AA;
SQ Query Match 99.4%; Score 630; DB 11; Length 457;
Best Local Similarity 99.1%; Pred. No. 1.6e-55;
Matches 111; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 ALDNTNYCFRNLENCVRLPYIDFRDLGKWKVHEPKGYANFCSGPCPYLRSADTTHT 60
Db 346 aldtncfrrnleencvrrplyidfrqdlgkwvhepkgyanfcsgpcpylrsadtthst 405
QY 61 VLGLYNTLNPEASPCCVQDLEPLTILYVGRTPKVEQLSNMVKSKCS 112
Db 406 vlglntlnpeaspcvcpqdlepltillyvgrtpkveqlsnmvvksckes 457
RESULT 21
AAR22038
ID AAR22038 standard; Protein; 413 AA.
XX AAR22038;
AC AAR22038;
XX 05-MAY-1992 (first entry)
DT Mutant Transforming Growth Factor beta-3 coding sequence.
XX TGF-beta 3; homodimer; ss.
KW Synthetic.
XX Key Location/Qualifiers
FH Region 1..296
FT /note= "amino acids 1-296 of TGF-beta3 precursor"
FT Modified-site 74..76
FT /label= glycosylation
FT Modified-site 135..137
FT /label= glycosylation
FT Modified-site 142..144
FT /label= glycosylation
FT Modified-site 158..160

FT Cleavage-site 297..300
FT /label= Factor_Xa_site
FT Region 302..404
FT /note= "amino acids 301-403 of TGF-beta3 precursor"
FT Misc-difference 405
FT /note= "wild-type = Met; may be substituted by
FT any other amino acid"
FT Region 406..413
FT /note= "amino acids 405-412 of TGF-beta3 precursor"
XX WO9200318-A.
PN 09-JAN-1992.
XX 25-JUN-1991; 91WO-US04541.
XX 25-JUN-1990; 90US-0543348.
PR (ONCO-) ONCOGENE SCI INC.
XX Iwata KK, Foulkes JG, Tendijke P, Haley JD;
PI WPI; 1992-041510/05.
XX N-PSDB; AAQ22229.
DR Transforming growth factor beta 3 proteins, precursors and
XX mutants - obdr. from polypeptide and antibodies, with optimal
PT therapeutic use due to genetic manipulation of coding sequence
XX Claim 12; Page 66; 107pp; English.
XX This sequence has been compiled from the description of a mutant TGF-
CC beta3 contained in the claims. The Factor Xa cleavage site may be
CC replaced by a similar protease recognition site, e.g. for collagenase.
CC The mutant protein may also include a hydrophobic transmembrane amino
CC acid sequence, e.g. from c-erbB2 and a "stop transfer"
CC sequence. The protease recognition site is located between the
CC C-terminal of the transmembrane region (when present) and the
CC N-terminal of the TGF-beta 3 precursor. Mature TGF-beta 3 can then be
CC efficiently cleaved from the membrane. See also AAQ20576 and AAR20622.
XX Sequence 413 AA;
SQ Query Match 98.9%; Score 627; DB 13; Length 413;
Best Local Similarity 99.1%; Pred. No. 2.8e-55;
Matches 111; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ALDNTNYCFRNLENCVRLPYIDFRDLGKWKVHEPKGYANFCSGPCPYLRSADTTHT 60
Db 302 aldtncfrrnleencvrrplyidfrqdlgkwvhepkgyanfcsgpcpylrsadtthst 361
QY 61 VLGLYNTLNPEASPCCVQDLEPLTILYVGRTPKVEQLSNMVKSKCS 112
Db 362 vlglntlnpeaspcvcpqdlepltillyvgrtpkveqlsnmvvksckes 413
RESULT 22
AAR04078
ID AAR04078 standard; protein; 112 AA.
XX AAR04078;
AC AAR04078;
XX 31-MAY-1989 (first entry)
DT Sequence of porcine TGF-beta 3.
DE Transforming growth factor beta-3 (TGF beta 3); tumour cells; growth
KW inhibition.
XX WO8912101-A.
PN

```
PD 14-DEC-1989.
XX
PF 08-JUN-1988; 88WO-US01945.
XX
PR 08-JUN-1988; 88WO-U001945.
XX
PA (GETH ) GENENTECH INC.
XX
PI Derynck RM, Goeddel DV;
XX
XX WPI; 1990-007474/01.
XX
XX Nucleotide sequence encoding transforming growth factor beta-3 used as a
PT probe, or to produce TGF beta 3, for inhibiting growth of certain normal
PT and neoplastic cells, eg A549.
XX
PS Disclosure; Fig. 3; 61pp; English.
XX
XX This sequence is that of porcine transforming growth factor-beta 3
CC (TGF-beta 3) polypeptide. It differs from human TGF-beta 1
CC sequence at positions 9-11,13,19,40,45,52,57,58,60,63,67,68,
CC 71,75,82,87,95 and 96. Nucleic acid sequence encoding subtype 3 of TGF
CC -beta (TGF-beta 3) is useful as a probe or to produce TGF-beta 3 for both
CC normal and neoplastic cell growth inhibition.
XX
SQ Sequence 112 AA;
Query Match 97.9%; Score 621; DB 11; Length 112;
Best Local Similarity 98.2%; Pred. No. 2.6e-55;
Matches 110; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 ALDTNYCFRNLENCVVRPLYIDFRQDLGKWKVHEPKGYIANFCSPGCPYLRSADTTHTST 60
DB 1 aldtncfrrnleencvvrplyidfrqdlgwkwvhepkgyianfcsgpcpylrsadtthss 60
QY 61 VLGLYNTLNPEASAPCCVPQDLEPLTILYYVGRTPKVEQLSNMVMVKSCKS 112
DB 61 vlgltyntlnpeasapccvpqdlepltilyyvgrtaveqlsnmvmvksckcs 112
RESULT 23
AAW78783
ID AAW78783 standard; Protein; 112 AA.
XX
AC AAW78783;
XX
DT 21-DEC-1998 (first entry)
XX
DE Pig transforming growth factor-beta 3 N-terminal sequence.
XX
KW Transforming growth factor-beta 3; TGF-beta 3; pig.
XX
OS Sus scrofa.
XX
PN US5801231-A.
XX
PD 01-SEP-1998.
XX
PF 22-MAR-1985; 85US-0715142.
XX
PR 13-MAR-1987; 87US-0025423.
XX
PR 22-MAR-1985; 85US-0715142.
XX
PR 04-AUG-1989; 89US-0389929.
XX
PR 04-MAR-1992; 92US-0845893.
XX
PR 05-NOV-1993; 93US-0147364.
XX
PR 30-MAY-1995; 95US-0454468.
XX
PA (GETH ) GENENTECH INC.
XX
PI Derynck RMA, Goeddel DV;
XX
XX WPI; 1998-494840/42.
XX
DR
```

```
XX
PT DNA encoding transforming growth factor-beta precursor sequence -
PT useful for analysis to perform manipulations to increase yield of
PT recombinant production of the protein
XX
PS Disclosure; Fig 3; 26pp; English.
XX
XX This is the amino acid sequence of pig transforming growth factor
CC beta-3 (TGF-beta 3, see also AAW78786). The sequence shows homology
CC to human TGF-beta 1 (see AAW78781), human TGF-beta 3 (see AAW78782)
CC and bovine TGF-beta 2 (see AAW78784) N-terminal sequences. The
CC invention relates to the recombinant production of TGF-beta. DNA
CC encoding TGF-beta has been isolated and cloned into vectors which
CC are replicated in bacteria and expressed in eukaryotic cells.
CC TGF-beta recovered from transformed cells can be used in known
CC therapeutic applications.
XX
SQ Sequence 112 AA;
Query Match 97.9%; Score 621; DB 19; Length 112;
Best Local Similarity 98.2%; Pred. No. 2.6e-55;
Matches 110; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 ALDTNYCFRNLENCVVRPLYIDFRQDLGKWKVHEPKGYIANFCSPGCPYLRSADTTHTST 60
DB 1 aldtncfrrnleencvvrplyidfrqdlgwkwvhepkgyianfcsgpcpylrsadtthss 60
QY 61 VLGLYNTLNPEASAPCCVPQDLEPLTILYYVGRTPKVEQLSNMVMVKSCKS 112
DB 61 vlgltyntlnpeasapccvpqdlepltilyyvgrtakveqlsnmvmvksckcs 112
RESULT 24
AAW46228
ID AAW46228 standard; Protein; 456 AA.
XX
AC AAW46228;
XX
DT 09-JUL-1994 (first entry)
XX
DE Pig TGF-beta-3.
XX
KW TGF-beta-1; TGF-beta-3; transforming growth factor beta-1;
KW transforming growth factor beta-3; recombinant; wound healing;
KW vulnerary.
XX
OS Sus scrofa.
XX
PN US5284763-A.
XX
PD 08-FEB-1994.
XX
PF 22-MAR-1985; 85US-0715142.
XX
PR 22-MAR-1985; 85US-0715142.
XX
PR 13-MAR-1987; 87US-0025423.
XX
PR 04-AUG-1989; 89US-0389929.
XX
PR 04-MAR-1992; 92US-0845893.
XX
PA (GETH ) GENENTECH INC.
XX
PI Derynck RMA, Goeddel DV;
XX
XX WPI; 1994-056343/07.
XX
DR N-PSDB; AAQ56925.
XX
XX Nucleic acid sequences encoding transforming growth factor-beta -
PT diagnostic probes, and for use in therapeutics
XX
XX Disclosure; Fig 5; 25pp; English.
XX
XX cDNA sequences were determined for human pre-TGF-beta-1 (AAQ56923),
```


CC e.g. arteriosclerosis, inflammation and psoriasis, or for the
CC treatment of burns to facilitate wound healing. TGI can also be
CC used as an immunomodulator. Although the protein has tumour
CC growth inhibitory activity, it is not transforming growth
CC factor-beta-1 or -beta-2. The peptide CM-1 (as featured) inhibits
CC the growth of human tumour cells but not of a mink lung cell line.
XX
SQ Sequence 112 AA;

Query Match 97.8%; Score 620; DB 17; Length 112;
Best Local Similarity 98.2%; Pred. No. 3.3e-55;
Matches 110; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ALDTNYCFNRLENCVRRPLYIDFRQDLGKWKVHEPKGYANFCSPCYLRSADTTHT 60
Db 1 aldtncyfrnleencvrrplyidfrqdlgkwkvhpkgyanfcspcyllrsadtthst 60
QY 61 VLGLYNTLNPEASAPCCVPQDLEPLTILYVYVGRTPKVEQLSNMVKSKCS 112
Db 61 vlglyntlnpeasawpcvvpqdleptilyyvgtrpkveqlsnmvvksckcs 112

RESULT 27
AAR86771
ID AAR86771 standard; Protein; 165 AA.
XX
AC AAR86771;
DT 12-JUN-1996 (first entry)
XX
DE Tissue-derived tumour growth inhibitor-1 precursor.
XX
KW Tumour growth inhibitor; carcinoma; melanoma; leukaemia;
KW arteriosclerosis; inflammation; psoriasis; therapy; vulnery;
KW immunomodulator.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Protein 1..165
FT /note= "tumour growth inhibitor precursor"
FT Misc-difference 53..54 /note= "residues 54-93 of the precursor protein are
FT not specified "
FT Protein 54..165
FT /note= "tumour growth inhibitor (see AAR86770)"
FT Peptide 62..81 /note= "peptide CM-1"
XX
XX EP684260-A2.
XX
XX 29-NOV-1995.
XX
XX 20-OCT-1987; 87EP-0109866.
XX
XX 20-OCT-1986; 86US-0922121.
XX
XX (ONCO-) ONCOGENE SCI INC.
XX
XX Gold LI, Iwata KK, Stephenson JR;
XX
XX WPI; 1996-000991/01.
XX
XX N-PSDB; AAT06496.
XX
XX Tissue-derived growth inhibitor and corresponding genes - useful for
XX detection of tumours, inhibition of tumour growth, treatment of
XX proliferative disorders and healing of burns and wounds.
XX
XX Claim 4; Fig 29; 83pp; English.
XX
XX The sequence represents the precursor of tumor growth inhibitor
XX (TGI) (see AAR86770), which is produced by recombinant DNA methods.
CC

CC However, amino acids 54-93 of the TGI precursor are not provided in
CC the specification. TGI, or its 205 amino acid precursor, can be
CC used to inhibit the growth of human tumour cells, e.g.
CC carcinoma, melanoma or leukaemia cells, in the treatment of
CC proliferative disorders e.g. arteriosclerosis, inflammation and
CC psoriasis, or for the treatment of burns to facilitate wound
CC healing. The proteins can also be used as immunomodulators.
CC Although the proteins have tumour growth inhibitory activity, they
CC are not transforming growth factor-beta-1 or -beta-2. The 20-amino
CC acid peptide CM-1 (as featured) inhibits the growth of human tumour
CC cells but not of a mink lung cell line.
XX
SQ Sequence 165 AA;

Query Match 97.8%; Score 620; DB 17; Length 165;
Best Local Similarity 98.2%; Pred. No. 5.1e-55;
Matches 110; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ALDTNYCFNRLENCVRRPLYIDFRQDLGKWKVHEPKGYANFCSPCYLRSADTTHT 60
Db 54 aldtncyfrnleencvrrplyidfrqdlgkwkvhpkgyanfcspcyllrsadtthst 113
QY 61 VLGLYNTLNPEASAPCCVPQDLEPLTILYVYVGRTPKVEQLSNMVKSKCS 112
Db 114 vlglyntlnpeasawpcvvpqdleptilyyvgtrpkveqlsnmvvksckcs 165

RESULT 28
AAR08264
ID AAR08264 standard; protein; 412 AA.
XX
AC AAR08264;
DT 05-MAR-1991 (first entry)
XX
DE Tumour growth inhibitor.
XX
KW TGI; Carcinoma; melanoma; leukaemia; arteriosclerosis; inflammation;
KW psoriasis.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Modified-site 74..76 /label= N-glycosylation site
FT Modified-site 0..137 /label= N-glycosylation site
FT Modified-site 142..144 /label= N-glycosylation site
FT Modified-site 158..160 /label= N-glycosylation site
XX
XX WO9014360-A.
XX
XX 29-NOV-1990.
XX
XX 17-MAY-1990; 90WO-US02753.
XX
XX 17-MAY-1989; 89US-0353410.
XX
XX 19-APR-1985; 85US-0725003.
XX
XX 07-APR-1986; 86US-0847931.
XX
XX 20-OCT-1986; 86US-0992121.
XX
XX 20-OCT-1987; 87US-0111022.
XX
XX 20-APR-1988; 88US-0183224.
XX
XX (ONCO-) ONCOGENE SCI INC.
XX
XX Iwata KK, Stephenson JR, Tendijke P, Franco R, Gold LI, Foulkes JG;
XX
XX WPI; 1990-375949/50.
XX
XX N-PSDB; AAQ06845.

PT Tissue-derived tumour growth inhibitors - comprise specified
PT protein sequences used to detect, and treat tumours, burns and
PT wounds.

XX
XX Claim 10; Fig 41; 190pp; English.

XX A plasmid carrying DNA encoding the TGI was isolated from a human
CC cDNA library prep. from the DNA of a chronic myelocytic leukaemia
CC cell line (K562). The sequence can be used to produce the TGI by
CC recombinant techniques. The protein may also be isolated from human
CC umbilical cord and placental tissues. It can be used to inhibit
CC tumour cell growth, to treat burns, to facilitate the healing
CC of wounds or to treat proliferative disorders. The protein and
CC Abs raised to it can be used for detection and typing of tumours.
CC The Abs can also be used to inhibit the activity of the TGI.

XX
SQ Sequence 412 AA;

Query Match 97.3%; Score 617; DB 11; Length 412;
Best Local Similarity 97.3%; Pred. No. 2.9e-54;
Matches 109; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 ALDTNYCFRNLENCVRRPLYIDFRQDLGWKWHPEKGYIYANFCSGPCPYLRSADTHST 60
Db 301 aldtncfrnleencvrrplyidfrqdlgwkwhepkgyanfcsgpcpylrsadtthst 360
OY 61 VLGLYNTLNPEASASPCVQDLEPLTILYVYGRTPKVEQLSNMVKCKCS 112
Db 361 vlglyntlnpeasaspcvqpdlleptillyvgrtpkvwsklsmvmvksckcs 412

RESULT 29

AAR04077
ID AAR04077 standard; protein; 112 AA.

XX AAR04077;

XX 31-MAY-1989 (first entry)

XX Sequence of human TGF-beta 3.

XX Transforming growth factor beta-3 (TGF beta 3); tumour cells; growth
KW inhibition.

XX W08912101-A.

XX 14-DEC-1989.

XX 08-JUN-1988; 88WO-US01945.

XX 08-JUN-1988; 88WO-U001945.

XX (GETH) GENENTECH INC.

XX Dernyck RM, Goeddel DV;

XX WPI; 1990-007474/01.

XX Nucleotide sequence encoding transforming growth factor beta-3 used as a
PT probe, or to produce TGF beta 3, for inhibiting growth of certain normal
PT and neoplastic cells, eg A549.

XX Disclosure; Fig. 3; 61pp; English.

XX This sequence is that of human transforming growth factor-beta 3
CC (TGF-beta 3) polypeptide. It differs from mature human TGF-beta
CC subtype 1 AA sequence at positions 9-11,13,19,40,45,52,57,58,60,63,67,68,
CC 71,75,82,87,and 95. The nucleic acid sequence encoding subtype 3 of TGF-
CC beta is useful as a probe or to produce TGF-beta 3 for both normal and
CC neoplastic cell growth inhibition.

XX Sequence 112 AA;

SQ Sequence 112 AA;

Query Match 96.5%; Score 612; DB 11; Length 112;
Best Local Similarity 97.3%; Pred. No. 2.1e-54;
Matches 109; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 ALDTNYCFRNLENCVRRPLYIDFRQDLGWKWHPEKGYIYANFCSGPCPYLRSADTHST 60
Db 1 aldtncfrnleencvrrplyidfrqdlgwkwhepkgyanfcsgpcpylrsadtthst 60
OY 61 VLGLYNTLNPEASASPCVQDLEPLTILYVYGRTPKVEQLSNMVKCKCS 112
Db 61 vlglyntlnpeasaspcvqpdlleptillyvgrtpkveqlsnmvmvksckcs 112

RESULT 30

AAR39642
ID AAR39642 standard; Protein; 112 AA.

XX AAR39642;

XX 26-AUG-1993 (first entry)

XX Transforming Growth Factor-beta1(44/45)beta3 hybrid.

XX hTGF-beta1; hTGF-beta3; hybrid protein; wound healing;
KW cancer treatment; bone repair; growth regulation.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Region 1..44

FT /note= "amino acids 1-44 of hTGF-beta1"

FT Region 45..112

FT /note= "amino acids 45-112 of hTGF-beta3"

XX EP542679-A.

XX 19-MAY-1993.

XX 03-NOV-1992; 92EP-0810845.

XX 11-NOV-1991; 91EP-0810870.

XX (CIBA) CIBA GEIGY AG.

XX McMaster GK, Cox D, Cerletti N, Kuhla J;

XX WPI; 1993-161126/20.

XX N-PSDB; AAQ41603.

XX New hybrid transforming growth factor-beta molecules - comprise
PT portions of mature TGF-beta isoforms; useful as wound healants,
PT cardioprotective, antiinflammatory and immunosuppressive agents etc.

XX Claim 8; Page 26-27; 48pp; English.

XX The invention covers hybrid TGF-beta molecules consisting of parts
CC of the human isoforms TGF-beta1, TGF-beta2 and TGF-beta3 (see AAQ41599,
CC AAQ41600 and AAQ41601, respectively). The hinge points between parts
CC derived from different parent isoforms are pref. between amino acids
CC 44 and 45, 56 and 57, 79 and 80, 90 and 91, or 22 and 23. Of the 30
CC possible hybrids using these hinge points and one part each
CC from two of the isoforms, 6 are preferred including the hybrid
CC TGF-beta1(44/45)beta3. The hybrid molecules promote cell migration,
CC inhibit the growth of A375 melanoma cells, accelerate the healing of
CC partial-thickness burn wounds and full-thickness incisional wounds and
CC increase formation of fibrous granular tissue.

XX See AAQ41602-Q41607 for the most pref. hybrids.

QY	1	ALDTNYCFRNLEENCVRPLYYIDFRQDLGKWVHEPKGYVAFNGCGPCPYLRSDTTHTST 60
		: : : : : : : : :
Db	1	alldtncfsstekncvcrqllydfkrldlgkwihpkgyhanfscgpcpylrdsadthst 60
QY	61	VGLGYNTLNPRASAPCCVPQDLPLTLTYVYVGRTPKVEQLSNMVKSCKCS 112
		: : : : : : :
Db	61	vlglyntlnpeasaspccvpqdgldpltilyyvgrtpkveqlsnmvmvskcs 112
RESULT	32	
AAAR91959		
ID	AAAR91959	standard; Protein; 112 AA.
XX		
AC	AAAR91959;	
XX		
DT	10-JUN-1996	(first entry)
XX		
DE		Human TGF-beta-like protein, TGF-beta-1-3.
XX		
KW		Transforming growth factor beta; TGF; regulator; method;
KW		proliferation; differentiation; wound healing; solvent.
XX		
OS		Homo sapiens.
XX		
FH		Key
FT	Peptide	Location/Qualifiers
FT		1..44
FT		/note= "N-terminal 44 amino acids of
FT		TGF-beta-1"
FT	Peptide	45..112
FT		/note= "C-terminal 68 amino acids of
FT		TGF-beta-3"
XX		
PN	W05603432-A1.	
XX		
PD	08-FEB-1996.	
XX		
PF	12-JUL-1995;	95WO-EP02718.
XX		
PR	25-JUL-1994;	94EP-0810438.
XX		
FA	(CIBA) CIBA GEIGY AG.	
XX		
FI	Cerletti N;	
XX		
DR	WPI; 1996-116999/12.	
DR	N-PSDB; AAT15465.	
XX		
PT		Prodn. of dimeric, biologically active transforming growth factor
PT		beta - by refolding denatured monomer in buffer contg. mild
PT		detergent and specific organic solvents to improve yields
XX		
PS	Claim 17; Page 40-41; 59pp; English.	
XX		
CC	AAAR91959 is transforming growth factor (TGF) beta-like protein,	
CC	TGF-beta-1-3. TGF beta-1-3 is a hybrid of TGF-1 and TGF-3. TGF beta	
CC	hybrids were made using a new process of producing dimeric,	
CC	biologically active TGF beta-like proteins. The new process involves	
CC	treating denatured TGF beta monomers with folding buffer contg. a	
CC	mild detergent (CHAPS, CHAPSO or digitonin) and at least one of the	
CC	solvents DMSO (dimethyl sulphoxide), DMSO2 (dimethylsulphone) and	
CC	DMF (dimethyl formamide). The detergent allows folding of the monomer	
CC	such that, after dimerisation, the TGF beta-like protein retains	
CC	biological activity and remains in soluble form. The method allows	
CC	relatively high yields of biologically active TGF beta-like proteins	
CC	in their native dimeric form. TGF-beta like proteins are multifunctional	
CC	regulators of cellular activity and a typical use is to stimulate wound	
CC	healing.	
XX		
SQ	Sequence	112 AA;

Query Match 93.8%; Score 595; DB 17; Length 112;

Best Local Similarity 92.9%; Pred. No. 1.1e-52;

QY 61 VLGLYNTLNPEASASPCCVQDLEPLTILYVGRTPKVEQLSNMVKSKCS 112
|| ||||:||||||| |||||:||||:||||:|||||
Db 61 vlslyntinpeasaspcvsgdleptilyigtkpieglsnmivksckcs 112
|| ||||:||||||| |||||:||||:||||:|||||

RESULT 37
AAR91961
ID AAR91961 standard; Protein; 112 AA.
XX AAR91961;
AC
XX
XX
DT 10-JUN-1996 (first entry)
XX
DE Human TGF-beta-like protein, TGF-beta-3-2.
XX
XX Transforming growth factor beta; TGF; regulator; method;
KW proliferation; differentiation; wound healing; solvent.
XX
XX Homo sapiens.
XX
XX
FH Key Location/Qualifiers
FT Peptide 1..44
FT /note= "N-terminal 44 amino acids of
FT TGF-beta-3"
FT Peptide 45..112
FT /note= "C-terminal 68 amino acids of
FT TGF-beta-2"
FT
FT
XX WO9603432-A1.
XX
XX
PD 08-FEB-1996.
XX
XX 12-JUL-1995; 95WO-EP02718.
XX
XX 25-JUL-1994; 94EP-0810438.
XX
XX (CIBA) CIBA GEIGY AG.
XX
XX Cerletti N;
XX
XX WPI: 1996-116999/12.
XX N-PSDB; AAT15467.
XX
XX Prodn. of dimeric, biologically active transforming growth factor
PT beta - by refolding denatured monomer in buffer contg. mild
PT detergent and specific organic solvents to improve yields
XX
XX Claim 17; Page 45-46; 59pp; English.
XX
XX AAR91961 is transforming growth factor (TGF) beta-like protein,
CC TGF-beta-3-2. TGF beta-3-2 is a hybrid of TGF-3 and TGF-2. TGF beta
CC hybrids were made using a new process of producing dimeric, beta
CC biologically active TGF beta-like proteins. The new process involves
CC treating denatured TGF beta monomers with folding buffer contg. a
CC mild detergent (CHAPS, CHAPSO or digitonin) and at least one of the
CC solvents DMSO (dimethyl sulphoxide), DMSO2 (dimethylsulphone) and
CC DMF (dimethyl formamide). The detergent allows folding of the monomer
CC such that, after dimerisation, the TGF beta-like protein retains
CC biological activity and remains in soluble form. The method allows
CC relatively high yields of biologically active TGF beta-like proteins
CC in their native dimeric form. TGF-beta like proteins are multifunctional
CC regulators of cellular activity and a typical use is to stimulate wound
CC healing.
XX
XX Sequence 112 AA;

Query Match 91.0%; Score 577; DB 17; Length 112;
Best Local Similarity 88.4%; Pred. No. 6.9e-51;
Matches 99; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

QY 1 ALDNTNCFRNLENCVVRPLYIDFRQDLGKWKVHEPKGYANFCSGPCPYLRSDTTHST 60
|||||:||||||| |||||:||||:||||:|||||

Db 1 aldtncfrcnleencvvrplyidfrqdlgkwkvhpkgyyanfcagacpylwsdqtqshr 60
QY 61 VLGLYNTLNPEASASPCCVQDLEPLTILYVGRTPKVEQLSNMVKSKCS 112
|| ||||:||||||| |||||:||||:||||:|||||
Db 61 vlslyntinpeasaspcvsgdqleptilyigtkpieglsnmivksckcs 112
|| ||||:||||||| |||||:||||:||||:|||||

RESULT 38
AAR92777
ID AAR92777 standard; Protein; 112 AA.
XX AAR92777;
AC
XX
XX 17-JUL-1996 (first entry)
DT
XX
DE Hybrid TGF-beta 3-2.
XX
XX Transforming growth factor type beta; TGF-beta 2; TGF-beta 3;
KW protein renaturation; protein folding.
XX
XX Synthetic.
XX
XX
FH Key Location/Qualifiers
FT Protein 1..33
FT /note= "amino acids 1-44 of human TGF-beta3"
FT Protein 45..112
FT /note= "amino acids 45-112 of human TGF-beta2"
FT
FT
XX WO9603433-A1.
XX
XX 08-FEB-1996.
XX
XX 12-JUL-1995; 95WO-EP02719.
XX
XX 25-JUL-1994; 94EP-0810439.
XX
XX (CIBA) CIBA GEIGY AG.
XX
XX Cerletti N;
XX
XX WPI: 1996-117000/12.
XX N-PSDB; AAT17239.
XX
XX Prodn. of dimeric biologically active transforming growth factor
PT by refolding denatured monomer in detergent-free folding buffer
PT contg. specific organic solvent to improve yield
XX
XX Example 10; Page 41-42; 54pp; English.
XX
XX A recombinant, non-soluble, monomeric hybrid of human transforming
CC growth factor-beta, TGF-beta 3-2 (AAR92777), is composed of the
CC N-terminal portion of TGF-beta 3 (see also AAR92772) and the C-terminal
CC portion of TGF-beta 2 (see also AAR92774). It was produced by E. coli
CC LC37 transformants carrying plasmid pPLMu.TGF-beta3(44/45)beta2,
CC which includes a coding sequence (AAT17239) for the hybrid. A
CC biologically active, dimeric form of TGF-beta3-2 was obtd. by refolding
CC the monomer in detergent-free buffer contg. DMSO and/or DMF. Hybrid
CC dimers TGF-beta 1-3 (AAR92775) and TGF-beta 2-3 (AAR92776) were
CC similarly produced.
XX
XX Sequence 112 AA;

Query Match 91.0%; Score 577; DB 17; Length 112;
Best Local Similarity 88.4%; Pred. No. 6.9e-51;
Matches 99; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

QY 1 ALDNTNCFRNLENCVVRPLYIDFRQDLGKWKVHEPKGYANFCSGPCPYLRSDTTHST 60
|||||:||||||| |||||:||||:||||:|||||

Db 1 aldtncfrcnleencvvrplyidfrqdlgkwkvhpkgyyanfcagacpylwsdqtqshr 60
|| ||||:||||||| |||||:||||:||||:|||||

QY 61 VLGLYNTLNPEASASPCCVQDLEPLTILYVGRTPKVEQLSNMVKSKCS 112
|| ||||:||||||| |||||:||||:||||:|||||

Db 61 vlslyntinpeasaspcvcsqdlptlilyyigtkpkieqlsnmvksckcs 112

RESULT 39

AAR11944
ID AAR11944 standard; Protein; 98 AA.

AC AAR11944;
XX

DT 23-JUL-1991 (first entry)
XX

DE Truncated TGF-beta #3.
XX

XX Transforming Growth Factor beta; AIDS.
KW

XX Synthetic.
OS

XX WO9105565-A.
PN

XX 02-MAY-1991.
PD

XX 18-OCT-1990; 90WO-US06006.
PF

XX 18-OCT-1989; 89US-0422962.
PR

XX (CREA-) CREATIVE BIOMOLECUL.
PA

XX Cohen CM;
PI

XX WPI; 1991-148530/20.
DR

XX Recombinant truncated transforming growth factor-beta analogues -
PT capable of inducing an anti-proliferative effect in mammalian
PT epithelial cells in vitro
XX

XX Claim 12; Page 27; 42pp; English.
PS

XX This sequence is an example of a highly generic protein (see
CC AAR11954). It can be used to control proliferation of tumour cell lines
CC or for enhancing growth rate of T- and B-lymphocytes in
CC immunosuppressed patients. The first 5 N-terminal residues can be
CC absent.
CC See also AAQ11774-5, AAR11942-RL1947 and AAR11954.
XX

XX Sequence 98 AA;
SQ

Query Match 87.5%; Score 555; DB 12; Length 98;
Best Local Similarity 100.0%; Pred. No. 9.7e-49;
Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 CCVRPLYIDFRQDLGKWKVHEPKGYANFCGPGPYLRSADTHTSVLGLYNTLNPEASA 74

Db 1 ccvrplyidfrqdlgkwwhepkgyanfcsgpcpylrsadtthstvtlglntlnpeasa 60

QY 75 SPCCVPDLEPTILYVGRTPKVEQLSNMVKSCKCS 112

Db 61 spccvpqdlptlilyyvgtrpkveqlsnmvksckcs 98

RESULT 40

AAV16699
ID AAV16699 standard; Peptide; 98 AA.

XX AAV16699;
AC

XX 17-AUG-1999 (first entry)
DT

XX WO9914235 Seq ID No: 152.
DE

XX Growth factor; GF; persephin; neuron growth; cellular degeneration;
KW peripheral neuropathy; amyotrophic lateral sclerosis; ischemic stroke;
KW Alzheimer's disease; Parkinson's disease; Huntington's disease; trauma;
XX

KW brain injury; spinal cord injury; nervous system tumour; infection;
KW multiple sclerosis; cardiac muscle degeneration; injury; neurotoxin;
KW metabolic disease; diabetes; renal dysfunction; neuriturin.

OS Unidentified.

XX WO9914235-A1.
PN

XX 25-MAR-1999.
PD

XX 15-SEP-1998; 98WO-US19163.
PF

XX 16-SEP-1997; 97US-0931858.
PR

XX (UNIW) UNIV WASHINGTON.
PA

XX Desauvage F, Johnson EM, Klein R, Kotzbauer PT;
PI Lampe PA, Milbrandt JD;

XX WPI; 1999-244023/20.
DR

XX New isolated persephin growth factor nucleic acids used to, e.g.
XX promote neuronal growth

XX Disclosure; Page 176-177; 222pp; English.
XX

CC The invention relates to a novel isolated and purified growth factor (GF)
CC that comprises persephin or a fragment or a conservatively substituted
CC variant. The persephin GF polypeptides can promote the survival and
CC growth of neurons and non-neuronal cells. The persephin GF polypeptides
CC or polynucleotides can be used for preventing or treating cellular
CC degeneration or insufficiency, e.g. neuronal degeneration resulting from
CC peripheral neuropathy, amyotrophic lateral sclerosis, Alzheimer's
CC disease, Parkinson's disease, Huntington's disease, ischemic stroke,
CC acute brain injury, acute spinal cord injury, nervous system tumours,
CC multiple sclerosis, or infection, hematopoietic cell degeneration or
CC insufficiency resulting from eosinopenia, anemias, thrombocytopenia, or
CC stem-cell insufficiencies, cardiac muscle degeneration or insufficiency
CC resulting from cardiomyopathy or congestive heart failure. They can also
CC be used for treating e.g. peripheral nerve trauma or injury, exposure to
CC neurotoxins, metabolic diseases such as diabetes or renal dysfunctions
CC and damage caused by infectious agents. The GF can also be used for
CC promoting the growth and/or differentiation of a cell in a culture
CC medium. The antisense polynucleotides can be used for treating a disease
CC condition mediated by expression of persephin by a population of cells.
CC The products can also be used for detection and diagnosis.

XX Sequence 98 AA;
SQ

Query Match 87.5%; Score 555; DB 20; Length 98;
Best Local Similarity 100.0%; Pred. No. 9.7e-49;
Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 CCVRPLYIDFRQDLGKWKVHEPKGYANFCGPGPYLRSADTHTSVLGLYNTLNPEASA 74

Db 1 ccvrplyidfrqdlgkwwhepkgyanfcsgpcpylrsadtthstvtlglntlnpeasa 60

QY 75 SPCCVPDLEPTILYVGRTPKVEQLSNMVKSCKCS 112

Db 61 spccvpqdlptlilyyvgtrpkveqlsnmvksckcs 98

RESULT 41

AA09521

ID AA09521 standard; Protein; 98 AA.

XX AA09521;
AC

XX 11-SEP-2000 (first entry)
DT

XX Human TGF-beta 3, SEQ ID NO:42.
DE

XX

KW TGF-beta superfamily; transforming growth factor-beta; developmental regulation; finger 2 subdomain; basic region;
 KW protein refolding; stability; solubility; osteogenic protein; OP;
 KW bone morphogenetic protein; BMP; growth/differentiation factor; GDF;
 KW inhibin; tissue morphogenesis; regeneration; bone; dental tissue;
 KW connective tissue; cartilage; vulnary.
 XX Homo sapiens.
 XX WO200020607-A2.
 XX 13-APR-2000.
 XX 07-OCT-1999; 99WO-US23371.
 XX 07-OCT-1999; 98US-0103418.
 PR 16-AUG-1999; 99US-0374958.
 XX (STYC) STRYKER CORP.
 XX Oppermann H, Tai M, McCartney J;
 XX WPI; 2000-303787/26.
 XX Transforming growth factor-beta superfamily member mutant induces tissue morphogenesis in e.g. bone, non-mineralized skeletal tissue, dental tissue and connective tissue and comprises a substitution in a region of the finger 2 domain -
 XX Claim 14; Page 141; 162pp; English.
 CC The invention relates to mutant TGF-beta (transforming growth factor-beta) superfamily members. These mutants comprise one or more amino acid substitutions in the base region of the finger 2 subdomain, and a C-terminal residue selected from Arg, Ile, Leu, Ser and Ala. In the finger 2 subdomain, basic residues (e.g., Arg, Lys), or residues containing an amide group (e.g., Gln, Asn), are substituted with acidic residues (e.g., Glu, Asp) or residues containing a hydroxyl group (e.g., Ser, Thr). TGF-beta superfamily proteins regulate developmental processes and include proteins such as the osteogenic proteins (OPs), bone morphogenetic proteins (BMPs), growth/differentiation factors (GDFs) and inhibins. Specific examples of TGF-beta superfamily mutants encompassed by the invention are the finger 2 subdomain mutants of human osteogenic protein-1 (OP-1) (AAB09576-B09615). Mutant TGF-beta proteins are used for inducing tissue morphogenesis in bone, non-mineralised skeletal tissue, dental tissue, connective tissue, brain, liver and nerve tissue. The proteins can be used in conjunction with a biocompatible matrix e.g., collagen, hydroxyapatite or carboxymethylcellulose for regenerating bone, cartilage and/or other mineralised skeletal or connective tissues e.g., ligament, tendon, muscle, fibrocartilage, joint capsule and intervertebral discs. The Op-1 mutants can be used to repair diseased or damaged mammalian tissue and to prevent or substantially inhibit immune/inflammatory response-mediated tissue damage and scar tissue formation following an injury. Compared to the wild-type TGF-beta superfamily members, the mutant proteins have improved in vitro refolding properties in a pH range of 6-9, increased solubility in aqueous solution and improved stability and/or activity. Sequences AAB09519-B09542 and AAB09553-B09558 represent a variety of wild-type TGF-beta superfamily proteins referred to in the specification.

Sequence 98 AA;

Query Match 87.5%; Score 555; DB 21; Length 98;
 Best Local Similarity 100.0%; Pred. No. 9.7e-49;
 Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 CCVRPLYIDFRDLGKWKVHEPKGYANFCGCPYLRSDTHTSTVLGLYNTLNPEASA 74
 Db 1 ccvrplyidfrdqlgkwwhepkgyanfcsgpcpylrsadtthstvglyntlnpeasa 60
 QY 75 SPCCVPDLEPLTILYVGRTPKVEQLSNMVKSCKCS 112
 Db 1 ccvrplyidfrdqlgkwwhepkgyanfcsgpcpylrsadtthstvglyntlnpeasa 60

Db 61 spccvpdgleptililyvgrtpkveqlsnmvmvksckcs 98

RESULT 42

AAB02787

ID AAB02787 standard; Protein; 98 AA.

XX AC AAB02787;

XX AC AAB02787;

XX 22-AUG-2000 (first entry)

XX Human TGF-beta3 amino acid sequence SEQ ID NO:42.

XX Tumour growth factor beta; TGF-beta; morphogenic protein; BMP; OP;
 KW bone morphogenic protein; osteogenic protein; mutant; modified;
 KW finger 2 sub-domain; finger 1 domain; heel domain; chimeric protein;
 KW osteogenic; proliferative; antiinflammatory; tissue morphogenesis;
 KW tissue repair; regeneration; proliferation; differentiation.

XX Homo sapiens.

XX WO200020591-A2.

XX 13-APR-2000.

XX 07-OCT-1999; 99WO-US23370.

XX 07-OCT-1998; 98US-0103418.

XX 16-AUG-1999; 99US-0374936.

XX (STYC) STRYKER CORP.

XX Oppermann H, Tai M, McCartney J;

XX WPI; 2000-303776/26.

XX Novel TGF-beta superfamily mutant chimeric protein, useful for inducing tissue morphogenesis in e.g. bone, comprises a dimer consisting of one monomer containing domains from two family members -

XX Disclosure; Page 128; 149pp; English.

XX The present invention describes a tumour growth factor beta (TGF-beta) superfamily chimeric protein (I) derived from at least 2 different members of the superfamily comprising a dimer with one monomer that contains a finger 2 domain derived from a first family member and a finger 1 domain and heel domain, both derived from a second family member. The monomer further comprises a conserved C-terminal cysteine skeleton. (I) has osteogenic, proliferative and antiinflammatory activities. The TGF-beta superfamily chimeric proteins (I) are useful for inducing tissue morphogenesis (i.e. molecules capable of tissue repair and regeneration and/or inhibiting inflammation) in bone, non-mineralised skeletal tissue, dental tissue, connective tissue, brain, liver and nerve and for inducing the proliferation and differentiation of uncommitted progenitor cells in a tissue-specific manner to support new tissue formation. AAB29887 to AAB29897 and AAB02748 to AAB02824 represent sequences used in the exemplification of the present invention.

XX Sequence 98 AA;

Query Match 87.5%; Score 555; DB 21; Length 98;
 Best Local Similarity 100.0%; Pred. No. 9.7e-49;
 Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 CCVRPLYIDFRDLGKWKVHEPKGYANFCGCPYLRSDTHTSTVLGLYNTLNPEASA 74
 Db 1 ccvrplyidfrdqlgkwwhepkgyanfcsgpcpylrsadtthstvglyntlnpeasa 60
 QY 75 SPCCVPDLEPLTILYVGRTPKVEQLSNMVKSCKCS 112
 Db 61 spccvpdgleptililyvgrtpkveqlsnmvmvksckcs 98

Db 61 vlslyntinpeasapccvssqdleptilyviqktpkieqlsnmivksckcs 112

AAR39645
ID AAR39645 standard; Protein; 112 AA.

XX

[illegible]

XX

XX 8

XX

FT	Region	1..44

FT	Region
45.112	

XX

XX
10-MAY-1963XX
PF
03-NOV-1992.

PR 11-NOV-1991; 91EP-0810870.

PA (CIBA) CIBA GEIGY AG.

PI McMaster GK, Cox D,
XX

DR N-PSDB; AAQ41606.

New hybrid transforming growth factor-beta molecules - comprise

FI
carcinoprotective, antiinflammatory and immunosuppressive agents etc.
XX

XX

derived from different parent isoforms are pref. between amino acids 44 and 45, 56 and 57, 79 and 80, 90 and 91, or 22 and 23. Of the 30 possible hybrids using these hinge points and one part each from two of the isoforms, 6 are preferred including the hybrid TGF-beta3(44/45)beta1. The hybrid molecules promote cell migration, inhibit the growth of A375 melanoma cells, accelerate the healing of partial-thickness burn wounds and full-thickness incisional wounds and increase formation of fibrous granular tissue. See AAQ411602-Q41607 for the most pref. hybrids.

[illegible]

Best Local Similarity 83.98; Pred. No. 5.8e-47;

[illegible]

Db 1 aldtncvfrnleencvrrplvidfradlqwkwyhepkayvanfclapcpv!wsltdavsk 60

1

```
OS Homo sapiens.
XX EP433225-A.
XX PN
XX 19-JUN-1991.
XX PD
XX 27-NOV-1990; 90EP-0810922.
XX PF
XX 06-DEC-1989; 89GB-0027546.
XX PR
XX (CIBA ) CIBA GEIGY AG.
XX PA
XX Cerletti N, McMaster GK, Cox D, Schmitz A, Meyhack B;
XX PI WPI; 1991-180005/25.
XX PN N-PSDB; AAQ11994.
XX DR
XX Prodn. of Transforming Growth Factor type-beta-like proteins - by
XX PT subjecting denatured monomeric form to refolding conditions
XX PS Example; Page 27; 35pp; English.
XX PS
XX The TGF-beta2 coding sequence was isolated from the CI-215 human
XX CC glioma cell line. It was incorporated into an appropriate vector to
XX CC transform Saccharomyces cerevisiae or E.coli. Monomeric TGF-beta1
XX CC was purified, denatured and dissolved in 140ml 50mM Tris/HCl pH8. 1M
XX CC NaCl, 5mM EDTA, 2mM reduced glutathione, 1mM oxidised glutathione
XX CC and 33mM Chaps. After 72 hrs at 4 deg C, pH was adjusted to 2.5 and
XX CC the mixture was conc. 10 times. The conc. soln was diluted to the
XX CC original vol. with 10mM HCl and conc to a final vol of 10 ml. The
XX CC supernatant from centrifugation at 5000g for 30 min contained
XX CC disulphide-linked dimeric TGF-beta2.
XX CC
XX SQ Sequence 112 AA;

Query Match 84.4%; Score 535; DB 12; Length 112;
Best Local Similarity 79.5%; Pred. No. 1.2e-46;
Matches 89; Conservative 14; Mismatches 9; Indels 0; Gaps 0;

QY 1 ALDNTNCFRNLENCVRLPYIDFRQDLGWKWWHEPKGYVYANFCSGPCPYLRSADTTHST 60
Db ||| |||:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 61 VLGLYNTLNPEASAPCCVPQDLEPLTILYVGRTPKVEQLSNMVKSCKS 112
Db || ||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 61 VLGLYNTLNPEASAPCCVPQDLEPLTILYVGRTPKVEQLSNMVKSCKS 112
Db || ||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 48
AAR39639
ID AAR39639 standard; Protein; 112 AA.
XX
XX AC AAR39639;
XX DT
XX 26-AUG-1993 (first entry)
XX DE
XX Mature human Transforming Growth Factor-beta2.
XX hTGF-beta2; hybrid protein; wound healing; cancer treatment;
XX KW bone repair; growth regulation.
XX OS
XX Homo sapiens.
XX OS
XX EP542679-A.
XX PN
XX 19-MAY-1993.
XX PD
XX 03-NOV-1992; 92EP-0810845.
XX PF
XX 11-NOV-1991; 91EP-0810870.
XX PR
XX (CIBA ) CIBA GEIGY AG.
XX PA
```

```
XX McMaster GK, Cox D, Cerletti N, Kuhla J;
XX PI WPI; 1993-161126/20.
XX DR N-PSDB; AAQ41600.
XX DR
XX New hybrid transforming growth factor-beta molecules - comprise
XX PT portions of mature TGF-beta isoforms; useful as wound healants,
XX PT cardioprotective, antiinflammatory and immunosuppressive agents etc.
XX PS Claim 4; Page 22-23; 48pp; English.
XX PS
XX The invention covers hybrid TGF-beta molecules consisting of parts
XX CC of the human isoforms TGF-beta1, TGF-beta2 and TGF-beta3 (see AAQ41599,
XX CC AAQ41600 and AAQ41601, respectively). The hinge points between parts
XX CC derived from different parent isoforms are pref. between amino acids
XX CC 44 and 45, 56 and 57, 79 and 80, 90 and 91, or 22 and 23. The hybrid
XX CC molecules promote cell migration, inhibit the growth of A375
XX CC melanoma cells, accelerate the healing of partial-thickness burn
XX CC wounds and full-thickness incisional wounds and increase formation
XX CC of fibrous granular tissue. See e.g. AAQ41602-Q41607 for pref. hybrids.
XX CC
XX SQ Sequence 112 AA;

Query Match 84.4%; Score 535; DB 14; Length 112;
Best Local Similarity 79.5%; Pred. No. 1.2e-46;
Matches 89; Conservative 14; Mismatches 9; Indels 0; Gaps 0;

QY 1 ALDNTNCFRNLENCVRLPYIDFRQDLGWKWWHEPKGYVYANFCSGPCPYLRSADTTHST 60
Db ||| |||:::|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 61 ALDAAYCFRNVDNCCLRPLYIDFKRDLGWKWWHEPKGYNANFCAGACPYLWSSDTQHSR 60
QY 61 VLGLYNTLNPEASAPCCVPQDLEPLTILYVGRTPKVEQLSNMVKSCKS 112
Db || ||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 61 VLGLYNTLNPEASAPCCVPQDLEPLTILYVGRTPKVEQLSNMVKSCKS 112
Db || ||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 49
AAR92774
ID AAR92774 standard; Protein; 112 AA.
XX
XX AC AAR92774;
XX DT
XX 17-JUL-1996 (first entry)
XX DE
XX Human TGF-beta 2.
XX KW
XX Transforming growth factor type beta; TGF-beta 2;
XX KW protein renaturation; protein folding.
XX OS
XX Homo sapiens.
XX OS
XX WO9603433-A1.
XX PN
XX 08-FEB-1996.
XX PD
XX 12-JUL-1995; 95WO-EP02719.
XX PF
XX 25-JUL-1994; 94EP-0810439.
XX PR
XX (CIBA ) CIBA GEIGY AG.
XX PA
XX Cerletti N;
XX PI
XX WPI; 1996-117000/12.
XX DR N-PSDB; AAT17236.
XX DR
XX Prodn. of dimeric biologically active transforming growth factor
XX PT by refolding denatured monomer in detergent-free folding buffer
XX PT contg. specific organic solvent to improve yield
XX PS Example 1B; Page 31-32; 54pp; English.
```

XX Non-soluble, monomeric transforming growth factor TGF-beta 2
 CC (AAR92774) was recovered from E. coli IC 137 (DSM 5658) transformants
 CC carrying plasmid pLMu.TGF-beta 2, which includes the coding
 CC sequence (AAT17236) for TGF-beta 2. A biologically active, dimeric
 CC form of TGF-beta 2 was obtd. by refolding this monomer in detergent-
 CC free buffer contg. DMSO and/or DMF. Dimers of TGF-beta 1 (AAR92773)
 CC and TGF-beta 3 (AAR92772), and hybrid dimers (see also AAR92775-77),
 CC were also produced.
 XX Sequence 112 AA;
 SQ

Query Match 84.4%; Score 535; DB 17; Length 112;
 Best Local Similarity 79.5%; Pred. No. 1.2e-46;
 Matches 89; Conservative 14; Mismatches 9; Indels 0; Gaps 0;

QY 1 ALDTNYCFRNLEENCCVRPLYIDFRQDLGKWKVHEPKGYIANFCSGPCPYLRSADTHST 60
 DB 1 aldaaycfrrvqncclrpdyldfrkdlgwkwhepkgyanfcagacpylwsdtghsr 60

QY 61 VLGLYNTLNPEASASPCCVQDLEPLTILYVGRTPKVEQLSNMVKSKCS 112
 DB 61 vislyntinpeasaspcvcsqdlptilyyigtkpkieqlsnmivksckcs 112

RESULT 50
 AAR91957
 ID AAR91957 standard; Protein; 112 AA.
 XX
 AC AAR91957;
 XX
 DT 10-JUN-1996 (first entry)
 DE Human transforming growth factor beta 2.
 XX
 KW Transforming growth factor beta; TGF; regulator; method;
 KW proliferation; differentiation; wound healing; solvent.
 XX
 OS Homo sapiens.
 XX
 PN WO9603432-A1.
 PD 08-FEB-1996.
 XX
 PF 12-JUL-1995; 95WO-EP02718.
 XX
 PR 25-JUL-1994; 94EP-0810438.
 XX
 PA (CIBA) CIBA GEIGY AG.
 XX
 PI Cerletti N;
 XX
 DR WPI; 1996-116999/12.
 DR N-PSDB; AAT15463.
 XX
 PT Prodn. of dimeric, biologically active transforming growth factor
 PT beta - by refolding denatured monomer in buffer contg. mild
 PT detergent and specific organic solvents to improve yields
 XX
 PS Claim 17; Page 35-36; 59pp; English.
 XX
 CC AAR91956-R91958 are the amino acid sequences of human transforming
 CC growth factor (TGF) beta-1, TGF beta-2 and TGF beta-3 which are used to
 CC produce TGF beta-like proteins in dimeric form. The TGF beta-like
 CC proteins produced are hybrids of 2 different types of TGF beta e.g.
 CC TGF beta-1-3, TGF beta-2-3, etc, or bone morphogenic proteins e.g.
 CC BMP-2. The TGF beta hybrids were made using a new process of producing
 CC dimeric, biologically active TGF beta-like proteins. The new process
 CC involves treating denatured TGF beta monomers with folding buffer contg.
 CC a mild detergent (CHAPS, CHAPSO or digitonin) and at least one of the
 CC solvents DMSO (dimethyl sulphoxide), DMSO2 (dimethylsulphone) and DMF
 CC (dimethyl formamide). The detergent allows folding of the monomer such

CC that, after dimerisation, the TGF beta-like protein retains biological
 CC activity and remains in soluble form. The method allows relatively high
 CC yields of biologically active TGF beta-like proteins in their native
 CC dimeric form. TGF-beta like proteins are multifunctional regulators of
 CC cellular activity and a typical use is to stimulate wound healing.
 XX Sequence 112 AA;
 SQ

Query Match 84.4%; Score 535; DB 17; Length 112;
 Best Local Similarity 79.5%; Pred. No. 1.2e-46;
 Matches 89; Conservative 14; Mismatches 9; Indels 0; Gaps 0;

QY 1 ALDTNYCFRNLEENCCVRPLYIDFRQDLGKWKVHEPKGYIANFCSGPCPYLRSADTHST 60
 DB 1 aldaaycfrrvqncclrpdyldfrkdlgwkwhepkgyanfcagacpylwsdtghsr 60

QY 61 VLGLYNTLNPEASASPCCVQDLEPLTILYVGRTPKVEQLSNMVKSKCS 112
 DB 61 vislyntinpeasaspcvcsqdlptilyyigtkpkieqlsnmivksckcs 112

RESULT 51
 AAW08174
 ID AAW08174 standard; Peptide; 112 AA.
 XX
 AC AAW08174;
 XX
 DT 26-AUG-1997 (first entry)
 DE TGF active fragment of a TGF-beta fusion protein.
 XX
 KW Transforming growth factor-beta fusion protein; wound healing;
 KW artificial skin; surgery recovery time.
 XX
 OS Homo sapiens.
 XX
 PN WO9639430-A1.
 PD 12-DEC-1996.
 XX
 PF 05-JUN-1996; 96WO-US08973.
 XX
 PR 06-JUN-1995; 95US-0470837.
 XX
 PA (CHEU/) CHEUNG D T.
 PA (HALL/) HALL F L.
 PA (NIMN/) NIMNI M E.
 PA (TUAN/) TUAN T.
 PA (WULL/) WU L.
 XX
 PI Cheung DT, Hall FL, Nimni ME, Tuan T, Wu L;
 XX
 DR WPI; 1997-043065/04.
 DR N-PSDB; AAT42772.
 XX
 PT Prepn. of transforming growth factor-beta fusion protein - useful to
 PT reduce surgery recovery time and to prepare artificial skin
 XX
 PS Claim 12; Page 47-48; 59pp; English.
 XX
 CC A novel transforming growth factor-beta (TGF-beta) fusion protein
 CC comprises a purification tag and a TGF active fragment. The present
 CC sequence represents a specifically claimed TGF active fragment.
 CC Additionally, the fusion protein may comprise proteinase-sensitive
 CC linker sites and binding domain so the protein sequence may contain
 CC some or all of the following elements: purification tag; proteinase
 CC site; ECM binding site; proteinase site; TGF-beta. TGF-beta promotes
 CC wound healing, and the fusion protein can be used to reduce surgery
 CC recovery time and in the preparation of artificial skin. The inclusion
 CC of a purification tag facilitates purification of the fusion protein.
 CC The proteinase site is included to permit cleavage and release of the
 CC purification tag after purification if desired. The extracellular

CC matrix binding site facilitates delivery of the fusion protein to the
 CC desired site of action. Delivery of the TGF-beta to the site to be
 CC treated reduces the amount of TGF-beta required to be administered to
 CC be effective and reduces the concentration of circulating TGF-beta
 CC which may result in undesirable effects.

XX Sequence 112 AA;

Query Match 84.4%; Score 535; DB 18; Length 112;
 Best Local Similarity 79.5%; Pred. No. 1.2e-46;
 Matches 89; Conservative 14; Mismatches 9; Indels 0; Gaps 0;

QY 1 ALDINYCFRNLENCVRRPLYIDFQDLGKWKVHEPKGYANFCGCPYLRSDTTHST 60
 ||| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Db 1 aldaaycfvncvqncclrpdyidfkrdlgkwkwihepkgyanfcagacpylwsdtqshr 60
 ||| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 VLGLYNTLNPEASAPCCVQDLEPLTILYVVGRTPKVEQLSNMVKCKCS 112
 || |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Db 61 vlslyntinpeasapccvsgdlepiltilyigktpkieqlsnmivksckcs 112
 || |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 52

AA08300
 ID AAY08300 standard; Protein; 112 AA.

XX AC AAY08300;

XX DT 14-JUL-1999 (first entry)

XX DE Human growth factor protein fragment TGF-Beta2.

XX KW Growth factor; human; dimer; cysteine knot; cellular inclusion body;
 KW pharmaceutical.

XX OS Homo sapiens.

XX PN DE19748734-A1.

XX PD 06-MAY-1999.

XX PF 05-NOV-1997; 97DE-1048734.

XX PR 05-NOV-1997; 97DE-1048734.

XX PA (GBFB) GBS BIOTECHNOLOGISCHE FORSCHUNG MBH.

XX PI Erdmann H, Kaerst U, Mueller C, Rinas U, Weich H;

XX DR WPI; 1999-278785/24.

XX PT Preparing active growth factor dimers from inclusion bodies in high
 PT yield

XX PS Claim 14; Page 12; 14pp; German.

XX This invention describes the novel preparation of biologically active
 CC dimers of recombinant human growth factors of the cysteine knot family
 CC starting from cellular inclusion bodies. Such dimers are are useful in
 CC pharmaceutical compositions and the method provides yields of 31-39.7%,
 CC in examples, compared with about 10% for the conventional method (see
 CC Biochemistry, 28 (1989) 2956). AAY08278-Y08301 are human growth factor
 CC protein fragments used in the method of the invention.

XX Sequence 112 AA;

Query Match 84.4%; Score 535; DB 20; Length 112;
 Best Local Similarity 79.5%; Pred. No. 1.2e-46;
 Matches 89; Conservative 14; Mismatches 9; Indels 0; Gaps 0;

QY 1 ALDINYCFRNLENCVRRPLYIDFQDLGKWKVHEPKGYANFCGCPYLRSDTTHST 60
 ||| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Db 1 aldaaycfvncvqncclrpdyidfkrdlgkwkwihepkgyanfcagacpylwsdtqshr 60
 ||| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 VLGLYNTLNPEASAPCCVQDLEPLTILYVVGRTPKVEQLSNMVKCKCS 112
 || |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Db 61 vlslyntinpeasapccvsgdlepiltilyigktpkieqlsnmivksckcs 112
 || |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 53

AAW97092

ID AAW97092 standard; Protein; 112 AA.

XX AC AAW97092;

XX DT 28-APR-1999 (first entry)

XX DE The mature form of transforming growth factor-beta-2.

XX KW Transforming growth factor-beta-2; TGF-beta-like protein;
 KW S-sulphonated TGF-beta-like protein; wound treatment; cancer;
 KW bone repair; tissue repair; bone marrow protective agent;
 KW cardioprotection; anti-inflammatory; immunosuppressive;
 KW ulcer; bed sore.

XX OS Homo sapiens.

XX PN EP891985-A1.

XX PD 20-JAN-1999.

XX PF 27-NOV-1990; 90EP-0810922.

XX PR 06-DEC-1989; 89GB-0027546.

XX PA (NOVS) NOVARTIS AG.

XX PI Cerletti N, Cox D, McMaster GK, Meyhack B, Schmitz A;

XX PN WPI; 1999-083520/08.

XX DR N-PSDB; AAX15246.

XX PT Producing biologically active dimeric Transforming Growth
 PT Factor-beta - by refolding new monomeric Transforming Growth
 PT Factor-beta, useful for treatment of wounds and cancer

XX PS Example 1; Page 29; 32pp; English.

XX The present sequence represents the mature form of transforming growth
 CC factor-beta-2. Dimeric, biologically active TGF-beta-like protein
 CC can be produced by subjecting the denatured monomeric form to refolding
 CC conditions. The new monomeric S-sulphonated TGF-beta-like protein is
 CC useful for the production of the dimeric, biologically active
 CC TGF-beta-like protein, which is useful for the treatment of wounds
 CC (surface or internal) and cancer in a mammal, in bone and tissue
 CC repair, as a bone marrow protective agent, a mediator of
 CC cardioprotection, for the production of an anti-inflammatory or
 CC immunosuppressive preparation. Treatment is useful for animals,
 CC especially humans, and wound treatment (e.g. ulcers, bed sores etc.) is
 CC particularly useful for the elderly.

XX Sequence 112 AA;

Query Match 84.4%; Score 535; DB 20; Length 112;
 Best Local Similarity 79.5%; Pred. No. 1.2e-46;
 Matches 89; Conservative 14; Mismatches 9; Indels 0; Gaps 0;

QY 1 ALDINYCFRNLENCVRRPLYIDFQDLGKWKVHEPKGYANFCGCPYLRSDTTHST 60
 ||| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Db 1 aldaaycfvncvqncclrpdyidfkrdlgkwkwihepkgyanfcagacpylwsdtqshr 60
 ||| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 VLGLYNTLNPEASAPCCVQDLEPLTILYVVGRTPKVEQLSNMVKCKCS 112
 || |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Db 61 vlslyntinpeasapccvsgdlepiltilyigktpkieqlsnmivksckcs 112
 || |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

```

RESULT 54
AAW84208
ID AAW84208 standard; Protein; 112 AA.
XX AC
XX AC AAW84208;
XX DT 25-MAR-1999 (first entry)
XX DE Transforming growth factor beta active fragment.
XX KW Proteinase site; bone morphogenetic fusion protein; bone binding site;
XX KW bone morphogenetic protein; transforming growth factor beta;
XX KW active fragment; wound healing; bone growth; purification tag.
XX OS Homo sapiens.
XX PN WO9855137-A1.
XX PD 10-DEC-1998.
XX PF 02-JUN-1998; 98WO-US11189.
XX PR 03-JUN-1997; 97US-0868452.
XX PA (HALL/) HALL F L.
XX PA (HANS/) HAN B.
XX PA (NIMN/) NIMNI M E.
XX PA (SHOR/) SHORS E C.
XX PA (WULL/) WU L.
XX PI Hall FL, Han B, Nimni ME, Shors EC, Wu L;
XX WPI: 1999-059875/05.
XX DR N-PSDB; AAV99376.
XX New bone morphogenetic fusion proteins - comprising a purification
XX tag and a bone morphogenetic active fragment, used for enhancing
XX wound healing or bone growth
XX PS Disclosure; Page 42-43; 64pp; English.
XX CC The present sequence represents a transforming growth factor beta active
XX fragment. The protein can be used in place of a bone morphogenetic
XX active fragment to create the fusion proteins of the invention. When a
XX bone morphogenetic active fragment is used, the fusion proteins are
XX designated bone morphogenetic fusion proteins. The bone morphogenetic
XX fusion protein may contain some or all of the following elements: a
XX purification tag, a proteinase site, an ECM/bone binding site, a second
XX proteinase site, and a bone morphogenetic protein active fragment.
XX The bone morphogenetic fusion proteins can be used for enhancing wound
XX healing or bone growth.
XX SQ Sequence 112 AA;

Query Match 84.4%; Score 535; DB 20; Length 112;
Best Local Similarity 79.5%; Pred. No. 1.2e-46;
Matches 89; Conservative 14; Mismatches 9; Indels 0; Gaps 0;

QY 1 ALDTNCFNLSENCVRPLYIDFRQDLGKWKVHPEKGYANFCSPCPYLSRSDTHST 60
   ||| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 aldaaycfnvqncclrpdydfkrdlgkwkwhpekgynanfcagacpylwsdtqhsr 60
   ||| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 61 VIGLVNTLNPASAPCCVPQDLEPLTILYVVGRTPKVQLSNMVKSCKCS 112
   || |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 vislyntinpeaspcvcsqdepltillylgktpkieqlsmivksckcs 112
   || |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 55
AA92011
ID AA92011 standard; Protein; 112 AA.
```

```

XX AC
XX AC AAY92011;
XX DT 19-JUL-2000 (first entry)
XX DE Human transforming growth factor beta 2 monomer.
XX KW human transforming growth factor beta 2 monomer; CKGF; mutant;
XX KW cysteine knot growth factor; hairpin loop; infertility.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX Misc-difference 1..20 /note= "optionally mutated to increase electrostatic
FT interaction between beta hairpin structure and
FT a receptor"
FT
FT Domain 21..40 beta_hairpin_loop_1
FT /label= "mutant optionally comprises one or more
FT /note= substitutions in these residues"
FT
FT Misc-difference 41..81 /note= "optionally mutated to increase electrostatic
FT interaction between beta hairpin structure and
FT a receptor"
FT
FT Domain 82..102 beta_hairpin_loop_3
FT /label= "mutant optionally comprises one or more
FT /note= substitutions in these residues"
FT
FT Misc-difference 103..112 /note= "optionally mutated to increase electrostatic
FT interaction between beta hairpin structure and
FT a receptor"
FT
XX WO2000017360-A1.
XX PN
XX 30-MAR-2000.
XX PD
XX 19-MAR-1999; 99WO-US05908.
XX PF
XX 22-SEP-1998; 98WO-US19772.
XX PR
XX (UYMA-) UNIV MARYLAND BALTIMORE.
XX PI Weintraub BD, Szkudlinski MW;
XX DR WPI: 2000-283585/24.
XX PT New mutant cysteine knot growth factor proteins comprising one or more
XX mutant subunits, useful for treating or preventing diseases e.g.
XX hypothyroidism and thyroid cancer
XX PS Claim 208; Page 301; 320pp; English.
XX CC This is the wild type human transforming growth factor beta 2 monomer.
XX Mutants comprise at least one electrostatic charge altering mutation in a
XX beta hairpin loop, resulting in increased bioactivity.
XX CC Mutant cysteine knot growth factor (CKGF) proteins comprising one or more
XX mutant subunits and having novel properties or improved pharmacological
XX properties, compared to wild type CKGFs, are claimed. The CKGF
XX superfamily comprises at least four families of growth factors: the
XX glycoprotein hormones, the platelet-derived growth factor (PDGF) family,
XX the neurotrophins and the transforming growth factor-beta family; the
XX families are known to be structurally similar (especially comprising the
XX cysteine knot topology) and it was shown that mutations at certain
XX positions in the CKGF hairpin loops of family members and other members
XX of the CKGF superfamily could significantly alter the biological
XX activities of the CKGF.
XX CC Mutant transforming growth factor family proteins or analogues are useful
XX for treatment of ovulatory dysfunction, luteal phase defect, unexplained
XX infertility, time-limited conception and in assisted reproduction.
XX SQ Sequence 112 AA;
```



```

Db      4 aldaaycfrnvqncclrpilyidfkrdlgkwkwihepkgyanfcagacpylwsddtqhsr 63
QY      61 VLGLYNTLNPEASAPCCVPQDLEPLTILYVGRTPKVEQLSNMVKSCKCS 112
      || |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      64 vlslyntinpeasapccvsqdiptilyyigktpkieqlsmivksckcs 115

RESULT  58
AAR20126
ID      AAR20126 standard; Protein; 390 AA.
XX      AC      AAR20126;
XX      DT      16-APR-1992 (first entry)
XX      DE      Sequence of hybrid transforming growth factor (TGF) beta-1/beta2.
XX      KW      Hypertension therapy; hypotensive agent; blood pressure modulator.
XX      OS      Monkey and Homo sapiens.
XX      FH      Key
XX      FT      Peptide      Location/Qualifiers
XX      FT      Protein      8..21
XX      FT      Protein      280..391
XX      PN      W09119513-A.
XX      PD      26-DEC-1991.
XX      PF      20-JUN-1991; 91WO-US04449.
XX      PR      20-JUN-1990; 90US-0541221.
XX      PA      (BRIM ) BRISTOL-MYERS SQUIB.
XX      PI      Oleson FB, Comereski CR;
XX      PS      WPI; 1992-024199/03.
XX      DR      N-PSDB; AAQ20291.
XX      PT      Use of transforming growth factor (TGF)-beta and their
XX      PT      antagonists - for modulating blood pressure, for treating
XX      PT      hypertension and hypotension
XX      PS      Disclosure; Fig 3; 42pp; English.
XX      CC      A new method for treating hypertension comprises administering a
XX      CC      transforming growth factor (TGF)-beta to an individual at a dose
XX      CC      effective for lowering blood pressure; the TGF-beta may be e.g.
XX      CC      mature TGF-beta, TGF-beta2, a mature TGF-beta1/beta2 hybrid, TGF-
XX      CC      beta2 precursor, a latent TGF-beta2 precursor, hybrid TGF-beta1/TGF-
XX      CC      beta2 precursor, a latent TGF-beta1 complex or a latent TGF-beta2
XX      CC      complex.
XX      SQ      Sequence      390 AA;

      Query Match      84.4%; Score 535; DB 13; Length 390;
      Best Local Similarity 79.5%; Pred. No. 4.8e-46;
      Matches 89; Conservative 14; Mismatches 9; Indels 0; Gaps 0;

QY      1 ALDTNYCFRNLENCVVRPLYIDFRQDLGKWVHEPKGYANFCSGPCPYLRSADTTHST 60
      ||| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      279 aldaaycfrnvqncclrpilyidfkrdlgkwkwihepkgyanfcagacpylwsddtqhsr 338
QY      61 VLGLYNTLNPEASAPCCVPQDLEPLTILYVGRTPKVEQLSNMVKSCKCS 112
      || |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      339 vlslyntinpeasapccvsqdiptilyyigktpkieqlsmivksckcs 390

RESULT  59
AAR83055
ID      AAR83055 standard; Protein; 414 AA.

```

```

XX      AC      AAR83055;
XX      DT      25-JUN-1996 (first entry)
XX      DE      Transforming growth factor-beta 2.
XX      KW      macrophage inducible nitric oxide synthase; iNOS; constitutive NOS;
XX      KW      interleukin-1-beta; transforming growth factor-beta; TGF-beta; IL1-beta;
XX      KW      nitric oxide production; hypotension; inflammation; septic shock;
XX      KW      treatment.
XX      OS      Mammalian sp.
XX      FH      Key
XX      FT      Protein      Location/Qualifiers
XX      FT      Protein      303..414
XX      FT      Protein      /note= "represents the mature active TGF beta-1 mol."
XX      PN      W09526745-A1.
XX      PD      12-OCT-1995.
XX      PF      05-APR-1994; 94WO-US03705.
XX      PR      05-APR-1994; 94WO-US03705.
XX      PA      (HARD ) HARVARD COLLEGE.
XX      PI      Lee M, Perrella MA;
XX      DR      WPI; 1995-358443/46.
XX      DR      N-PSDB; AAT05877.
XX      PT      Treatment of hypotension, esp. in septic shock - by administering
XX      PT      transforming growth factor-beta e.g. to inhibit inducible nitric
XX      PT      oxide synthase gene transcription
XX      PS      Disclosure; Fig 18; 52pp; English.
XX      CC      Transforming growth factor-beta 2 (TGF-beta 2) has been found to inhibit
XX      CC      inducible nitric oxide synthase (iNOS) gene transcription, esp. in
XX      CC      interleukin-1-beta (IL1-beta) stimulated rat smooth muscle cells, and at
XX      CC      a dose which does not inhibit constitutive NOS. TGF-beta 1 (AAR83054) or
XX      CC      2 or their active fragments (esp. derived from the carboxy-terminal 112
XX      CC      amino acids), can be used in the treatment of hypotension, such as that
XX      CC      associated with severe inflammation or septic shock.
XX      SQ      Sequence      414 AA;

      Query Match      84.4%; Score 535; DB 16; Length 414;
      Best Local Similarity 79.5%; Pred. No. 5.1e-46;
      Matches 89; Conservative 14; Mismatches 9; Indels 0; Gaps 0;

QY      1 ALDTNYCFRNLENCVVRPLYIDFRQDLGKWVHEPKGYANFCSGPCPYLRSADTTHST 60
      ||| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      303 aldaaycfrnvqncclrpilyidfkrdlgkwkwihepkgyanfcagacpylwsddtqhsr 362
QY      61 VLGLYNTLNPEASAPCCVPQDLEPLTILYVGRTPKVEQLSNMVKSCKCS 112
      || |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      363 vlslyntinpeasapccvsqdiptilyyigktpkieqlsmivksckcs 414

RESULT  60
AAR73597
ID      AAR73597 standard; Protein; 414 AA.
XX      AC      AAR73597;
XX      DT      20-DEC-1995 (first entry)
XX      DE      Human TGF-beta 2 protein.

```

KW	Transforming growth factor-beta; Human TGF-beta protein; TGF-beta 1;	
KW	TGF-beta 2; TGF-beta 3; osteogenic cell source; OCS; bone deficiency;	
KW	bone-inducing cofactor.	
XX		
OS	Homo sapiens.	
XX		
PN	US5409896-A.	
XX		
PD	25-APR-1995.	
XX		
PF	12-NOV-1993; 930S-0401906.	
XX		
PR	01-SEP-1989; 89US-0401906.	
PR	12-NOV-1991; 91US-0790856.	
PR	18-MAY-1993; 930S-0063841.	
PR	12-NOV-1993; 930S-0132405.	
XX		
PA	(GETH) GENENTECH INC.	
XX		
PI	Ammann AJ, Rudman CG;	
XX		
DR	WPI; 1995-169610/22.	
XX		
PT	Compsn. for treating skeletal tissue deficiency - comprising	
PT	transforming growth factor-beta and an osteogenic cell source in a	
PT	carrier	
XX		
PS	Disclosure; Column 17-20; 19pp; English.	
XX		
CC	This sequence represents human transforming growth factor-beta 2	
CC	(TGF-beta 2). The sequences for human TGF-beta 1 (see AAR73596) and	
CC	human TGF-beta 3 (see AAR73598) are claimed within the scope of the	
CC	invention. The invention is a composition consisting of a TGF-beta	
CC	protein and an osteogenic cell source (OCS) formulated in an acceptable	
CC	carrier other than a bone morphogenic cofactor. This composition can be	
CC	used for the restoration of bone deficiency. This provides for the	
CC	generation of mature bone only where it is required, without the	
CC	inclusion of a specific bone-inducing cofactor. This method can be used	
CC	with any of the 5 human TGF-beta's or with TGF-beta from other species.	
XX		
SQ	Sequence 414 AA;	
Query Match 84.4%; Score 535; DB 16; Length 414;		
Best Local Similarity 79.5%; Pred. No. 5.1e-46;		
Matches 89; Conservative 14; Mismatches 9; Indels 0; Gaps 0;		
QY	1 ALDTNYCFRNLENCVVRPLYIDFRQDLGKWKVHEPKGYVANFCGCPYLRSDTTHST 60	
Db	303 aldaaycfrnvqncclrpilydfkrdlgkwkwihepkgyanfcagacpylwsdsdtghsr 362	
QY	61 VLGLYNTLNPEASASPCVPPQDLEPLTILYVVGRTPKVQLSNMVVKCKCS 112	
Db	363 vislyntinpeasaspcvvsqdlleptillyigktpkieqlsnmivksccks 414	
RESULT 61		
AAP91899		
ID	AAP91899 standard; protein; 442 AA.	
XX		
AC	AAP91899;	
XX		
DT	23-DEC-1990 (first entry)	
XX		
DE	Sequence encoded by human transforming growth factor (TGF) beta-2	
DE	precursor 442 cDNA in pPC-21.	
XX		
KW	Cell differentiation; cell proliferation.	
XX		
OS	Homo sapiens.	
XX		
XX		
FH	Key Location/Qualifiers	
FT	Region 20..442	
Query Match 84.4%; Score 535; DB 10; Length 442;		
Best Local Similarity 79.5%; Pred. No. 5.5e-46;		
Matches 89; Conservative 14; Mismatches 9; Indels 0; Gaps 0;		
QY	1 ALDTNYCFRNLENCVVRPLYIDFRQDLGKWKVHEPKGYVANFCGCPYLRSDTTHST 60	
Db	331 aldaaycfrnvqncclrpilydfkrdlgkwkwihepkgyanfcagacpylwsdsdtghsr 390	
QY	61 VLGLYNTLNPEASASPCVPPQDLEPLTILYVVGRTPKVQLSNMVVKCKCS 112	
Db	391 vislyntinpeasaspcvvsqdlleptillyigktpkieqlsnmivksccks 442	
RESULT 62		
AAR05748		
ID	AAR05748 standard; protein; 442 AA.	
XX		
AC	AAR05748;	
XX		
DT	02-NOV-1990 (first entry)	
XX		
DE	Human TGF-Beta2-442 precursor.	
XX		
KW	Human TGF-Beta2 precursor; cancer; tumorcide; ss.	
XX		
OS	Synthetic.	
XX		
FH	Key Location/Qualifiers	
FT	Protein 331..442	
FT	Peptide 4..19	
Peptide /note="Claimed"		
FT	4..19	
FT	/note="Signal"	
FT	20..21	
FT	116..144	
FT	/note="This entire SQ is replaced with Asn in simian	
FT	TGF-beta-2-414"	
FT		
FT	72	
FT	/note="Potential glycosylation site"	
FT	168	
FT	/note="Potential glycosylation site"	
FT	269	
FT	/note="Potential glycosylation site"	
FT	331..442	
XX		
PN	DE3833897-A.	
XX		
PD	03-MAY-1989.	
XX		
PF	05-OCT-1988; 88DE-3833897.	
XX		
PR	18-AUG-1988; 88US-0234065.	
XX		
PA	(ONCO-) ONCOGEN.	
XX		
PI	Purchio AF, Madisen L, Webb N;	
XX		
DR	WPI; 1989-138796/19.	
XX		
DR	N-PSDB; AAN90767.	
XX		
PT	New DNA sequence encoding transforming growth factor beta 2 -	
PT	used for large scale expression in eucaryotic cells	
XX		
PS	Claim 4; Fig 1a; 27pp; German.	
XX		
CC	PolyA-RNA was isolated from the tamoxifen-treated, human prostatic	
CC	adenocarcinoma line PC-3 and converted to cDNA. TGF DNA is pref. used	
CC	for control of the SV40 promoter. and expressed in CHO cells. The simian	
CC	SQ is also claimed.	
XX		
SQ	Sequence 442 AA;	

```
FT XX /label=Sinal peptide
PN XX EP376785-A.
XX
XX PD 04-JUL-1990.
XX
XX PF 14-DEC-1989; 89EP-0403480.
XX
XX PR 16-DEC-1988; 89US-0285140.
XX
XX PR 05-DEC-1989; 89US-0446020.
XX
XX PA (ONCO-) ONCOGEN LTD PARTNER.
XX
XX PI Purchio AF, Madisen L, Webb N;
XX
XX WPI; 1990-203127/27.
XX
XX DR N-PSDB; AAQ05126.
XX
XX PT Cloning and expression of transforming growth factor beta 2 -
XX used for treatment of tumors or for augmenting wound healing.
XX
XX PS Claim 1; Fig 1a; 58pp; English.
XX
XX CC TGF-Beta2 may be used in treatment of tumors at effective doses,
XX and may also be useful in augmenting wound healing by stimulating
XX cell proliferation. The growth factor can be produced at high
XX levels from a CHO expression system.
XX
XX SQ Sequence 442 AA;

Query Match 84.4%; Score 535; DB 11; Length 442;
Best Local Similarity 79.5%; Pred. No. 5.5e-46;
Matches 89; Conservative 14; Mismatches 9; Indels 0; Gaps 0;

QY 1 ALDTNYCFRNLENCVRLPYIDFRQDLGWKWWHEPKYGYANFCSGPCPYLRSADTTHTST 60
Db 331 aldaaycfrnvqdnccrlpyidfrkdlgwkwihpkgyanfcagacpylwssdtqhsr 390

QY 61 VLGLYNTLNPEASASPCCVQDLEPLTILYYVGRTPKVEQLSNMVKSKCS 112
Db 391 vlslyntlnpeasapccvsgdpleltilyyigktpkieqlsnmivksckcs 442

RESULT 63
AAR20125
ID AAR20125 standard; Protein; 442 AA.
XX
XX AC AAR20125;
XX
XX DT 16-APR-1992 (first entry)
XX
XX DE Sequence of human transforming growth factor (TGF) beta-2-442.
XX
XX KW Hypertension therapy; hypotensive agent; blood pressure modulator.
XX
XX OS Homo sapiens.
XX
XX FH Key Location/Qualifiers
XX FT Peptide 4..19
XX FT Protein 330..442
XX
XX PN W09119513-A.
XX
XX XX 26-DEC-1991.
XX
XX PF 20-JUN-1991; 91WO-US04449.
XX
XX PR 20-JUN-1990; 90US-0541221.
XX
XX PA (BRIM ) BRISTOL-MYERS SQUIB.
XX
XX PI Oleson FB, Comerreski CR;
```

```
XX WPI; 1992-024199/03.
XX DR N-PSDB; AAQ20290.
XX
XX PT Use of transforming growth factor (TGF)-beta and their
XX antagonists - for modulating blood pressure, for treating
XX hypertension and hypotension
XX
XX PS Disclosure; Fig 2; 42pp; English.
XX
XX CC A new method for treating hypertension comprises administering a
XX transforming growth factor (TGF)-beta to an individual at a dose
XX effective for lowering blood pressure; the TGF-beta may be e.g.
XX mature TGF-beta, TGF-beta2, a mature TGF-beta/beta2 hybrid, TGF-
XX beta1 precursor, a latent TGF-beta2 precursor, hybrid TGF-beta/TGF-
XX beta2 precursor, a latent TGF-beta1 complex or a latent TGF-beta2
XX complex.
XX
XX SQ Sequence 442 AA;

Query Match 84.4%; Score 535; DB 13; Length 442;
Best Local Similarity 79.5%; Pred. No. 5.5e-46;
Matches 89; Conservative 14; Mismatches 9; Indels 0; Gaps 0;

QY 1 ALDTNYCFRNLENCVRLPYIDFRQDLGWKWWHEPKYGYANFCSGPCPYLRSADTTHTST 60
Db 331 aldaaycfrnvqdnccrlpyidfrkdlgwkwihpkgyanfcagacpylwssdtqhsr 390

QY 61 VLGLYNTLNPEASASPCCVQDLEPLTILYYVGRTPKVEQLSNMVKSKCS 112
Db 391 vlslyntlnpeasapccvsgdpleltilyyigktpkieqlsnmivksckcs 442

RESULT 64
AAR79922
ID AAR79922 standard; Protein; 442 AA.
XX
XX AC AAR79922;
XX
XX DT 28-MAY-1996 (first entry)
XX
XX DE Human transforming growth factor-2.
XX
XX KW TGF-beta1; TGF-beta2; transforming growth factor; protein;
XX cell differentiation; cell proliferation; CHO; Chinese hamster;
XX ovary; COS; monkey kidney; animal; mammal.
XX
XX OS Homo sapiens.
XX
XX FH Key Location/Qualifiers
XX FT Peptide 4..19
XX FT Cleavage-site /note= "signal peptide"
XX FT 20..21
XX FT Peptide /note= "putative signal sequence cleavage site"
XX FT 331..442
XX FT /note= "mature peptide"
XX
XX PN EP676474-A1.
XX
XX XX 11-OCT-1995.
XX
XX PF 14-DEC-1989; 89EP-0104223.
XX
XX PR 05-DEC-1989; 89US-0446020.
XX
XX PR 16-DEC-1988; 88US-0285140.
XX
XX PA (ONCO ) ONCOGEN LP.
XX
XX PI Madisen L, Purchio AF, Webb N;
XX
XX WPI; 1995-346094/45.
XX
XX DR N-PSDB; AAT04116.
```

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XX Hybrid transforming growth factor beta-1/TGF-beta-2 precursor - used
PT to produce biologically active, mature TGF-beta-2
PS Disclosure: Fig.1a; 52pp; English.
XX
XX This sequence is expressed in a host cell, preferably a
CC COS or CHO cell, so the host cell produces active TGF-beta2. The
CC produced TGF-beta2 protein can be used to regulate cellular
CC differentiation and proliferation.
XX
XX Sequence 442 AA;

Query Match      84.4%; Score 535; DB 16; Length 442;
Best Local Similarity 79.5%; Pred. No. 5.5e-46;
Matches 89; Conservative 14; Mismatches 9; Indels 0; Gaps 0;

QY 1 ALDTNYCFRNLENCVRRPLYIDFRDLGKWKVHEPKGYANFCGPPYLRSDTTHST 60
   ||| |||||: |||: |||||: |||||: |||||: |||||: |||||: |||||: |||||
Db 331 aldaaycfrrvqncclrpdyidfrdlgkwkwihepkgyanfcagacpylwssdtqhsr 390

QY 61 VLGLYNTLNPEASAPCCVPQDLEPLTILYVGRTPKVEQLSNMVKCKCS 112
   || |||||: |||||: |||||: |||||: |||||: |||||: |||||: |||||
Db 391 vislyntinpeasapccvsgdqleptililyigktpkieqlsnmivksckcs 442

RESULT 65
AAP91900
ID AAP91900 standard; protein; 391 AA.
XX
AC AAP91900;
XX
XX 23-DEC-1990 (first entry)
XX
DE Sequence encoded by human transforming growth factor (TGF)
DE beta-1/TGF-beta-2 precursor DNA.
XX
XX Cell differentiation; cell proliferation.
XX
XX Homo sapiens.
XX
FH Key Location/Qualifiers
FT Region 30..391
FT Peptide /note="Claimed"
FT 8..21
FT /note="Signal"
FT Protein 279..291
XX
XX DE3833897-A.
XX
XX PN
XX PD
XX 03-MAY-1989.
XX
XX PF 05-OCT-1988; 88DE-3833897.
XX
XX PR 18-AUG-1988; 88US-0234065.
XX
XX PA (ONCO-) ONCOGEN.
XX
XX Purchio AF, Madisen L, Webb N;
XX
XX WPI; 1989-138796/19.
XX
XX DR N-PSDB; AAN90768.
XX
XX New DNA sequence encoding transforming growth factor beta 2 -
XX used for large scale expression in eucaryotic cells
XX
XX Claim 10; Fig 1b; 27pp; German.
XX
XX PolyA-RNA was isolated from the tamoxifen-treated, human prostatic
XX adenocarcinoma line PC-3 and converted to cDNA. TGF DNA is pref. used
XX for control of the SV40 promoter. and expressed in CHO cells.
XX

```

```

SQ Sequence 391 AA;

Query Match      84.1%; Score 533; DB 10; Length 391;
Best Local Similarity 79.5%; Pred. No. 7.6e-46;
Matches 89; Conservative 13; Mismatches 10; Indels 0; Gaps 0;

QY 1 ALDTNYCFRNLENCVRRPLYIDFRDLGKWKVHEPKGYANFCGPPYLRSDTTHST 60
   ||| |||||: |||: |||||: |||||: |||||: |||||: |||||: |||||
Db 280 aldaaycfrrvqncclrpdyidfrdlgkwkwihepkgyanfcagacpylwssdtqhsr 339

QY 61 VLGLYNTLNPEASAPCCVPQDLEPLTILYVGRTPKVEQLSNMVKCKCS 112
   || |||||: |||||: |||||: |||||: |||||: |||||: |||||: |||||
Db 340 vislyntinpeasapccvsgdqleptililyigktpkieqlsnmivksckcs 391

RESULT 66
AAR05665
ID AAR05665 standard; protein; 390 AA.
XX
AC AAR05665;
XX
XX 14-AUG-1990 (first entry)
XX
XX Human Transforming growth factor from TGF-Beta2-442 cDNA.
XX
XX HIV; AIDS; SIV; vaccine; AZT; CD4; cytokines; growth
XX factors; ds.
XX
FH Key Location/Qualifiers
FT Peptide 279..390
XX
XX EP356935-A.
XX
XX PD 07-MAR-1990.
XX
XX PF 25-AUG-1989; 89EP-0115719.
XX
XX PR 25-AUG-1988; 88US-0236698.
XX
XX PA (ONCO-) ONCOGEN LTD PARTNER.
XX
XX Brankovan V, Lioubin M, Purchio A;
XX
XX WPI; 1990-068723/10.
XX
XX DR N-PSDB; AAQ03510.
XX
XX Compens. contg. transforming growth factor beta -
XX used for inhibitions of HIV infection and replication in vivo.
XX
XX TGF-beta may be used in vivo to prevent formation of synctia and
XX inhibit HIV infection. TGF may also be used with other HIV treatments
XX (AZT, soluble CD4 etc.).
XX
XX Disclosure; Fig 2; 20pp; English.
XX
XX Sequence 390 AA;

Query Match      83.9%; Score 532; DB 11; Length 390;
Best Local Similarity 79.5%; Pred. No. 9.6e-46;
Matches 89; Conservative 13; Mismatches 10; Indels 0; Gaps 0;

QY 1 ALDTNYCFRNLENCVRRPLYIDFRDLGKWKVHEPKGYANFCGPPYLRSDTTHST 60
   ||| |||||: |||: |||||: |||||: |||||: |||||: |||||: |||||
Db 279 aldaaycfrrvqncclrpdyidfrdlgkwkwihepkgyanfcagacpylwssdtqhsr 338

QY 61 VLGLYNTLNPEASAPCCVPQDLEPLTILYVGRTPKVEQLSNMVKCKCS 112
   || |||||: |||||: |||||: |||||: |||||: |||||: |||||: |||||
Db 339 vislyntinpeasapccvsgdqleptililyigktpkieqlsnmivksckcs 390

RESULT 67

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```
AAR05666
ID AAR05666 standard; protein; 390 AA.
XX
AC AAR05666;
XX
DT 14-AUG-1990 (first entry)
XX
DE Hybrid transforming growth factor TGF-beta1/beta2.
XX
KW HIV; AIDS; SIV; vaccine; AZT; CD4; cytokines; growth
KW factors; ds.
XX
FH Key Location/Qualifiers
FT Peptide 379..390
XX
XX EP356935-A.
XX
PD 07-MAR-1990.
XX
XX 25-AUG-1989; 89EP-0115719.
XX
XX 25-AUG-1988; 88US-0236698.
XX
XX (ONCO-) ONCOGEN LTD PARTNER.
XX
PI Brankovan V, Lioubin M, Purchio A;
XX
DR WPI; 1990-068723/10.
DR N-PSDB; AAQ03511.
XX
XX Compsns. contg. transforming growth factor beta -
PT used for inhibitions of HIV infection and replication in vivo.
XX
XX TGF-beta may be used in vivo to prevent formation of synctia and
CC inhibit HIV infection. TGF may also be used with other HIV treatments
CC (AZT, soluble CD4 etc.).
XX
XX Disclosure; Fig 3; 20pp; English.
PS
XX Sequence 390 AA;
XX

Query Match 83.9%; Score 532; DB 11; Length 390;
Best Local Similarity 79.5%; Pred. No. 9.6e-46;
Matches 89; Conservative 13; Mismatches 10; Indels 0; Gaps 0;

QY 1 ALDTNYCFRNLENCVRLYIDFRDLGWKWHPEKGYANFCSPGCPYLRSADTHST 60
   ||| |||||: |||:|||||:|||||:|||||:|||||: |||||: ||| ||
Db 279 aldpaycfrrvghncclrlplyldfkrdlgkwihpkgyanfcagacpylwsdqtghr 338

QY 61 VLGLYNTLNPEASASPCCVQDLEPLTILYYVGRTPKVEQLSNMVKCKCS 112
   || |||||:|||||:|||||:|||||:|||||: |||||: |||||: |||||
Db 339 vlslyntlnpeasaspcvcsqdlptilyyigtkpkieqlsnmivksckcs 390

RESULT 68
AAR05749
ID AAR05749 standard; protein; 390 AA.
XX
AC AAR05749;
XX
DT 02-NOV-1990 (first entry)
XX
DE Human TGF-Beta2 expressed by TGF-Betal/TGF-Beta2 hybrid precursor.
XX
KW Human TGF-Beta2 precursor; cancer; tumoricide; ss.
XX
XX Synthetic.
OS
XX Key Location/Qualifiers
FH Protein 279..390
FT Peptide 8..21
   /label=Signal peptide
```

```
XX EP376785-A.
XX
XX 04-JUL-1990.
XX
XX 14-DEC-1989; 89EP-0403480.
XX
XX 16-DEC-1988; 88US-0285140.
XX
XX 05-DEC-1989; 89US-0446020.
XX
XX (ONCO-) ONCOGEN LTD PARTNER.
XX
XX Purchio AF, Madisen L, Webb N;
XX
XX WPI; 1990-203127/27.
XX
XX N-PSDB; AAQ05127.
XX
XX Cloning and expression of transforming growth factor beta 2 -
PT used for treatment of tumors or for augmenting wound healing.
XX
XX Claim 15; Fig 1b; 58pp; English.
XX
XX TGF-Beta2 may be used in treatment of tumors at effective doses,
CC and may also be useful in augmenting wound healing by stimulating
CC cell proliferation. The growth factor can be produced at high
CC levels from a CHO expression system.
XX
XX Sequence 390 AA;
XX

Query Match 83.9%; Score 532; DB 11; Length 390;
Best Local Similarity 79.5%; Pred. No. 9.6e-46;
Matches 89; Conservative 13; Mismatches 10; Indels 0; Gaps 0;

QY 1 ALDTNYCFRNLENCVRLYIDFRDLGWKWHPEKGYANFCSPGCPYLRSADTHST 60
   ||| |||||: |||:|||||:|||||:|||||:|||||: |||||: ||| ||
Db 279 aldpaycfrrvghncclrlplyldfkrdlgkwihpkgyanfcagacpylwsdqtghr 338

QY 61 VLGLYNTLNPEASASPCCVQDLEPLTILYYVGRTPKVEQLSNMVKCKCS 112
   || |||||:|||||:|||||:|||||:|||||: |||||: |||||: |||||
Db 339 vlslyntlnpeasaspcvcsqdlptilyyigtkpkieqlsnmivksckcs 390

RESULT 69
AAR27522
ID AAR27522 standard; Protein; 390 AA.
XX
AC AAR27522;
XX
XX 10-MAR-1993 (first entry)
XX
XX TGF-beta 1/beta 2 chimeric protein.
XX
XX Transforming growth factor; TGF; TGF-beta; TGF-5 beta; simian;
KW Simian virus 40; SV40; expression vector; Chinese Hamster ovary; CHO;
KW vascular endothelial cell.
XX
XX Synthetic.
OS
XX Key Location/Qualifiers
FH Peptide 1..29
FT /note= "Signal peptide, pre-pro-protein"
FT Region 30..278
FT /note= "pro-protein"
FT Protein 279..390
FT /note= "Mature TGF-5 beta"
FT Modified-site 82
FT /note= "N-glycosylation site"
FT Modified-site 136
FT /note= "N-glycosylation site"
FT Modified-site 176
FT /note= "N-glycosylation site"
FT Misc-difference 287
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XX FH Key Location/Qualifiers
XX FT Misc-difference 287..298
XX PN /note="TGF-beta2 derived sequence"
XX PD EP374044-A.
XX PD 20-JUN-1990.
XX PF 13-DEC-1989; 89EP-0403463.
XX PR 15-DEC-1988; 88US-0284972.
XX PA (ONCO-) ONCOGEN LTD PARTNER.
XX PI Purchio AF, Madisen L;
XX DR WPI; 1990-187401/25.
XX DR N-PSDB; AAQ04908.
XX PT New chimeric transforming growth factor -
XX PT with TGF-beta biological activity and increased secretion
XX PS efficiency.
XX PS Claim 2; Fig 1; 18pp; English.
XX CC Chimeric gene has TGF activity and may be more desirable than its
XX CC parents TGF-beta1 and TGF-beta2. CHO cells expressing the product
XX CC from a plasmid vector (pbeta/dhfr) are 2.5 times more bioactive
XX CC than normal. The product is useful in treatment of cancer and wound
XX CC healing.
XX CC See also EP-373994.
XX CC Sequence 390 AA;
XX SQ

Query Match 79.3%; Score 503; DB 11; Length 390;
Best Local Similarity 75.9%; Pred. No. 7.9e-43;
Matches 85; Conservative 14; Mismatches 13; Indels 0; Gaps 0;

QY 1 ALDTNYCFRNLENCVRLPYIDFRQDLGKWKVHEPKGYVANFCSGPCPYLRSADTTHST 60
DB 279 aldtncyfrnvqncclrlpyidfrkdlgkwkwihepkgyhanfclgpcpyiwsldtgysk 338
QY 61 VLGLYNTLNPEASAPCCVPQDLEPLTILYVGRTPKVEQLSNMVKSKCS 112
DB 339 vlalynqhnpgasaapccvpqaleplivyyvgrkpkveqlsnmivsvkcs 390

RESULT 72
AAR04076
ID AAR04076 standard; protein; 112 AA.
XX AC
XX AC AAR04076;
XX DT 31-MAY-1989 (first entry)
XX XX Sequence of mature human TGF-beta 1.
XX DE
XX DE Transforming growth factor beta-3 (TGF beta 3); tumour cells; growth
XX KW inhibition.
XX KW WO8912101-A.
XX PN
XX PN 14-DEC-1989.
XX PD
XX PD 08-JUN-1988; 88WO-US01945.
XX PF
XX PF 08-JUN-1988; 88WO-US01945.
XX PR
XX PR (GETH ) GENENTECH INC.
XX PA
XX PA Dernyck RM, Goeddel DV;

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XX WPI; 1990-007474/01.
XX Nucleotide sequence encoding transforming growth factor beta-3 used as a
XX probe, or to produce TGF beta 3, for inhibiting growth of certain normal
XX and neoplastic cells, eg A349.
XX Disclosure; Fig. 3; 61pp; English.
XX This sequence is that of mature human transforming growth factor-beta 1
XX (TGF-beta 1) polypeptide. It differs from human and porcine TGF-beta
XX subtype 3 sequences at positions 9-11,13,19,40,45,52,57,58,60,63,67,68,
XX 71,75,82,87, and 95. In addition porcine TGF-beta 3 has an AA substitution
XX at posn. 96. The N-terminal AA sequence of bovine TGF-beta 2 differs from
XX that of human TGF-beta 1 at posns 4,5,9,13, and 19.
XX The nucleic acid sequence encoding the second subtype of TGF-beta (TGF-
XX beta 3) is useful as a probe or to produce TGF-beta 3 for both normal and
XX neoplastic cell growth inhibition.
XX SQ Sequence 112 AA;

Query Match 78.9%; Score 500; DB 11; Length 112;
Best Local Similarity 76.8%; Pred. No. 3.9e-43;
Matches 86; Conservative 11; Mismatches 15; Indels 0; Gaps 0;

QY 1 ALDTNYCFRNLENCVRLPYIDFRQDLGKWKVHEPKGYVANFCSGPCPYLRSADTTHST 60
DB 1 aldtncyssstekncvcrqlyidfrkdlgkwkwihepkgyhanfclgpcpyiwsldtgysk 60
QY 61 VLGLYNTLNPEASAPCCVPQDLEPLTILYVGRTPKVEQLSNMVKSKCS 112
DB 61 vlalynqhnpgasaapccvpqaleplivyyvgrkpkveqlsnmivsvkcs 112

RESULT 73
AAR08142
ID AAR08142 standard; protein; 112 AA.
XX AC
XX AC AAR08142;
XX DT 28-FEB-1991 (first entry)
XX DE Platelet-derived human TGF-beta monomer.
XX XX Transforming growth factor; cartilages inducing factor; CIF;
XX KW polycythemia; thrombocytosis; splenomegaly.
XX OS Homo sapiens.
XX PN US4971952-A.
XX PD 20-NOV-1990.
XX PF 27-OCT-1988; 88US-0263635.
XX PR 06-MAR-1986; 86US-0836672.
XX PR 07-AUG-1985; 85US-0763337.
XX PA (CLGE ) COLLAGEN CORP.
XX PI Bentze H, Ellingsworth L, Armstrong R;
XX XX WPI; 1990-368150/49.
XX DR
XX DR Treating inflammation associated with transplants, etc. - using
XX PT cartilage inducing factor polypeptide homodimer cpd.
XX PS Disclosure; Fig 1; 14pp; English.
XX CC The TGF-beta may be used to derive cartilage inducing factors (CIFs)
XX CC useful for inhibition of acute/chronic inflammation, treatment of red
XX CC blood cell dysfunction associated with polycythemia, thrombocytosis

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CC or splenomegaly.
XX Sequence 112 AA;
SQ

Query Match 78.9%; Score 500; DB 11; Length 112;
Best Local Similarity 76.8%; Pred. No. 3.9e-43;
Matches 86; Conservative 11; Mismatches 15; Indels 0; Gaps 0;

QY 1 ALDNTYCFRNLENCVVRPLYIDFRQDLGKWKVHEPKGYANFCSGPCPYLRSADTTHTST 60
   ||||| : ||||| ||||| ||||| ||||| ||||| ||||| ||||| : || : |
Db 1 aldtncfsteknccvrrqlyidfrkdlgkwkwihepkgyhanfclgpcpyiwsldtqysk 60

QY 61 VLGLYNFLNPEASASPCCVQDLEPLTILYYVGRTPKVEQLSNMVKSCKCS 112
   || || || || || || || || || || || || || || || || || || || || ||
Db 61 vlalynqhnpgasaapccvpqaleplivyyvgrkpkveqlsnmivrsckcs 112

RESULT 74
AAR22134
ID AAR22134 standard; peptide; 112 AA.
AC AAR22134;
DT 10-JUL-1992 (first entry)
XX
DE PDGI subunit a.
KW Platelet derived growth inhibitor alpha; TGF-beta; trypsin;
KW pepsin; cell proliferation; eczema; immunosuppressant; ss.
XX
OS Homo sapiens.
XX
PN EP475719-A.
XX
PD 18-MAR-1992.
XX
PF 10-JAN-1991; 91EP-0308239.
XX
PR 11-SEP-1990; 90JP-0238944.
XX
PA (NAKA/) NAKAMURA T.
XX
PI Nakamura T;
XX
DR WPI; 1992-090304/12.
XX
PT New platelet-derived growth regulating peptide-alpha - used for
PT treatment of eczema, stimulation of bone growth and as
PT immunosuppressant
XX
PS Claim 2; Page 11; 21pp; English.
XX
CC The peptide is subunit a of PDGI alpha. It can be obtd. by treating
CC transforming growth factor (TGF) beta with chymotrypsin or pepsin,
CC or can be isolated from human blood platelets or by recombinant
CC expression of DNA obtd. using RNA extd. from blood plasma. PDGI
CC alpha is comprised of subunits a, b and c bonded b-a-c. PDGI alpha
CC can be used for controlling cell proliferation without the cancerous
CC activity (transformation activity) associated with TGF-beta. PDGI-
CC alpha can be used for activation and acceleration of the
CC proliferation of epithelium cells in treating eczema, for
CC stimulating osseous growth for bone formation or as an immuno-
CC suppressant for immune diseases.
CC See also AAR22135, 6.
XX
SQ Sequence 112 AA;

Query Match 78.9%; Score 500; DB 13; Length 112;
Best Local Similarity 76.8%; Pred. No. 3.9e-43;
Matches 86; Conservative 11; Mismatches 15; Indels 0; Gaps 0;

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QY 1 ALDNTYCFRNLENCVVRPLYIDFRQDLGKWKVHEPKGYANFCSGPCPYLRSADTTHTST 60
   ||||| : ||||| ||||| ||||| ||||| ||||| ||||| ||||| : || : |
Db 1 aldtncfsteknccvrrqlyidfrkdlgkwkwihepkgyhanfclgpcpyiwsldtqysk 60

QY 61 VLGLYNFLNPEASASPCCVQDLEPLTILYYVGRTPKVEQLSNMVKSCKCS 112
   || || || || || || || || || || || || || || || || || || || || ||
Db 61 vlalynqhnpgasaapccvpqaleplivyyvgrkpkveqlsnmivrsckcs 112

RESULT 75
AAR43263
ID AAR43263 standard; protein; 112 AA.
XX
AC AAR43263;
DT 27-APR-1994 (first entry)
XX
DE TGF-beta.
XX
KW TGF; transforming growth factor; scar formation; CNS;
KW central nervous system; infusion; antagonist; brain;
KW spinal cord; regeneration; decorin; Arg-Gly-Asp.
XX
OS Homo sapiens.
XX
PN WO9319783-A.
XX
PD 14-OCT-1993.
XX
PF 01-APR-1993; 93WO-US03068.
XX
PR 01-APR-1992; 92US-0860704.
XX
PA (WHIT-) WHITTIER INST DIABETES & ENDOCRINOLOGY.
XX
PI Baird A, Logan A;
XX
DR WPI; 1993-336598/42.
XX
PT Inhibiting or enhancing scar formation in the CNS - by infusion
PT of transforming growth factor-beta antagonists, e.g.
PT anti-(TGF-beta)-antibodies, or TGF-beta itself, respectively
XX
PS Disclosure; Page 5; 32pp; English.
XX
CC The mature form of TGF-beta is comprised of two identical chains,
CC each of 112 amino acids. Since TGF-beta is a regulator of scar
CC prodn. after a penetrating injury to the brain or spinal cord, which
CC scar prodn. can preclude neuronal recovery. TGF-beta antagonists
CC have potential use as adjuncts to those therapies designed to
CC promote regeneration and reconnection of damaged neural pathways.
XX
SQ Sequence 112 AA;

Query Match 78.9%; Score 500; DB 14; Length 112;
Best Local Similarity 76.8%; Pred. No. 3.9e-43;
Matches 86; Conservative 11; Mismatches 15; Indels 0; Gaps 0;

QY 1 ALDNTYCFRNLENCVVRPLYIDFRQDLGKWKVHEPKGYANFCSGPCPYLRSADTTHTST 60
   ||||| : ||||| ||||| ||||| ||||| ||||| ||||| ||||| : || : |
Db 1 aldtncfsteknccvrrqlyidfrkdlgkwkwihepkgyhanfclgpcpyiwsldtqysk 60

QY 61 VLGLYNFLNPEASASPCCVQDLEPLTILYYVGRTPKVEQLSNMVKSCKCS 112
   || || || || || || || || || || || || || || || || || || || || ||
Db 61 vlalynqhnpgasaapccvpqaleplivyyvgrkpkveqlsnmivrsckcs 112

RESULT 76
AAR42311
ID AAR42311 standard; peptide; 112 AA.
XX
AC AAR42311;

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Db 61 vlalynqhnpgasaapccvpqalelpivyyvgrkpkveqlsnmivrsckcs 112

RESULT	84
AA92010	AA92010
ID	AA92010 standard; Protein; 112 AA.
XX	AA92010;
AC	AA92010;
XX	19-JUL-2000 (first entry)
DT	19-JUL-2000 (first entry)
XX	Human transforming growth factor beta 1 monomer.
DE	human transforming growth factor beta 1 monomer; CKGF; mutant;
KW	cystine knot growth factor; hairpin loop; infertility.
XX	
OS	Homo sapiens.
XX	
Key	Location/Qualifiers
FH	Misc-difference 1..20
FT	/note= "optionally mutated to increase electrostatic interaction between beta hairpin structure and a receptor"
FT	
FT	Domain
FT	21..40
FT	/label= beta_hairpin_loop_1
FT	/note= "mutant optionally comprises one or more substitutions in these residues"
FT	
FT	Misc-difference 41..81
FT	/note= "optionally mutated to increase electrostatic interaction between beta hairpin structure and a receptor"
FT	
FT	Domain
FT	82..102
FT	/label= beta_hairpin_loop_3
FT	/note= "mutant optionally comprises one or more substitutions in these residues"
FT	
FT	Misc-difference 103..112
FT	/note= "optionally mutated to increase electrostatic interaction between beta hairpin structure and a receptor"
FT	
XX	
PN	WO200017360-A1.
XX	30-MAR-2000.
XX	19-MAR-1999; 99WO-US05908.
PF	22-SEP-1998; 98WO-US19772.
XX	(UYMA-) UNIV MARYLAND BALTIMORE.
XX	Weintraub BD, Szkudlinski MW;
PI	WPI; 2000-283585/24.
XX	New mutant cystine knot growth factor proteins comprising one or more mutant subunits, useful for treating or preventing diseases e.g. hypothyroidism and thyroid cancer
PT	Claim 193; Page 300; 320pp; English.
PS	This is the wild type human transforming growth factor beta 1 monomer. Mutants comprise at least one electrostatic charge altering mutation in beta hairpin loop, resulting in increased bioactivity.
XX	Mutant cystine knot growth factor (CKGF) proteins comprising one or more mutant subunits and having novel properties or improved pharmacological properties, compared to wild type CKGFs, are claimed. The CKGF superfamily comprises at least four families of growth factors: the glycoprotein hormones, the platelet-derived growth factor (PDGF) family, the neurotrophins and the transforming growth factor-beta family; the families are known to be structurally similar (especially comprising the cystine knot topology) and it was shown that mutations at certain positions in the CKGF hairpin loops of family members and other members of the CKGF superfamily could significantly alter the biological activities of the CKGF.
XX	Mutant transforming growth factor family proteins or analogues are used

CC for treatment of ovulatory dysfunction, luteal phase defect, unexplained
XX infertility, time-limited conception and in assisted reproduction.
SQ Sequence 112 AA;

Query Match 78.9%; Score 500; DB 21; Length 112;
Best Local Similarity 76.8%; Pred. No. 3.9e-43;
Matches 86; Conservative 11; Mismatches 15; Indels 0; Gaps 0;

QY 1 ALDNTNYCFRNLENCVRRPLYIDFRQDLGKWKVHEPKGYVANFCSGPCPYLRSADTTHST 60
DB 1 aldtncysfsteckncvrrqlyidfrkdkgkwihpkgyhanfcigpcpylwsldtgysk 60

QY 61 VLGLYNTLNPEASASPCVQDLEPLTILYVYGRTPKVEQLSNMVKSKCS 112
DB 61 vlalynqhngpasaapccvpqaleplivyyvgrkpkveqlsnmivrskcs 112

RESULT 85
AAY67950
ID AAY67950 standard; protein; 112 AA.
AC AAY67950;
XX
XX 03-APR-2000 (first entry)
XX Human transforming growth factor SEQ ID NO:2.
XX
XX Human; transforming growth factor; Pax4 gene; expression; potentiator;
KW Insulin; pancreatic beta cell; diabetes.
XX
XX Homo sapiens.
XX
XX WC9966073-A1.
XX
XX 23-DEC-1999.
XX
XX 15-JUN-1999; 99WO-JP03182.
XX
XX 16-JUN-1998; 98JP-0167976.
XX
XX (YAMA) YAMANOUCHI PHARM CO LTD.
XX
XX Ueda Y;
XX
XX WPI; 2000-097752/08.
XX
XX Screening potential Pax4 gene potentiators, used in treatment of, e.g.
PT diabetes -
XX
XX Disclosure; Page 29; 38pp; Japanese.

XX The present invention describes the a method for screening potential
XX inhibitors of the expression of the Pax4 gene by contacting the
XX potential inhibitor with pancreatic beta cells and measuring the
XX expression of the gene in these cells is new. Substances identified
XX by the screening method potentiate the expression of the Pax4 gene in
XX pancreatic beta cells and accelerate the expression of insulin gene in
XX those cells. The method can be used in the treatment of disorders in
XX which the exhaustion of pancreatic beta cells is involved, such as
XX diabetes. The present sequence represents the human transforming growth
XX factor protein which is used in the exemplification of the present
XX invention.

XX Sequence 112 AA;
Query Match 78.9%; Score 500; DB 21; Length 112;
Best Local Similarity 76.8%; Pred. No. 3.9e-43;
Matches 86; Conservative 11; Mismatches 15; Indels 0; Gaps 0;

QY 1 ALDNTNYCFRNLENCVRRPLYIDFRQDLGKWKVHEPKGYVANFCSGPCPYLRSADTTHST 60

DB 1 aldtncysfsteckncvrrqlyidfrkdkgkwihpkgyhanfcigpcpylwsldtgysk 60
QY 61 VLGLYNTLNPEASASPCVQDLEPLTILYVYGRTPKVEQLSNMVKSKCS 112
DB 61 vlalynqhngpasaapccvpqaleplivyyvgrkpkveqlsnmivrskcs 112

RESULT 86
AAB35937
ID AAB35937 standard; protein; 112 AA.
XX
AC AAB35937;
XX
XX 26-FEB-2001 (first entry)
XX
XX TGF-beta 1 amino acid sequence.
XX
XX Heparin binding; vascular graft; matrix; cell adhesion; growth factor;
KW wound healing; dermal wound; wound healing; TGF-beta 1.
XX
XX Unidentified.
XX
XX WO200064481-A1.
XX
XX 02-NOV-2000.
XX
XX 22-APR-1999; 99WO-IB00800.
XX
XX 22-APR-1999; 99WO-IB00800.
XX
XX (ETHZ-) ETH ZURICH & UNIV ZURICH.
XX
XX Sakiyama SE, Hubbell JA;
XX
XX WPI; 2001-024627/03.

XX Matrix for controlled release of growth factor for wound healing, has
XX substrate that attaches heparin binding peptide, protein growth factor
XX that bind heparin with low affinity, and heparin or heparin-like
XX polymer -
XX
XX Example 5; Page 21; 48pp; English.

XX This invention relates to a matrix comprising a substrate capable of
XX providing attachment of a heparin binding peptide (HBP), a peptide
XX comprising a binding domain which binds heparin with high affinity,
XX heparin or heparin-like polymer, and a protein growth factor or peptide
XX fragment which has a domain that binds heparin with low affinity.
XX Included in the invention is a vascular graft comprising the matrix,
XX which is capable of supporting cell adhesion. The matrix is used for
XX delivering low heparin binding affinity growth factor proteins or
XX peptides in a controlled manner suitable for wound healing. The matrix
XX can be used in an article for treating dermal wounds, and in an
XX implantable sterilized composition capable of supporting cell adhesion.
XX The present sequence represents a growth factor protein. The protein is
XX used in an example illustrating that non-heparin-binding growth factors
XX can be released in a controlled manner from heparin-based drug delivery
XX systems based on their low affinity for heparin.

XX Sequence 112 AA;

Query Match 78.9%; Score 500; DB 22; Length 112;
Best Local Similarity 76.8%; Pred. No. 3.9e-43;
Matches 86; Conservative 11; Mismatches 15; Indels 0; Gaps 0;

QY 1 ALDNTNYCFRNLENCVRRPLYIDFRQDLGKWKVHEPKGYVANFCSGPCPYLRSADTTHST 60
DB 1 aldtncysfsteckncvrrqlyidfrkdkgkwihpkgyhanfcigpcpylwsldtgysk 60
QY 61 VLGLYNTLNPEASASPCVQDLEPLTILYVYGRTPKVEQLSNMVKSKCS 112

N.B. The present sequence is does not appear in the specification,
but is derived from the sequences mentioned above.

Sequence 122 AA;

Query Match 78.9%; Score 500; DB 18; Length 122;
Best Local Similarity 76.8%; Pred. No. 4.2e-43;
Matches 86; Conservative 11; Mismatches 15; Indels 0; Gaps

QY 1 ALDTNYCFRNLESCCVRPLYIDFRODLGWKWHPEPKGYIANFCGCPCLRSADTTHST 60
||||| : ||||| ||||| : ||||| : ||||| : ||||| : || :
Db 11 aldtncfsstekccvrlqldfkdlgwkihepkgyhanfcgpcpylswldtqysk 70

QY 61 VLGLYNLTNPASAPCCVPQDPLEPTILYYVGRTPKEQLSNMVMVKCKCS 112
|| | || | || | || | || | : || | || | || | || | || | : || | || |
Db 71 vlalynhgasaapccvpqaaleplivyygrkpkeqlsnmivrsccks 122

RESULT 90
AAW08177
ID AAW08177 standard; Peptide; 124 AA.
XX AC AAW08177;
XX DT 26-AUG-1997 (first entry)
XX TF TGF-beta fusion protein 22:15:30.
KW Transforming growth factor-beta fusion protein; wound healing;
RW artificial skin; surgery recovery time.
OS Homo sapiens.
XS Synthetic.
FH Key Location/Qualifiers
FT Region 1..6 /label= Purification_tag
FT Region 7..12 /label= Proteinase_site
FT Region 13..123 /label= TGF-beta1_active_fragment
XX WO9639430-A1.
XX PD 12-DEC-1996.
XX PF 05-JUN-1996; 96WO-US08973.
XX PR 06-JUN-1995; 95US-0470837.
XX PA (CHEU/) CHEUNG D T.
PA (HALL/) HALL F L.
PA (NIMNI/) NIMNI M E.
PA (TUAN/) TUAN T.
PA (WULL/) WU L.
XX PI Cheung DT, Hall FL, Nimni ME, Tuan T, Wu L;
XX WPI; 1997-043065/04.
XX Prepn. of transforming growth factor-beta fusion protein - useful to
reduce surgery recovery time and to prepare artificial skin
PS Example 1; Page -: 59pp; English.
XX

A novel transforming growth factor-beta (TGF-beta) fusion protein comprises a purification tag and a TGF active fragment. Additionally, the fusion protein may comprise proteinase-sensitive linker sites and binding domain so the protein sequence may contain some or all of the following elements: purification tag;proteinase site;ECM binding site;proteinase site:TGF-beta. The present sequence represents a fusion protein made up from a purification tag (AAW18225), a proteinase site

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CC (AAW08170) and a TGF active fragment (AAW08173). TGF-beta promotes
CC wound healing, and the fusion protein can be used to reduce surgery
CC recovery time and in the preparation of artificial skin. The inclusion
CC of a purification tag facilitates purification of the fusion protein.
CC The proteinase site is included to permit cleavage and release of the
CC purification tag after purification if desired. The extracellular
CC matrix binding site facilitates delivery of the fusion protein to the
CC desired site of action. Delivery of the TGF-beta to the site to be
CC treated reduces the amount of TGF-beta required to be administered to
CC be effective and reduces the concentration of circulating TGF-beta
CC which may result in undesirable effects.
CC N.B. The present sequence is does not appear in the specification,
CC but is derived from the sequences mentioned above.
XX Sequence 124 AA;
SQ
    Query Match          78.9%; Score 500; DB 18; Length 124;
    Best Local Similarity 76.8%; Pred. No. 4.3e-43;
    Matches 86; Conservative 11; Mismatches 15; Indels 0; Gaps 0;
QY 1 ALDTNYCFRNLENCVRLYIDFRDLGKWKVHEPKGYANFCGPGPYLRSADTTHT 60
Db 13 aldtncfsstekncvrlqidfrkdlgkwkwihepkgyhanfcgpcpyiwsldtcqysk 72
QY 61 VLGLYNTLNPEASAPCCVPQDLEPLTILYVVGRTPKVEQLSNMVKSCKCS 112
Db 73 vialynqhnpgasapccvpqaleplivyvgrkpkveqlsnmivrsckcs 124
RESULT 91
AAW08188
ID AAW08188 standard; Peptide; 128 AA.
XX AC AAW08188;
XX FH Key Location/Qualifiers
FT Region 1..6
FT /label= Purification_tag
FT Region 7..10
FT /label= Proteinase_site
FT Region 11..16
FT /label= Extracellular_matrix_binding_site
FT Region 17..128
FT /label= TGF-betal_active_fragment
XX W09639430-A1.
XX PN
XX PD 12-DEC-1996.
XX PF 05-JUN-1996; 96WO-US089973.
XX PR 06-JUN-1995; 95US-0470837.
XX (CHEU/) CHEUNG D T.
XX (HALL/) HALL F L.
XX (NIMN/) NIMNI M E.
XX (TUAN/) TUAN T.
XX (WULL/) WU L.
XX Cheung DT, Hall FL, Nimni ME, Tuan T, Wu L;
XX WPI; 1997-043065/04.
DR
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XX Prepn. of transforming growth factor-beta fusion protein - useful to
PT reduce surgery recovery time and to prepare artificial skin
XX Disclosure; Page -: 59pp; English.
XX A novel transforming growth factor-beta (TGF-beta) fusion protein
CC comprises a purification tag and a TGF active fragment. Additionally,
CC the fusion protein may comprise proteinase-sensitive linker sites and
CC binding domain so the protein sequence may contain some or all of the
CC following elements: purification tag;proteinase site;ECM binding site;
CC proteinase site:TGF-beta. The present sequence represents a fusion
CC protein made up from a purification tag (AAW18225), a proteinase site
CC (AAW08169), an extracellular matrix binding site (AAW08171) and a TGF
CC active fragment (AAW08173). TGF-beta promotes wound healing, and the
CC fusion protein can be used to reduce surgery recovery time and in the
CC preparation of artificial skin. The inclusion of a purification tag
CC facilitates purification of the fusion protein. The proteinase site
CC is included to permit cleavage and release of the purification tag
CC after purification if desired. The extracellular matrix binding site
CC facilitates delivery of the fusion protein to the desired site of
CC action. Delivery of the TGF-beta to the site to be treated reduces
CC the amount of TGF-beta required to be administered to be effective
CC and reduces the concentration of circulating TGF-beta which may result
CC in undesirable effects.
CC N.B. The present sequence is does not appear in the specification,
CC but is derived from the sequences mentioned above.
XX Sequence 128 AA;
SQ
    Query Match          78.9%; Score 500; DB 18; Length 128;
    Best Local Similarity 76.8%; Pred. No. 4.5e-43;
    Matches 86; Conservative 11; Mismatches 15; Indels 0; Gaps 0;
QY 1 ALDTNYCFRNLENCVRLYIDFRDLGKWKVHEPKGYANFCGPGPYLRSADTTHT 60
Db 17 aldtncfsstekncvrlqidfrkdlgkwkwihepkgyhanfcgpcpyiwsldtcqysk 76
QY 61 VLGLYNTLNPEASAPCCVPQDLEPLTILYVVGRTPKVEQLSNMVKSCKCS 112
Db 77 vialynqhnpgasapccvpqaleplivyvgrkpkveqlsnmivrsckcs 128
RESULT 92
AAW08185
ID AAW08185 standard; Peptide; 130 AA.
XX AC AAW08185;
XX FH Key Location/Qualifiers
FT Region 1..6
FT /label= Purification_tag
FT Region 7..12
FT /label= Proteinase_site
FT Region 13..18
FT /label= Extracellular_matrix_binding_site
FT Region 19..130
FT /label= TGF-betal_active_fragment
XX W09639430-A1.
XX PN
XX PD 12-DEC-1996.
DR
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XX PF 05-JUN-1996; 96WO-US08973.
XX PR 06-JUN-1995; 95US-0470837.
XX XX
XX PA (CHEU/) CHEUNG D T.
XX PA (HALL/) HALL F L.
XX PA (NIMN/) NIMNI M E.
XX PA (TUAN/) TUAN T.
XX PA (WULL/) WU L.
XX XX
XX PI Cheung DT, Hall FL, Nimni ME, Tuan T, Wu L;
XX XX WPI; 1997-043065/04.
XX DR
XX PT Prepn. of transforming growth factor-beta fusion protein - useful to
XX PT reduce surgery recovery time and to prepare artificial skin
XX PS Disclosure; Page -: 59pp; English.
XX XX
XX CC A novel transforming growth factor-beta (TGF-beta) fusion protein
XX CC comprises a purification tag and a TGF active fragment. Additionally,
XX CC the fusion protein may comprise proteinase-sensitive linker sites and
XX CC binding domain so the protein sequence may contain some or all of the
XX CC following elements: purification tag; proteinase site; ECM binding site;
XX CC proteinase site; TGF-beta. The present sequence represents a fusion
XX CC protein made up from a purification tag (AAW18225), a proteinase site
XX CC (AAW08170), an extracellular matrix binding site (AAW08171) and a TGF
XX CC active fragment (AAW08173). TGF-beta promotes wound healing, and the
XX CC fusion protein can be used to reduce surgery recovery time and in
XX CC the preparation of artificial skin. The inclusion of a purification
XX CC tag facilitates purification of the fusion protein. The proteinase
XX CC site is included to permit cleavage and release of the purification
XX CC tag after purification if desired. The extracellular matrix binding
XX CC site facilitates delivery of the fusion protein to the desired site
XX CC of action. Delivery of the TGF-beta to the site to be treated reduces
XX CC the amount of TGF-beta required to be administered to be effective
XX CC and reduces the concentration of circulating TGF-beta which may
XX CC result in undesirable effects.
XX CC N.B. The present sequence is does not appear in the specification,
XX CC but is derived from the sequences mentioned above.
XX SQ Sequence 130 AA;

Query Match 78.9%; Score 500; DB 18; Length 130;
Best Local Similarity 76.8%; Pred. No. 4.6e-43;
Matches 86; Conservative 11; Mismatches 15; Indels 0; Gaps 0;

QY 1 ALDTNYCFRNLENCVVRPLYIDFRQDLGKWKVHEPKGYANFCGPGCPYLRSADTTHST 60
Db 19 aldtncyfsstekncvvrqlyidfrkdlgkwkwihepkgyhanfcigpcpylwsldtqysk 78

QY 61 VLGLYNTLNPEASAPCCVPQDLEPLTILYVYVGRTPKVEQLSNMVKSCKCS 112
Db 79 vlalynqhnpgasaapccvpqaleplipivvyvgrkpkveqlsnmivrsckcs 130

RESULT 93
AAW08182
ID AAW08182 standard; Peptide; 131 AA.
XX AC AAW08182;
XX XX
XX DT 26-AUG-1997 (first entry)
XX DE TGF-beta fusion protein 22:13:20:30.
XX XX
XX KW Transforming growth factor-beta fusion protein; wound healing;
XX KW artificial skin; surgery recovery time.
XX OS Homo sapiens.
XX OS Synthetic.

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XX FH Location/Qualifiers
XX FT 1..6
XX FT /label= Purification_tag
XX FT 7..10
XX FT /label= Proteinase_site
XX FT 11..19
XX FT /label= Extracellular_matrix_binding_site
XX FT 20..131
XX FT /label= TGF-beta1_active_fragment
XX XX
XX PN WO9639430-A1.
XX XX 12-DEC-1996.
XX XX
XX PF 05-JUN-1996; 96WO-US08973.
XX XX
XX PR 06-JUN-1995; 95US-0470837.
XX XX
XX PA (CHEU/) CHEUNG D T.
XX PA (HALL/) HALL F L.
XX PA (NIMN/) NIMNI M E.
XX PA (TUAN/) TUAN T.
XX PA (WULL/) WU L.
XX XX
XX PI Cheung DT, Hall FL, Nimni ME, Tuan T, Wu L;
XX XX WPI; 1997-043065/04.
XX DR
XX PT Prepn. of transforming growth factor-beta fusion protein - useful to
XX PT reduce surgery recovery time and to prepare artificial skin
XX PS Disclosure; Page -: 59pp; English.
XX XX
XX CC A novel transforming growth factor-beta (TGF-beta) fusion protein
XX CC comprises a purification tag and a TGF active fragment. Additionally,
XX CC the fusion protein may comprise proteinase-sensitive linker sites and
XX CC binding domain so the protein sequence may contain some or all of the
XX CC following elements: purification tag; proteinase site; ECM binding site;
XX CC proteinase site; TGF-beta. The present sequence represents a fusion
XX CC protein made up from a purification tag (AAW18225), a proteinase site
XX CC (AAW08169), an extracellular matrix binding site (AAW08172) and a TGF
XX CC active fragment (AAW08173). TGF-beta promotes wound healing, and the
XX CC fusion protein can be used to reduce surgery recovery time and in the
XX CC preparation of artificial skin. The inclusion of a purification tag
XX CC facilitates purification of the fusion protein. The proteinase site is
XX CC included to permit cleavage and release of the purification tag after
XX CC purification if desired. The extracellular matrix binding site
XX CC facilitates delivery of the fusion protein to the desired site of
XX CC action. Delivery of the TGF-beta to the site to be treated reduces the
XX CC amount of TGF-beta required to be administered to be effective and
XX CC reduces the concentration of circulating TGF-beta which may result in
XX CC undesirable effects.
XX CC N.B. The present sequence is does not appear in the specification,
XX CC but is derived from the sequences mentioned above.
XX SQ Sequence 131 AA;

Query Match 78.9%; Score 500; DB 18; Length 131;
Best Local Similarity 76.8%; Pred. No. 4.6e-43;
Matches 86; Conservative 11; Mismatches 15; Indels 0; Gaps 0;

QY 1 ALDTNYCFRNLENCVVRPLYIDFRQDLGKWKVHEPKGYANFCGPGCPYLRSADTTHST 60
Db 20 aldtncyfsstekncvvrqlyidfrkdlgkwkwihepkgyhanfcigpcpylwsldtqysk 79

QY 61 VLGLYNTLNPEASAPCCVPQDLEPLTILYVYVGRTPKVEQLSNMVKSCKCS 112
Db 80 vlalynqhnpgasaapccvpqaleplipivvyvgrkpkveqlsnmivrsckcs 131

RESULT 94

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AAW08189
ID AAW08189 standard; Peptide; 132 AA.

XX AC AAW08189;

XX DT 26-AUG-1997 (first entry)

XX DE TGF-beta fusion protein 22:13:18:13:30.

XX KW Transforming growth factor-beta fusion protein; wound healing;
artificial skin; surgery recovery time.

XX OS Homo sapiens.

XX OS Synthetic.

XX FH Key Location/Qualifiers
FT Region 1..6
FT Region /label= Purification_tag
FT Region 7..10
FT Region /label= Proteinase_site
FT Region 11..16
FT Region /label= Extracellular_matrix_binding_site
FT Region 17..20
FT Region /label= Proteinase_site
FT Region 21..132
FT Region /label= TGF-beta1_active_fragment

XX PN W09G39430-A1.

XX PD 12-DEC-1996.

XX PF 05-JUN-1996; 96WO-US08973.

XX PR 06-JUN-1995; 95US-0470837.

XX PA (CHEU/) CHEUNG D T.

XX PA (HALL/) HALL F L.

XX PA (NIMN/) NIMNI M E.

XX PA (TUAN/) TUAN T.

XX PA (WULL/) WU L.

XX PI Cheung DT, Hall FL, Nimmi ME, Tuan T, Wu L;

XX WPI; 1997-043065/04.

XX PT Prepn. of transforming growth factor-beta fusion protein - useful to
reduce surgery recovery time and to prepare artificial skin

XX PS Disclosure; Page -: 59pp; English.

XX CC A novel transforming growth factor-beta (TGF-beta) fusion protein
comprises a purification tag and a TGF active fragment. Additionally,
the fusion protein may comprise proteinase-sensitive linker sites and
binding domain so the protein sequence may contain some or all of the
following elements: purification tag; proteinase site; ECM binding site;
proteinase site; TGF-beta. The present sequence represents a fusion
protein made up from a purification tag (AAW18225), a proteinase site
(AAW08169), an extracellular matrix binding site (AAW08171), another
proteinase site (AAW08169) and a TGF active fragment (AAW08173).
TGF-beta promotes wound healing, and the fusion protein can be used to
reduce surgery recovery time and in the preparation of artificial skin.
The inclusion of a purification tag facilitates purification of the
fusion protein. The proteinase site is included to permit cleavage and
release of the purification tag after purification if desired. The
extracellular matrix binding site facilitates delivery of the fusion
protein to the desired site of action. Delivery of the TGF-beta to the
site to be treated reduces the amount of TGF-beta required to be
administered to be effective and reduces the concentration of circulating
TGF-beta which may result in undesirable effects.
N.B. The present sequence is does not appear in the specification,
XX CC but is derived from the sequences mentioned above.

XX Sequence 132 AA;

Query Match 78.9%; Score 500; DB 18; Length 132;
Best Local Similarity 76.8%; Pred. No. 4.6e-43;
Matches 86; Conservative 11; Mismatches 15; Indels 0; Gaps 0;

QY 1 ALDTNYCFRNLNCCVRRPLYIDFRQDLGWKWHPEKGYANFCSGPCPYLRSADTHST 60
||||| : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| : || : |

Db 21 aldtncfsstekncvrrqlyidfrkdlgwkwihpkyhanfclgpcpylwsldtgysk 80

QY 61 VLGLYNTLNPASPCCVQDLEPLTLIYYVGRTPKVEQLSNMVKSCKCS 112
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 81 vlalynghnpgsaaapccvpqaleplivyyvgrkpkveqlsnmivrsckcs 132

RESULT 95

AAW08178

ID AAW08178 standard; Peptide; 133 AA.

XX AC AAW08178;

XX DT 26-AUG-1997 (first entry)

XX DE TGF-beta fusion protein 22:15:20:30.

XX KW Transforming growth factor-beta fusion protein; wound healing;
artificial skin; surgery recovery time.

XX OS Homo sapiens.

XX OS Synthetic.

XX FH Key Location/Qualifiers
FT Region 1..6
FT Region /label= Purification_tag
FT Region 7..12
FT Region /label= Proteinase_site
FT Region 13..21
FT Region /label= Extracellular_matrix_binding_site
FT Region 22..133
FT Region /label= TGF-beta1_active_fragment

XX PN W09G39430-A1.

XX PD 12-DEC-1996.

XX PF 05-JUN-1996; 96WO-US08973.

XX PR 06-JUN-1995; 95US-0470837.

XX PA (CHEU/) CHEUNG D T.

XX PA (HALL/) HALL F L.

XX PA (NIMN/) NIMNI M E.

XX PA (TUAN/) TUAN T.

XX PA (WULL/) WU L.

XX PI Cheung DT, Hall FL, Nimmi ME, Tuan T, Wu L;

XX WPI; 1997-043065/04.

XX PT Prepn. of transforming growth factor-beta fusion protein - useful to
reduce surgery recovery time and to prepare artificial skin

XX PS Example 1; Page -: 59pp; English.

XX CC A novel transforming growth factor-beta (TGF-beta) fusion protein
comprises a purification tag and a TGF active fragment. Additionally,
the fusion protein may comprise proteinase-sensitive linker sites and
binding domain so the protein sequence may contain some or all of the
following elements: purification tag; proteinase site; ECM binding site;
proteinase site; TGF-beta. The present sequence represents a fusion
protein made up from a purification tag (AAW18225), a proteinase site
(AAW08170), an extracellular matrix binding site (AAW08172) and a TGF
active fragment (AAW08173). TGF-beta promotes wound healing, and the

CC fusion protein can be used to reduce surgery recovery time and in the
 CC preparation of artificial skin. The inclusion of a purification tag
 CC facilitates purification of the fusion protein. The proteinase site is
 CC included to permit cleavage and release of the purification tag after
 CC purification if desired. The extracellular matrix binding site
 CC facilitates delivery of the fusion protein to the desired site of
 CC action. Delivery of the TGF-beta to the site to be treated reduces the
 CC amount of TGF-beta required to be administered to be effective and
 CC reduces the concentration of circulating TGF-beta which may result in
 CC undesirable effects.
 CC N.B. The present sequence is does not appear in the specification,
 CC but is derived from the sequences mentioned above.
 XX Sequence 133 AA;
 SQ

Query Match 78.9%; Score 500; DB 18; Length 133;
 Best Local Similarity 76.8%; Pred. No. 4.7e-43;
 Matches 86; Conservative 11; Mismatches 15; Indels 0; Gaps 0;

QY 1 ALDNTNYCFRNLENCVRLPYIDFRQDLGWKWHPEKGYANFCGCPYLRSADTTHST 60
 ||||| : ||||| ||||| ||||| ||||| ||||| ||||| ||||| : || :
 Db 22 aldnycfsstekncvrlqyidfrkdlgwkwihpekyhanfclgpcpyiwsldtqysk 81
 ||||| : ||||| ||||| ||||| ||||| ||||| ||||| ||||| : || :
 QY 61 VLGLYNTLNPEASAPCCVPQDLPLTILYVGRTPKVEQLSNMVKSKCS 112
 || ||| || ||||| ||||| ||||| ||||| ||||| ||||| : |||||
 Db 82 vlalynqhnpgasaapccvpqaleplpivyyvgrkpkveqlsnmivrsckcs 133
 || ||| || ||||| ||||| ||||| ||||| ||||| ||||| : |||||

RESULT 96
 AAW08187
 ID AAW08187 standard; Peptide: 134 AA.
 XX
 AC AAW08187;
 XX
 DT 26-AUG-1997 (first entry)
 XX
 DE TGF-beta fusion protein 22:15:18:13:30.
 XX Transforming growth factor-beta fusion protein; wound healing;
 KW artificial skin; surgery recovery time.
 XX Homo sapiens.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Region 1..6
 FT /label= Purification_tag
 FT Region 7..12
 FT /label= Proteinase_site
 FT Region 13..18
 FT /label= Extracellular_matrix_binding_site
 FT Region 19..22
 FT /label= Proteinase_site
 FT Region 23..134
 FT /label= TGF-beta_active_fragment
 XX
 PN W09639430-A1.
 XX
 PD 12-DEC-1996.
 XX
 XX 05-JUN-1996; 96WO-US08973.
 XX
 XX 06-JUN-1995; 95US-0470837.
 PR
 XX (CHEU/) CHEUNG D T.
 PA (HALL/) HALL F L.
 PA (NIMN/) NIMNI M E.
 PA (TUAN/) TUAN T.
 PA (WULL/) WU L.
 XX
 PI Cheung DT, Hall FL, Nimni ME, Tuan T, Wu L;
 XX

DR WPI; 1997-043065/04.
 XX
 PT Prepn. of transforming growth factor-beta fusion protein - useful to
 PT reduce surgery recovery time and to prepare artificial skin
 XX
 XX Disclosure; Page -: 59pp; English.
 XX
 CC A novel transforming growth factor-beta (TGF-beta) fusion protein
 CC comprises a purification tag and a TGF active fragment. Additionally,
 CC the fusion protein may comprise proteinase-sensitive linker sites and
 CC binding domain so the protein sequence may contain some or all of the
 CC following elements: purification tag; proteinase site; ECM binding site;
 CC proteinase site; TGF-beta. The present sequence represents a fusion
 CC protein made up from a purification tag (AAW18225), a proteinase site
 CC (AAW08170), an extracellular matrix binding site (AAW08171), another
 CC proteinase site (AAW08169) and a TGF active fragment (AAW08173).
 CC TGF-beta promotes wound healing, and the fusion protein can be used to
 CC reduce surgery recovery time and in the preparation of artificial skin.
 CC The inclusion of a purification tag facilitates purification of the
 CC fusion protein. The proteinase site is included to permit cleavage and
 CC release of the purification tag after purification if desired. The
 CC extracellular matrix binding site facilitates delivery of the fusion
 CC protein to the desired site of action. Delivery of the TGF-beta to the
 CC site to be treated reduces the amount of TGF-beta required to be
 CC administered to be effective and reduces the concentration of circulating
 CC TGF-beta which may result in undesirable effects.
 CC N.B. The present sequence is does not appear in the specification,
 CC but is derived from the sequences mentioned above.
 XX Sequence 134 AA;
 SQ

Query Match 78.9%; Score 500; DB 18; Length 134;
 Best Local Similarity 76.8%; Pred. No. 4.7e-43;
 Matches 86; Conservative 11; Mismatches 15; Indels 0; Gaps 0;

QY 1 ALDNTNYCFRNLENCVRLPYIDFRQDLGWKWHPEKGYANFCGCPYLRSADTTHST 60
 ||||| : ||||| ||||| ||||| ||||| ||||| ||||| ||||| : || :
 Db 23 aldnycfsstekncvrlqyidfrkdlgwkwihpekyhanfclgpcpyiwsldtqysk 82
 ||||| : ||||| ||||| ||||| ||||| ||||| ||||| ||||| : || :
 QY 61 VLGLYNTLNPEASAPCCVPQDLPLTILYVGRTPKVEQLSNMVKSKCS 112
 || ||| || ||||| ||||| ||||| ||||| ||||| ||||| : |||||
 Db 83 vlalynqhnpgasaapccvpqaleplpivyyvgrkpkveqlsnmivrsckcs 134
 || ||| || ||||| ||||| ||||| ||||| ||||| ||||| : |||||

RESULT 97
 AAW08190
 ID AAW08190 standard; Peptide: 134 AA.
 XX
 AC AAW08190;
 XX
 DT 26-AUG-1997 (first entry)
 XX
 DE TGF-beta fusion protein 22:13:18:15:30.
 XX Transforming growth factor-beta fusion protein; wound healing;
 KW artificial skin; surgery recovery time.
 XX Homo sapiens.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Region 1..6
 FT /label= Purification_tag
 FT Region 7..10
 FT /label= Proteinase_site
 FT Region 11..16
 FT /label= Extracellular_matrix_binding_site
 FT Region 17..22
 FT /label= Proteinase_site
 FT Region 23..134
 FT /label= TGF-beta_active_fragment
 XX

```

PN WO9639430-A1.
XX
XX PD
XX OS
XX PF 12-DEC-1996.
XX
XX PF 05-JUN-1996; 96WO-US08973.
XX
XX PR 06-JUN-1995; 95US-0470837.
XX
XX PA (CHEU/) CHEUNG D T.
XX PA (HALL/) HALL F L.
XX PA (NIMN/) NIMNI M E.
XX PA (TUAN/) TUAN T.
XX PA (WULL/) WU L.
XX
PI Cheung DT, Hall FL, Nimni ME, Tuan T, Wu L;
XX WPI; 1997-043065/04.
XX
XX Prepn. of transforming growth factor-beta fusion protein - useful to
XX reduce surgery recovery time and to prepare artificial skin
XX
XX PS Disclosure; Page -: 59pp; English.
XX
XX CC A novel transforming growth factor-beta (TGF-beta) fusion protein
XX comprises a purification tag and a TGF active fragment. Additionally,
XX the fusion protein may comprise proteinase-sensitive linker sites and
XX binding domain so the protein sequence may contain some or all of the
XX following elements: purification tag; proteinase site; ECM binding site;
XX proteinase site; TGF-beta. The present sequence represents a fusion
XX protein made up from a purification tag (AAW18225), a proteinase site
XX (AAW08169), an extracellular matrix binding site (AAW08171), another
XX proteinase site (AAW08170) and a TGF active fragment (AAW08173).
XX TGF-beta promotes wound healing, and the fusion protein can be used to
XX reduce surgery recovery time and in the preparation of artificial skin.
XX The inclusion of a purification tag facilitates purification of the
XX fusion protein. The proteinase site is included to permit cleavage and
XX release of the purification tag after purification if desired. The
XX extracellular matrix binding site facilitates delivery of the fusion
XX protein to the desired site of action. Delivery of the TGF-beta to the
XX site to be treated reduces the amount of TGF-beta required to be
XX administered to be effective and reduces the concentration of circulating
XX TGF-beta which may result in undesirable effects.
XX N.B. The present sequence is does not appear in the specification,
XX but is derived from the sequences mentioned above.
XX
XX SQ Sequence 134 AA;

Query Match 78.9%; Score 500; DB 18; Length 134;
Best Local Similarity 76.8%; Pred. No. 4.7e-43;
Matches 86; Conservative 11; Mismatches 15; Indels 0; Gaps 0;

QY 1 ALDNTYCFNRLENCVRRPLYIDFRDLGKWKVHPEKGYANFCSPGCPYLRSDPTHTST 60
DB 23 aldtncyfstekncvcrrglyidfrkdlgwkwihpekgvhanfclgpcpylwsldtqysk 82
QY 61 VLGLYNTLNPEASAPCCVPQDLEPLTILYYVGRTPKVEQLSNMVKSCKCS 112
DB 83 vialynqhpgasapccvpqaleplivyyvgrtpkveqlsnmivrskcs 134

RESULT 98
AAW08183
ID AAW08183 standard; Peptide; 135 AA.
XX
XX AC AAW08183;
XX
XX DT 26-AUG-1997 (first entry)
XX
XX DE TGF-beta fusion protein 22:13:20:13:30.
XX
XX KW Transforming growth factor-beta fusion protein; wound healing;
XX artificial skin; surgery recovery time.

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XX
XX OS Homo sapiens.
XX OS Synthetic.
XX
XX FH Key Location/Qualifiers
XX FT Region 1..6
XX FT /label= Purification_tag
XX FT Region 7..10
XX FT /label= Proteinase_site
XX FT Region 11..19
XX FT /label= Extracellular_matrix_binding_site
XX FT Region 20..23
XX FT /label= Proteinase_site
XX FT Region 24..135
XX FT /label= TGF-beta1_active_fragment
XX
XX PN WO9639430-A1.
XX
XX XX 12-DEC-1996.
XX
XX XX 05-JUN-1996; 96WO-US08973.
XX
XX XX 06-JUN-1995; 95US-0470837.
XX
XX XX (CHEU/) CHEUNG D T.
XX PA (HALL/) HALL F L.
XX PA (NIMN/) NIMNI M E.
XX PA (TUAN/) TUAN T.
XX PA (WULL/) WU L.
XX
XX Cheung DT, Hall FL, Nimni ME, Tuan T, Wu L;
XX WPI; 1997-043065/04.
XX
XX Prepn. of transforming growth factor-beta fusion protein - useful to
XX reduce surgery recovery time and to prepare artificial skin
XX
XX PS Disclosure; Page -: 59pp; English.
XX
XX CC A novel transforming growth factor-beta (TGF-beta) fusion protein
XX comprises a purification tag and a TGF active fragment. Additionally,
XX the fusion protein may comprise proteinase-sensitive linker sites and
XX binding domain so the protein sequence may contain some or all of the
XX following elements: purification tag; proteinase site; ECM binding site;
XX proteinase site; TGF-beta. The present sequence represents a fusion
XX protein made up from a purification tag (AAW18225), a proteinase site
XX (AAW08169), an extracellular matrix binding site (AAW08172), another
XX proteinase site (AAW08169) and a TGF active fragment (AAW08173).
XX TGF-beta promotes wound healing, and the fusion protein can be used to
XX reduce surgery recovery time and in the preparation of artificial skin.
XX The inclusion of a purification tag facilitates purification of the
XX fusion protein. The proteinase site is included to permit cleavage and
XX release of the purification tag after purification if desired. The
XX extracellular matrix binding site facilitates delivery of the fusion
XX protein to the desired site of action. Delivery of the TGF-beta to the
XX site to be treated reduces the amount of TGF-beta required to be
XX administered to be effective and reduces the concentration of circulating
XX TGF-beta which may result in undesirable effects.
XX N.B. The present sequence is does not appear in the specification,
XX but is derived from the sequences mentioned above.
XX
XX SQ Sequence 135 AA;

Query Match 78.9%; Score 500; DB 18; Length 135;
Best Local Similarity 76.8%; Pred. No. 4.8e-43;
Matches 86; Conservative 11; Mismatches 15; Indels 0; Gaps 0;

QY 1 ALDNTYCFNRLENCVRRPLYIDFRDLGKWKVHPEKGYANFCSPGCPYLRSDPTHTST 60
DB 24 aldtncyfstekncvcrrglyidfrkdlgwkwihpekgvhanfclgpcpylwsldtqysk 83
QY 61 VLGLYNTLNPEASAPCCVPQDLEPLTILYYVGRTPKVEQLSNMVKSCKCS 112

```

Db 84 vialynhnpasapccvpqalepivvyvgrkpkveqlsnmivrsckcs 135

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RESULT 99
AAW08186
ID AAW08186 standard; Peptide; 136 AA.
AC AAW08186;
XX
XX
XX
XX 26-AUG-1997 (first entry)
DE TGF-beta fusion protein 22:15:18:15:30.
XX
XX Transforming growth factor-beta fusion protein; wound healing;
KW artificial skin; surgery recovery time.
XX
XX Homo sapiens.
OS Synthetic.
XX
XX Key Location/Qualifiers
FH Region 1..6
FT /label= Purification_tag
FT 7..12
FT /label= Proteinase_site
FT 13..18
FT /label= Extracellular_matrix_binding_site
FT 19..24
FT /label= Proteinase_site
FT 25..136
FT /label= TGF-beta1_active_fragment
XX
XX WO9639430-A1.
XX
XX 12-DEC-1996.
XX
XX 05-JUN-1996; 96WO-US08973.
XX
XX 06-JUN-1995; 95US-0470837.
XX
XX (CHEU/) CHEUNG D T.
PA (HALL/) HALL F L.
PA (NIMN/) NIMNI M E.
PA (TUAN/) TUAN T.
PA (WULL/) WU L.
XX
XX Cheung DT, Hall FL, Nimni ME, Tuan T, Wu L;
PI WPI; 1997-043065/04.
XX
XX Prepn. of transforming growth factor-beta fusion protein - useful to
PT reduce surgery recovery time and to prepare artificial skin
XX
XX Disclosure; Page -: 59pp; English.
XX
XX A novel transforming growth factor-beta (TGF-beta) fusion protein
CC comprises a purification tag and a TGF active fragment. Additionally,
CC the fusion protein may comprise proteinase-sensitive linker sites and
CC binding domain so the protein sequence may contain some or all of the
CC following elements: purification tag; proteinase site; ECM binding site;
CC proteinase site: TGF-beta. The present sequence represents a fusion
CC protein made up from a purification tag (AAW18225), a proteinase site
CC (AAW08170), an extracellular matrix binding site (AAW08171), another
CC proteinase site (AAW08170) and a TGF active fragment (AAW08173).
CC TGF-beta promotes wound healing, and the fusion protein can be used to
CC reduce surgery recovery time and in the preparation of artificial skin.
CC The inclusion of a purification tag facilitates purification of the
CC fusion protein. The proteinase site is included to permit cleavage and
CC release of the purification tag after purification if desired. The
CC extracellular matrix binding site facilitates delivery of the fusion
CC protein to the desired site of action. Delivery of the TGF-beta to the
CC site to be treated reduces the amount of TGF-beta required to be
CC administered to be effective and reduces the concentration of circulating

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CC TGF-beta which may result in undesirable effects.
 CC N.B. The present sequence is does not appear in the specification,
 CC but is derived from the sequences mentioned above.
 XX
 SQ Sequence 136 AA;

Query Match 78.9%; Score 500; DB 18; Length 136;
 Best Local Similarity 76.8%; Pred. No. 4.8e-43;
 Matches 86; Conservative 11; Mismatches 15; Indels 0; Gaps 0;

QY 1 ALDTNYCFRNLENCVRRPLYIDFRQDLGWKWWHPKGYANFCGPGCPYLSADTTHST 60
 ||||| : ||||| ||||| ||||| ||||| ||||| ||||| ||||| : ||| : |
 Db 25 aldtncfsstekccvrrqlyidfrkdgkwkwihepkgyhanfcigpcpyiwsldtqysk 84
 QY 61 VLGLYNTLNPEASAPCCVPQDLEPLTLYYVGRTPKVEQLSNMVMVKCKCS 112
 ||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| : |||||
 Db 85 vialynhnpasapccvpqalepivvyvgrkpkveqlsnmivrsckcs 136

RESULT 100
 AAW08180
 ID AAW08180 standard; Peptide; 137 AA.
 XX
 AC AAW08180;
 XX
 XX 26-AUG-1997 (first entry)
 DT
 XX
 DE TGF-beta fusion protein 22:15:20:13:30.
 XX
 XX Transforming growth factor-beta fusion protein; wound healing;
 KW artificial skin; surgery recovery time.
 XX
 XX Homo sapiens.
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FH Region 1..6
 FT /label= Purification_tag
 FT 7..12
 FT /label= Proteinase_site
 FT 13..21
 FT /label= Extracellular_matrix_binding_site
 FT 22..25
 FT /label= Proteinase_site
 FT 26..137
 FT /label= TGF-beta1_active_fragment
 XX
 XX WO9639430-A1.
 XX
 XX 12-DEC-1996.
 XX
 XX 05-JUN-1996; 96WO-US08973.
 XX
 XX 06-JUN-1995; 95US-0470837.
 XX
 XX (CHEU/) CHEUNG D T.
 PA (HALL/) HALL F L.
 PA (NIMN/) NIMNI M E.
 PA (TUAN/) TUAN T.
 PA (WULL/) WU L.
 XX
 XX Cheung DT, Hall FL, Nimni ME, Tuan T, Wu L;
 PI WPI; 1997-043065/04.
 XX
 XX Prepn. of transforming growth factor-beta fusion protein - useful to
 PT reduce surgery recovery time and to prepare artificial skin
 XX
 XX Disclosure; Page -: 59pp; English.
 XX
 XX A novel transforming growth factor-beta (TGF-beta) fusion protein
 CC comprises a purification tag and a TGF active fragment. Additionally,

CC the fusion protein may comprise proteinase-sensitive linker sites and
 CC binding domain so the protein sequence may contain some or all of the
 CC following elements: purification tag; proteinase site; ECM binding site;
 CC proteinase site; TGF-beta. The present sequence represents a fusion
 CC protein made up from a purification tag (AAW18225), a proteinase site
 CC (AAW08170), an extracellular matrix binding site (AAW08172), another
 CC proteinase site (AAW08169) and a TGF active fragment (AAW08173).
 CC TGF-beta promotes wound healing, and the fusion protein can be used to
 CC reduce surgery recovery time and in the preparation of artificial skin.
 CC The inclusion of a purification tag facilitates purification of the
 CC fusion protein. The proteinase site is included to permit cleavage and
 CC release of the purification tag after purification if desired. The
 CC extracellular matrix binding site facilitates delivery of the fusion
 CC protein to the desired site of action. Delivery of the TGF-beta to the
 CC site to be treated reduces the amount of TGF-beta required to be
 CC administered to be effective and reduces the concentration of circulating
 CC TGF-beta which may result in undesirable effects.
 CC N.B. the present sequence is does not appear in the specification,
 CC but is derived from the sequences mentioned above.

XX Sequence 137 AA;

Query Match 78.9%; Score 500; DB 18; Length 137;
 Best Local Similarity 76.8%; Pred. No. 4.8e-43;
 Matches 86; Conservative 11; Mismatches 15; Indels 0; Gaps 0;

QY	1	ALDTNYCFRNLENCVRPLYIDFRQDLGWKWHPEKGYANFCGPGCPYLRSDTTHST	60
Db	26	alldtnycfsstekncvrglyidfrkdlgwkwihpkyhanfclgpcpyiwsldtqysk	85
QY	61	VLGLYNTLNPEASPCCPQDLEPLTILYYVGRTPKVEQLSNMVKCKCS	112
Db	86	vlalynqhnpgasaapccvpqaleplivyyvgrkpkveqlsnmivrsckcs	137

Search completed: October 30, 2001, 08:51:22
 Job time: 151 sec

OM of: TGFB3P to: GenEmbl.* out_format : pfs

Date: Oct 30, 2001 9:34 AM

About: Results were produced by the GenCore software, version 4.5,
Copyright (c) 1993-2000 Compugen Ltd.

Command line parameters:
-MODEL=frame+p2n.model -DEV=xlh
-Q/cgn2_1/USPTO.spool/DUFFY097/runat_29102001_162247_25250/app_query.fasta_1.159
-DB=GenEmbl -QFMT=fastap -SUFFIX=rge -GAPOP=12.000 -GAPOP=4.000
-MINMATCH=0.100 -LOOPEL=0.000 -LOOPEXT=0.000 -QGAPOP=4.500
-QGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500 -FGAPOP=6.000
-FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500 -DELOP=6.000
-DELEXT=7.000 -START=1 -MATRIX=blosom62 -TRANS=human40.cdi
-LIST=100 -DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0
-ALIGN=100 -MODE=LOCAL -OUTFMT=pfs -NORM=ext -MINLEN=0
-MAXLEN=2000000000 -USER=DUFFY097 @CGNL_15962 -NCPU=6 -ICPU=3
-THREADS=1
-LOGREADS=1
-WARN_TIMEOUT=120 -WARN_TIMEOUT=30 -NO_XLPXY -WAIT

Search information block:
Query: TGFB3P
Query length: 113
Database: GenEmbl.*
Database sequences: 1344157
Database length: -856060004
Search time (sec): 1231.360000

score_list:	Sequence	Strd	Orig	Zscore	Escore	Len
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	gb_pat1:A23753	+	633.00	1192.04	3.7e-58	339
	gb_pat1:A48553	+	633.00	1192.04	3.7e-58	339
	gb_pat1:A48567	+	633.00	1192.04	3.7e-58	339
	gb_pat1:A59779	+	633.00	1192.04	3.7e-58	339
	gb_pat1:AR036688	+	633.00	1192.04	3.7e-58	339
	gb_pat1:AR036856	+	633.00	1192.04	3.7e-58	339
	gb_pat1:BC005513	+	633.00	1178.32	2.1e-57	2164
	gb_pat1:HM07GFB3A	+	633.00	1177.17	2.5e-57	2529
	gb_pat1:HM07GFB3B	+	633.00	1177.04	2.5e-57	2574
	gb_pat1:HM07GFB3C	+	633.00	1176.21	2.8e-57	2879
	gb_pat2:T03320	+	630.00	1173.62	3.9e-57	1899
	gb_pat2:REU03491	+	630.00	1171.20	5.3e-57	2633
	gb_ov:CHKTGFB	+	629.00	1170.68	5.7e-57	2187
	gb_ov:SSGTGFB3	+	621.00	1154.32	4.6e-56	2585
	gb_pat2:T05432	+	620.00	1164.62	1.2e-56	498
	gb_pat2:T03319	+	604.00	1124.15	2.2e-54	1981
	gb_pat1:A48555	+	595.00	1120.27	3.7e-54	336
	gb_pat1:A48569	+	595.00	1120.27	3.7e-54	336
	gb_pat1:A48571	+	591.00	1112.70	9.7e-54	336
	gb_pat1:A48557	+	591.00	1112.70	9.7e-54	336
	gb_pat1:A48571	+	591.00	1112.70	9.7e-54	336
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	gb_pat1:A48565	+	535.00	1006.77	7.7e-48	339
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	gb_pat1:A11707	+	535.00	1006.70	7.8e-48	342
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	gb_ov:AGMGFB2A	+	535.00	995.35	3.3e-47	1585
	gb_pat1:A05308	+	535.00	994.85	3.5e-47	1695
	gb_pat1:A11709	+	535.00	994.85	3.5e-47	1695

gb_pr9:HSCTSF	+	535.00	994.85	3.5e-47	1695	Y00083 Human mRNA for glob
gb_pat2:HM07GFB2A	+	535.00	991.78	5.3e-47	2569	I08281 Sequence 3 from Pate
gb_pr10:HM07GFB2A	+	535.00	991.77	5.3e-47	2570	M19154 Human transforming g
gb_r01:AF135598	+	530.00	987.62	9.0e-47	1255	AF135598 Rattus norvegicus
gb_r01:AF153013	+	530.00	981.70	1.9e-46	2796	AF153013 Rattus norvegicus
gb_r01:AF153012	+	530.00	981.48	2.0e-46	2880	AF153012 Rattus norvegicus
gb_r01:MMTGF2B	+	530.00	978.57	2.9e-46	4267	X57413 Mouse mRNA for trans
gb_r02:RN0132718	+	528.00	983.73	1.5e-46	1274	AF132718 Rattus norvegicus
gb_ov:SLTGF2B	+	523.00	981.55	2.0e-46	477	X70142 S. scrofa mRNA for tr
gb_ov:SLTGF2B	+	516.00	955.42	5.6e-45	2724	X51817 Xenopus laevis TGF-b
gb_pat2:IO8275	+	503.00	934.96	7.7e-44	1561	I08275 Sequence 3 from Pate
gb_r01:MUSGFRNA	+	503.00	934.88	7.8e-44	1579	M13177 Mouse transforming g
gb_r02:RNTGFB1	+	503.00	934.88	7.8e-44	1585	X52498 Rat mRNA for transfo
gb_r01:MM0009862	+	503.00	932.79	1.0e-43	2094	AJ009862 Mus musculus mRNA
gb_r01:OCAP000133	+	500.00	940.59	3.7e-44	339	AF000133 Oryctolagus cunicul
gb_pat1:A18277	+	500.00	940.59	3.7e-44	339	I18277 H.sapiens TGF-beta 1
gb_pat1:A23751	+	500.00	940.59	3.7e-44	339	A23751 TGF-beta1 coding regi
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gb_pat1:A48563	+	500.00	940.59	3.7e-44	339	A48563 Sequence 1 from Paten
gb_pat1:AR036686	+	500.00	940.59	3.7e-44	339	AR036686 Sequence 29 from pa
gb_pat2:IO56854	+	500.00	940.59	3.7e-44	339	I56854 Sequence 1 from paten
gb_r01:HM07GFB	+	500.00	935.78	6.9e-44	650	M38449 Human transforming gr
gb_pat2:IO5434	+	500.00	935.24	7.4e-44	699	I05434 Sequence 4 from Paten
gb_pat2:IO3312	+	500.00	933.69	9.0e-44	862	I03312 Sequence 3 from Paten
gb_ov:BOVTGFB	+	500.00	931.77	1.2e-43	1117	M36271 Bovine transforming
gb_ov:OATGFB1	+	500.00	931.41	1.2e-43	1173	X76916 O. aries mRNA for tra
gb_ov:DOGTGFB1A	+	500.00	930.26	1.4e-43	1369	L34956 Canine transforming
gb_r01:AGMTGFB	+	500.00	929.29	1.6e-43	1561	M16658 Simian transforming
gb_ov:SSGTGFB	+	500.00	929.09	1.6e-43	1605	Y00111 Porcine mRNA for tra
gb_ov:GGTGFB1	+	500.00	928.45	1.8e-43	1750	X12373 Porcine mRNA for tra
gb_r01:BC0001125	+	500.00	928.32	1.8e-43	1780	BC000125 Homo sapiens, Simi
gb_r01:BC0011180	+	500.00	928.32	1.8e-43	1780	BC001180 Homo sapiens, Simi
gb_pat1:A06669	+	500.00	928.15	1.8e-43	1821	E03028 DNA encoding human p
gb_pat1:EO3028	+	500.00	925.70	2.5e-43	2537	A06669 Synthetic mRNA for p
gb_r01:HSCTGFB1	+	500.00	925.11	2.7e-43	2745	X02812 Human mRNA for trans
gb_ov:PICTGFB1A	+	500.00	923.96	3.1e-43	3206	M23703 Sus scrofa transform
gb_ov:ECRGFB1	+	499.00	929.52	1.5e-43	1173	X99438 E.caballus mRNA for
gb_pat1:EO00973	+	497.00	920.05	5.2e-43	2527	E00973 cDNA encoding human
gb_pat1:A23756	+	496.00	933.10	9.8e-44	336	A23756 TGF-beta2(44/45)beta
gb_ov:SHPGFBIW	+	492.00	925.58	2.6e-43	334	L36038 Ovis aries transformi
gb_ov:AF175709	+	491.00	914.30	1.1e-42	1187	AF175709 Equus caballus tra
gb_ov:CCU66874	+	489.00	911.20	1.6e-42	1083	U66874 Cyprinus carpio tran
gb_r01:MATGFB1	+	488.00	915.50	9.3e-43	469	X60296 M.auratus mRNA for tr
gb_r01:AF191297	+	488.00	906.44	3.0e-42	1597	AF191297 Cavia porcellus tr
gb_r01:IO8268	+	487.00	904.72	3.7e-42	1560	I08268 Sequence 2 from Pate
gb_r01:AY007214	+	482.00	897.23	9.7e-42	1197	AY007214 Mesocricetus aurat
gb_pat2:IO62216	+	476.00	883.92	5.3e-41	1560	I06216 Sequence 2 from Pate
gb_pat2:IO62221	+	476.00	883.88	5.4e-41	1569	I06221 Sequence 3 from Pate
gb_ov:AF152592	+	463.00	873.08	2.2e-40	244	AF152592 Capreolus capreolus
gb_ov:CHKTGFB4	+	461.00	857.17	1.7e-39	1256	M31160 Chicken transforming
gb_ov:XLGTGFB5	+	439.00	809.76	7.2e-37	2754	J05180 X.laevis transforming
gb_ov:AF276986	+	435.00	819.31	2.1e-37	273	AF276986 Capra hircus TGF be
gb_r01:AF161218	+	420.00	790.20	8.9e-36	302	AF161218 Meriones unguiculat
gb_r01:AF097509	+	420.00	788.94	1.0e-35	358	AF097509 Cavia porcellus int
gb_ov:CEU62111	+	412.00	776.21	5.3e-35	259	U62111 Cervus elaphus trans
gb_r01:AF169347	+	401.00	754.89	8.2e-34	278	AF169347 Cavia porcellus tra
gb_r01:AC079432	-	401.00	705.66	4.5e-31	215287	AC079432 Mus musculus chr
gb_r01:AF04363	+	396.00	732.89	1.4e-32	1514	AF04363 Morone chrysops x
gb_r01:AF046214	+	389.00	732.42	1.5e-32	270	AF046214 Mesocricetus aurat
gb_ov:OMTGF2B	+	389.00	721.68	5.8e-32	1152	X99303 O.mykiss mRNA for tr

seq_name: gb_pat1:A18281

seq_documentation_block:	
LOCUS	A18281
DEFINITION	H.sapiens TGF-beta 2 peptide seq
ACCESSION	A18281
VERSION	A18281.1
KEYWORDS	GI:513241
SOURCE	synthetic construct.
ORGANISM	artificial sequence.
REFERENCE	1 (bases 1 to 339)

339 bp mRNA PAT ID No.3.

17-MAY-1994

AUTHORS Cerletti,N., McMaster,G.K., Cox,D., Schmitz,A. and Meyhack,B.
TITLE Process for the production of biologically active protein (e.g.
TGF)
JOURNAL Patent: EP 0433225-A 6 19-JUN-1991;
CIBA-GEIGY AG
FEATURES Location/Qualifiers
source 1..339
/organism="synthetic construct"
/db_xref="taxon:32630"
CDS 1..339
/note="protein sequence is in conflict with the conceptual
translation"
/codon_start=1
/transl_table=11
/product="TGF-beta 2"
/protein_id="CAA01387.1"
/db_xref="GI:4529905"
/translation="ALDNTVCFRNLNCCVRLPYIDFRDLGKWHVHEPKGYANFC
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NMVKSCKCS"
BASE COUNT 74 a 104 c 86 g 75 t
ORIGIN

alignment_scores:
Quality: 633.00 Length: 112
Ratio: 5.652 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
TGFB3P x A18281 ..

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1 GCCTTGGACACCAATCTACTGCTCCGCAACTTGGAGGAGAACTGCTGTGT 50
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51 LeuArgSerAlaAspThrHisSerThrValLeuGlyLeuTyrAsnTh 67
|||||
151 CTCGCCAGTGCAGACACACCCAGCAGCGTCTGGGCTGGAAGTGGGTCC 200
67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
|||||
201 TCTGAACCTTGAAGCATCTGCCTCGCTTGCCTGCGTCCGCCAGGACCTGG 250
84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
|||||
251 AGCCCTTGACCATCTCTACTATGTTGGGAGGACCCCAAGTGGAGCAG 300
101 LeuSerAsnMetValValLysSerCysLysCysSer 112
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301 CTCCTCAACATGGTGGTGAAGTCTTGTAAATGTAGC 336

seq_name: gb_pat1:A23753
seq_documentation_block:
LOCUS A23753 339 bp mRNA PAT 25-JAN-1995
DEFINITION TGF-beta3 coding region.
ACCESSION A23753
VERSION A23753.1 GI:825587
KEYWORDS human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 (bases 1 to 339)
AUTHORS McMaster,G.K., Cox,D., Cerletti,N. and Kuhla,J.
TITLE Novel hybrid transforming growth factors
JOURNAL Patent: EP 0542679-A 3 19-MAY-1993;
CIBA-GEIGY AG
FEATURES Location/Qualifiers
source 1..339
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 74 a 104 c 86 g 75 t
ORIGIN

alignment_scores:
Quality: 633.00 Length: 112
Ratio: 5.652 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
TGFB3P x A23753 ..

Align seg 1/1 to: A23753 from: 1 to: 339

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17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTyrLysTyrValH 34
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51 GCGCCCCCTCTACATTGACTTCGACAGGATCTGGGCTGGAAGTGGGTCC 100
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51 LeuArgSerAlaAspThrHisSerThrValLeuGlyLeuTyrAsnTh 67
|||||
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67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
|||||
201 TCTGAACCTTGAAGCATCTGCCTCGCTTGCCTGCGTCCGCCAGGACCTGG 250
84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
|||||
251 AGCCCTTGACCATCTCTACTATGTTGGGAGGACCCCAAGTGGAGCAG 300
101 LeuSerAsnMetValValLysSerCysLysCysSer 112
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seq_name: gb_pat1:A48553

seq_documentation_block:
LOCUS A48553 339 bp DNA PAT 07-MAR-1997
DEFINITION Sequence 5 from Patent WO9603432.
ACCESSION A48553
VERSION A48553.1 GI:2302323
KEYWORDS unidentified.
SOURCE unidentified.
ORGANISM unidentified.

REFERENCE 1 (bases 1 to 339)
AUTHORS Cerletti,N.
TITLE NOVEL PROCESS FOR THE PRODUCTION OF BIOLOGICALLY ACTIVE DIMERIC
PROTEI
JOURNAL Patent: WO 9603432-A 5 08-FEB-1996;
CIBA GEIGY AG (CH)
COMMENT Other publication AU 3109595 960222.
FEATURES Location/Qualifiers
source 1..339
/organism="unidentified"

CDS

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/db_xref="taxon:32644"
1..336
/notes="Protein sequence is in conflict with the conceptual
translation"
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/db_xref="GI:2302324"
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BASE COUNT      74 a 104 c 86 g 75 t
ORIGIN
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alignment_scores:

Quality:	633.00	Length:	112
Ratio:	5.652	Gaps:	0
Percent Similarity:	100.000	Percent Identity:	100.000

alignment_block:
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Align seg 1/1 to: A48553 from: 1 to: 339

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51 GCGCCCTCTACATTGACTTCGACAGGATCTGGCTGGAAGTGGGTCC 100

34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
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67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
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84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
|||||
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301 CTCCTCAACATGGTGGTGAAGTCTTGTAATGTAGC 336
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seq_name: gb_pat1:A48567

seq_documentation_block: 339 bp DNA PAT 07-MAR-1997

LOCUS A48567

DEFINITION Sequence 5 from Patent WO9603433.

ACCESSION A48567

VERSION A48567.1 GI:2302337

KEYWORDS

SOURCE unidentified.

ORGANISM unidentified.

REFERENCE 1 (bases 1 to 339)

AUTHORS Cerletti, N.

TITLE NEW PROCESS FOR THE PRODUCTION OF BIOLOGICALLY ACTIVE PROTEIN

JOURNAL Patent: WO 9603433-A 5 08-FEB-1996;

COMMENT CIBA GEIGY AG (CH)

FEATURES Other publication AU 3109695 960222.

source Location/Qualifiers

1..339

/organism="unidentified"

CDS

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/db_xref="taxon:32644"
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/notes="Protein sequence is in conflict with the conceptual
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BASE COUNT      74 a 104 c 86 g 75 t
ORIGIN
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Ratio:	5.652	Gaps:	0
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TGFB3P x A48567 ..

Align seg 1/1 to: A48567 from: 1 to: 339

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17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
|||||
51 GCGCCCTCTACATTGACTTCGACAGGATCTGGCTGGAAGTGGGTCC 100

34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
|||||
101 ATGAACCTAAGGCTACTATGCCAACTTCGTCAAGCCCTTGCCCATAC 150

51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
|||||
151 CTCGCGAGTCGACACACCAACCCAGACCGTGTGGGACTGTACACAC 200

67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
|||||
201 TCTGAACCTTGAAGCATCTGCCTCGCCTTGTGCTGCCCGCAGACCTGG 250

84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
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251 AGCCCTTGACCATCCCTGCTACTATGTTGGGAGGACCCCAAGTGGAGCAG 300

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seq_name: gb_pat1:A59779

seq_documentation_block: 339 bp DNA PAT 06-MAR-1998

LOCUS A59779

DEFINITION Sequence 1 from Patent WO9705166.

ACCESSION A59779

VERSION A59779.1 GI:3715005

KEYWORDS

SOURCE unidentified.

ORGANISM unidentified.

REFERENCE 1 (bases 1 to 339)

AUTHORS Mittl, P., Gruetter, M. and Arvinde, T.

TITLE TRANSFORMING GROWTH FACTOR BETA CRYSTALS

JOURNAL Patent: WO 9705166-A 1 13-FEB-1997;

COMMENT CIBA GEIGY AG (CH)

FEATURES Location/Qualifiers

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74 a 104 c 86 g 75 t

alignment_scores:
  Quality: 633.00      Length: 112
  Ratio: 5.652        Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

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17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
|||||
51 GCGCCCTCTACATTGACTTCCGACAGGATCTGGGCTGGAAGTGGGTCC 100

34 isGluProLysGlyTyrAlaAsnPheCysSerGlyProCysProTyr 50
|||||
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67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
|||||
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84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
|||||
251 AGCCCTTGACCATCTCTACTATGTTGGGAGGACCCCAAGTGGAGCAG 300

101 LeuSerAsnMetValLysSerCysLysCysSer 112
|||||
301 CTCTCCAACATGGTGGTGAAGTCTTGTAAATGTAGC 336

seq_name: gb_pat1:AR036688

seq_documentation_block:
LOCUS AR036688 339 bp DNA PAT 29-SEP-1999
DEFINITION Sequence 33 from patent US 5800811.
ACCESSION AR036688
VERSION AR036688.1 GI:5954544
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 339)
AUTHORS Hall,F.L., Nimmi,M.E., Tuan,T., Wu,L. and Cheung,D.T.
TITLE Artificial skin prepared from collagen matrix containing transforming growth factor-beta having a collagen binding site
JOURNAL Patent: US 5800811-A 33 01-SEP-1998;
FEATURES
source Location/Qualifiers
BASE COUNT 74 a 104 c 86 g 75 t
ORIGIN

alignment_scores:
  Quality: 633.00      Length: 112
  Ratio: 5.652        Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

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51 GCGCCCTCTACATTGACTTCCGACAGGATCTGGGCTGGAAGTGGGTCC 100

34 isGluProLysGlyTyrAlaAsnPheCysSerGlyProCysProTyr 50
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seq_name: gb_pat1:AR036688

seq_documentation_block:
LOCUS AR036688 339 bp DNA PAT 29-SEP-1999
DEFINITION Sequence 33 from patent US 5800811.
ACCESSION AR036688
VERSION AR036688.1 GI:5954544
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 339)
AUTHORS Hall,F.L., Nimmi,M.E., Tuan,T., Wu,L. and Cheung,D.T.
TITLE Artificial skin prepared from collagen matrix containing transforming growth factor-beta having a collagen binding site
JOURNAL Patent: US 5800811-A 33 01-SEP-1998;
FEATURES
source Location/Qualifiers
BASE COUNT 74 a 104 c 86 g 75 t
ORIGIN

alignment_scores:
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Percent Similarity: 100.000 Percent Identity: 100.000

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TGFB3P x I56856
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51 LeuArgSerAlaAspThrHisSerThrValLeuGlyLeuTyrAsnTh 67
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67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
|||||
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seq_name: gb_pat2:I56856

seq_documentation_block:
LOCUS I56856 339 bp DNA PAT 07-OCT-1997
DEFINITION Sequence 3 from patent US 5650494.
ACCESSION I56856
VERSION I56856.1 GI:2477269
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 339)
AUTHORS Cerletti,N., McMaster,G.Kent, Cox,D., Schmitz,A. and Meyhack,B.
TITLE Process for refolding recombinantly produced TGF-beta-like proteins
JOURNAL Patent: US 5650494-A 3 22-JUL-1997;
FEATURES
source Location/Qualifiers
BASE COUNT 74 a 104 c 86 g 75 t
ORIGIN

alignment_scores:
  Quality: 633.00      Length: 112
  Ratio: 5.652        Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

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17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
|||||
51 GCGCCCTCTACATTGACTTCCGACAGGATCTGGGCTGGAAGTGGGTCC 100

34 isGluProLysGlyTyrAlaAsnPheCysSerGlyProCysProTyr 50
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101 ATGAACCTAAGGCTACTATGCCAACTTCTGCTCAGGCCCTTGCCCATAC 150

51 LeuArgSerAlaAspThrHisSerThrValLeuGlyLeuTyrAsnTh 67
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67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
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84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
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251 AGCCCTTGACCATCTCTACTATGTTGGGAGGACCCCAAGTGGAGCAG 300

101 LeuSerAsnMetValLysSerCysLysCysSer 112
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51 LeuArgSerAlaAspThrHisSerThrValLeuGlyLeuTyrAsnTh 67
151 CTCGCGAGTGCAGACACACACCCAGCAGCGTGTGGGACTGTACACAC 200
67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeu 84
201 TCTGAACCTGAAGCATCTGCTCGCCTTGTGGTGGCCAGGACCTGG 250
84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
251 AGCCCTTGACCATCTCTACTATGTTGGAGGACCCCAAGTGGAGCAG 300
101 LeuSerAsnMetValValLysSerCysLysCysSer 112
301 CTCTCCCAACATGGTGGTGAAGCTCTTGAATGTAGC 336
seq_name: gb_rol:BC005513
seq_documentation_block:
LOCUS BC005513 2164 bp mRNA ROD 03-APR-2001
DEFINITION Mus musculus, similar to transforming growth factor, beta 3, clone
IMAGE:3492763, mRNA, partial cds.
ACCESSION BC005513
VERSION BC005513.1 GI:13529607
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 2164)
Strausberg, R.
Direct Submission
Submitted (27-MAR-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
R. M.
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 8 Row: f Column: 13.
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34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
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852 AGCAACCTAAGGGTGTACTATGCCAATCTTGTCTAGGCCCTTGCCCATAC 901
51 LeuArgSerAlaAspThrHisSerThrValLeuGlyLeuTyrAsnTh 67
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902 CTCGCGAGTGCAGACACACCCAGCAGCGTGTGGACTGTACACAC 951
67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
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952 CTGAACCCAGAGCGTCTGCTCGCCATGCTGCGTCCGCCAGGACCTGG 1001
84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
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1002 AGCCCTTGACCATCTTGTACTATGTGGCAGAACCCCAAGTGGAGCAG 1051
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seq_documentation_block:
LOCUS HUMTGF3A 2529 bp mRNA PRI 14-JAN-1995
DEFINITION Human transforming growth factor-beta 3 (TGF-beta3); mRNA, complete
cds.
ACCESSION J03241
VERSION J03241.1 GI:339551
KEYWORDS transforming growth factor.
SOURCE Human placental and umbilical cord (cell line A673), cDNA to mRNA,
from library lambda-gt10.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 2529)
ten Dijke, P., Hansen, P., Iwata, K.K., Pieler, C. and Foulkes, J.G.
Identification of another member of the transforming growth factor
type beta gene family
```

JOURNAL MEDLINE	Proc. Natl. Acad. Sci. U.S.A. 85 (13), 4715-4719 (1988) 88263019
COMMENT	Draft entry and computer-readable sequence [1] kindly submitted by C.Pieler 12-SEPT-1988 The authors have found that this transforming growth factor contains multiple growth inhibitory elements.

DEFINITION	Human mRNA for transforming growth factor-beta 3 (TGF-beta 3).
ACCESSION	X14149
VERSION	X14149.1 GI:37095
KEYWORDS	growth factor; transforming growth factor; transforming growth factor-beta 3.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
AUTHORS	Chen, E.Y.
TITLE	Direct Submission
JOURNAL	Submitted (23-MAR-1989) Chen E.Y., Genentech Inc., 460 Pt. San Bruno Blvd., San Francisco, CA 94080, USA
REFERENCE	2 (bases 1 to 2574)
AUTHORS	Derynck, R., Lindquist, P.B., Lee, A., Wen, D., Tamm, J., Graycar, J.L., Rhee, L., Mason, A.J., Miller, D.A., Coffey, R.J., Moses, H.L. and Chen, E.Y.
TITLE	A new type of transforming growth factor-beta, TGF-beta 3
JOURNAL	EMBO J. 7 (12), 3737-3743 (1988)
MEDLINE	89091120
COMMENT	See <03241> for alternative sequence of TGF-beta 3.
FEATURES	Location/Qualifiers
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 1204 GGGCCCCCTCTACATTGACTCCGACAGATCTGGCTGGGAAGTGGGTCC 1253
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 1304 CTCCTCAGTTGAGACACCAACCCACAGCAGCGTGTGGGACTGTACAACAC 1353

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 85 (13), 4715-4719 (1988)
MEDLINE 88263019
COMMENT Draft entry and computer-readable sequence [1] kindly submitted by C.Pieler 12-SEPT-1988 The authors have found that this transforming growth factor contains multiple growth inhibitory elements.

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67 IleuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
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seq_documentation_block:
LOCUS MUSTGB3 2879 bp mRNA ROD 27-APR-1993
DEFINITION mouse transforming growth factor beta-3 mRNA, complete cds.
ACCESSION M32745
VERSION M32745.1 GI:201949
KEYWORDS transforming growth factor.
SOURCE Mouse cell line AKR-2B, cDNA to mRNA.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 2879)
AUTHORS Miller,D.A., Lee,A., Matsui,Y., Chen,E.Y., Moses,H.L. and Derynck,R.
TITLE Complementary DNA cloning of the murine transforming growth factor-beta-3 (TGF-beta-3) precursor and the comparative expression of TGF-beta-3 and TGF-beta-1 messenger RNA in murine embryos and adult tissues
JOURNAL Mol. Endocrinol. 3, 1926-1934 (1989)
MEDLINE 90190650
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LOCUS I03320 1899 bp ss-DNA PAT 21-MAY-1993
DEFINITION Sequence 11 from Patent US 4886747.
ACCESSION I03320
VERSION I03320.1 GI:270714
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1899)
AUTHORS Derynck,R.M.A. and Goeddel,D.V.
TITLE Nucleic acid encoding TGF-.beta. and its uses
JOURNAL Patent: US 4886747-A 11 12-DEC-1989;
Genentech, Inc.;
South San Francisco, CA
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DEFINITION Rattus norvegicus Wistar transforming growth factor beta-3 mRNA,
complete cds.
ACCESSION U03491
VERSION U03491.1 GI:424131
KEYWORDS Norway rat.
SOURCE Rattus norvegicus
ORGANISM Rattus norvegicus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 2633)
AUTHORS Wang,J., Kuliszewski,M., Yee,W., Sedlackova,L., Xu,J., Tseu,I. and Post,M.
TITLE Cloning and expression of glucocorticoid-induced genes in fetal rat lung fibroblasts. Transforming growth factor-beta 3
J. Biol. Chem. 270 (6), 2722-2728 (1995)
MEDLINE 95155340
REFERENCE 2 (bases 1 to 2633)
AUTHORS Post,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-1993) M. Post, The Hospital for Sick Children, Paediatrics & Research Institute, 555 University Avenue, Toronto, Ontario M5G 1X8, Canada

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LOCUS CHKTFGB 2187 bp mRNA VRT 28-APR-1993
DEFINITION Chicken transforming growth factor beta (TGF-beta-3) mRNA, complete
cds.
ACCESSION M31154
VERSION M31154.1 GI:212758
KEYWORDS transforming growth factor-beta.
SOURCE Chicken embryo chondrocyte, cdNA to mRNA.
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
REFERENCE 1 (bases 1 to 2187)
AUTHORS Jakowlew,S.B., Dillard,P.J., Kondaiah,P., Sporn,M.B. and Roberts,A.B.
TITLE Complementary deoxyribonucleic acid cloning of a novel transforming
growth factor-beta messenger ribonucleic acid from chick embryo
chondrocytes
Mol. Endocrinol. 2, 747-755 (1988)
JOURNAL
MEDLINE 89096966
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940 GCCCTGGATACCACTACTGCTTCGGGAACCTGGAGGAGAACTGCTGTGT 989
17 lArpProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
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990 GCGTCTCTTTACATTGACTTCCGACAGGACCTGGGCTGGAATGGGTCC 1039
34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
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1040 ATGAGCTTAAGGCTACTTTGCAAACTTCTGTTCGGGCCCATGTCCTGAC 1089
51 LeuArgSerAlaAspPheThrHisSerThrValLeuGlyLeuTyrAsnTh 67
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1090 CTTCCGAGTGCAGACACCACTTCACAGCACGGTGTGGGCTGTGACAAC 1139
67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
|||||
1140 GCTGAACCCGAGGATCGCTTACCGCTGTGTGCTCCACAGACCTGG 1189
84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
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1190 AGCCACTGACGATCTGTACTATGTTGGGAGGACACCCAAAGTGGACG 1239
101 LeuSerAsnMetValLysSerCysLysCysSer 112
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1240 CTCCTCAATATGGTGGTGAATCCTGCAAGTGCAGC 1275
seq_name: gb_om:SSTGFB3M
seq_documentation_block:
LOCUS SSTGFB3M 2585 bp mRNA MAM 12-SEP-1993
DEFINITION Porcine mRNA for transforming growth factor-beta 3 (TGF-beta 3).
ACCESSION X14150
VERSION X14150.1 GI:2127
KEYWORDS growth factor; transforming growth factor; transforming growth factor-beta 3.
SOURCE pig.
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
Chen,E.Y.
Direct Submission
Submitted (23-MAR-1989) Chen E.Y., Genentech Inc., 460 Pt. San Bruno Blvd., San Francisco, CA 94080, USA
2 (bases 1 to 2585)
Derynck,R., Lindquist,P., Lee,A., Wen,D., Tamm,J., Graycar,J.L., Rhee,L., Mason,A.J., Miller,D.A., Coffey,R.J., Moses,H.L. and Chen,E.Y.
A new type of transforming growth factor-beta, TGF-beta 3

JOURNAL EMBO J. 7 (12), 3737-3743 (1988)
MEDLINE 89091120
COMMENT See <X14149> and <J03241> for human TGF-beta 3 mRNA sequence.
FEATURES
Location/Qualifiers
source
1. .2585
/organism="Sus scrofa"
/db_xref="taxon:9823"
/tissue_type="ovary"
/clone_lib="lambda gt10"
268. .1497
CDS
/note="TGF-beta 3 (AA 1-409)"
/codon_start=1
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/db_xref="GI:2128"
/db_xref="SWISS-PROT:P15203"
/translation="MHQRLAVLVLLALNFATVLSMSTCTTLDHDKIKRKRVEAIRGO
ILSKRLTSPDPSPMLANIPQVLDLYNSTRLELLEVEHGERGDDCTGENTSEYAKE
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RSQRTELFQITQPDDEHIAKQRYIDGNLPTRGAAEWLSEDDVDTVREWLDRRESNLG
LEISHCPCITFQPDGDIENIQEVMIEIKFGVDEDDPGRGDLRLKKKHEHPHLI
LMMIPDLNDPGLQAKRRALDTNYCFRNLBENCVRPLYIDFRODLGKWKWYHEPK
GYVANFCSGPCPYLRASADTTTHSSVLGLYNTLNPEASASPCCPQDLEPLTILYVGR
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BASE COUNT 620 a 705 c 699 g 561 t
ORIGIN
alignment_scores:
Quality: 621.00 Length: 112
Ratio: 5.595 Gaps: 0
Percent Similarity: 99.107 Percent Identity: 98.214
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17 lArpProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
|||||
1209 GCGCCCTCTCTACATTGACTTCCGACAGATCTGGCTGGAAGTGGGTCC 1258
34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
|||||
1259 ATGAACCTAAGGGCTACTATGCCAATCTGCTCAGGCCCTTGGCCGTAC 1308
51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
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1309 CTCGCGAGTGCAGACACCAACCCACAGCTTCGGTGTCTGGGGCTGTACAAC 1358
67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
|||||
1359 CCTGAACCCGAGGCTCGGCCCTCTCCGCTGTGCTGCTCCCAAGACCTGG 1408
84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
|||||
1409 AGCCCTTGACCATCTGTACTACGTTCGGGAGGACCGCAAGGTGGAGCAG 1458
101 LeuSerAsnMetValLysSerCysLysCysSer 112
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1459 CTCCTCAATATGGTGGTGAAGTCTGCAAGTGCAGC 1494
seq_name: gb_pat2:I05432
seq_documentation_block:
LOCUS I05432 498 bp PAT
DEFINITION Sequence 2 from Patent EP 0267463.
ACCESSION I05432
VERSION I05432.1 GI:590974
KEYWORDS

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SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 498)
AUTHORS     Iwata,K.K., Gold,L.I. and Stephenson,J.R.
TITLE       Tissue-derived tumor growth inhibitors, methods of preparation and
            uses thereof
JOURNAL     Patent: EP 0267463-A2 2 18-MAY-1988;
FEATURES    Location/Qualifiers
            source
            1..498
            /organism="unknown"
BASE COUNT  122 a 137 c 129 g 110 t
ORIGIN

alignment_scores:
    Quality: 620.00      Length: 112
    Ratio: 5.586        Gaps: 0
Percent Similarity: 99.107 Percent Identity: 98.214

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17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
|||||
210 GCGCCCTCTCTACATTGACTTCCGACAGGATCTGGGCTGGAAGTGGGTCC 259
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34 isGluProLysGlyTyrTyrAlaAsnPheCysSerClyProCysProTyr 50
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260 ATGAACCTAAGGGCTACTATGCAACTTCTGCTCAGCCCTTGCCCATAC 309
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51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
|||||
310 CTCGCCAGTGCAGACACACACAGCAGCGTGTGGGACTGTACAAACAC 359
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67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
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360 TCTGAACCCCTGAAGCATCTGCTGGCGCTGCTGCGTGCCTCCAGGACCTGG 409
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84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
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410 AGCCCTGTACCATCTGTACTATGTGGGAGGACCCCAAGTGGAGCAG 459
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101 LeuSerAspMetValValLysSerCysLysCysSer 112
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460 CTCTCCACATGGTGTGAAGTCTTGTAAATGTAGC 495

seq_name: gb_pat2:I03319

seq_documentation_block:
LOCUS      I03319
DEFINITION Sequence 10 from Patent US 4886747.
ACCESSION  I03319
VERSION     I03319.1 GI:270713
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 1981)
AUTHORS     Derynck,R.M.A. and Goeddel,D.V.
TITLE       Nucleic acid encoding TGF-beta, and its uses
JOURNAL     Patent: US 4886747-A 10 12-DEC-1989;
            Genentech, Inc.;
            South San Francisco, CA
FEATURES    Location/Qualifiers
            source
            1..1981
            /organism="unknown"

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BASE COUNT  466 a 570 c 556 g 389 t
ORIGIN

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    Quality: 604.00      Length: 112
    Ratio: 5.491        Gaps: 0
Percent Similarity: 98.214 Percent Identity: 95.536

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Align seg 1/1 to: I03319 from: 1 to: 1981

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17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
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|||||
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67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
|||||
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84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
|||||
1409 AGCCCTGTACCATCTGTACTATGTGGGAGGACCCCAAGTGGAGCAG 1458
|||||
101 LeuSerAspMetValValLysSerCysLysCysSer 112
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1459 CTCTCAACATGGTGTGAAGTCTCTCAAGTGCAGC 1494

seq_name: gb_pat1:A23755

seq_documentation_block:
LOCUS      A23755
DEFINITION TGF-beta1(44/45)beta3 hybrid coding region.
ACCESSION  A23755
VERSION     A23755.1 GI:825589
KEYWORDS    .
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 336)
AUTHORS     McMaster,G.K., Cox,D., Cerletti,N. and Kuhla,J.
TITLE       Novel hybrid transforming growth factors
JOURNAL     Patent: EP 0342679-A 5 19-MAY-1993;
            CIBA-GEIGY AG
FEATURES    Location/Qualifiers
            source
            1..336
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BASE COUNT  75 a 109 c 86 g 66 t
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Percent Similarity: 97.321 Percent Identity: 92.857

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17 largProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
51 GCGCAGCTGTACATTGCTTCCGCAAGGACCTCGCTGGAAGTGGATCC 100
34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
101 ACGAGCCCAAGGGTACCATGCCAACTTCTGCTCAGGCCCTTGCCCATAC 150
51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
151 CTCCGAGTGCAGACACACACAGCAGCGTGTGGGACTGTACAACAC 200
67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
201 TCTGAACCCCTGAAGCATCTGCCTCGCTTGTGCGTGCCTCCAGGACCTGG 250
84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
251 AGCCCTGACCATCTGTACTATGTTGGGAGGACCCCAAGTGGAGCAG 300
101 LeuSerAsnMetValValLysSerCysLysCysSer 112
301 CTCTCCAACTGGTGGTGAAGTCTTGTAAATGTAGC 336
seq_name: gb_pat1:A48555
seq_documentation_block: 336 bp DNA PAT 07-MAR-1997
LOCUS A48555
DEFINITION Sequence 7 from Patent WO9603432.
ACCESSION A48555
VERSION A48555.1 GI:2302325
KEYWORDS
SOURCE unidentified.
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 336)
AUTHORS Cerletti, N.
TITLE NOVEL PROCESS FOR THE PRODUCTION OF BIOLOGICALLY ACTIVE DIMERIC PROTEIN
JOURNAL Patent: WO 9603432-A 7 08-FEB-1996;
COMMENT CIBA GEIGY AG (CH)
FEATURES
source Location/Qualifiers
mat_peptide /organism="unidentified"
1. .336 /db_xref="taxon:32644"
CDS /product="N-TERMINAL 44 AMINO ACIDS OF HUMAN TGF-BETA1"
/note="Protein sequence is in conflict with the conceptual translation"
/codon_start=1
/product="HYBRID TGF-BETA NAMED TGF-BETA1-3"
/protein_id="CAA03116.1"
/db_xref="GI:2302326"
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133. .336
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BASE COUNT 75 a 109 c 86 g 66 t
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Ratio: 5.459 Gaps: 0
Percent Similarity: 97.321 Percent Identity: 92.857
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17 largProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
51 GCGCAGCTGTACATTGCTTCCGCAAGGACCTCGCTGGAAGTGGATCC 100
34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
101 ACGAGCCCAAGGGTACCATGCCAACTTCTGCTCAGGCCCTTGCCCATAC 150
51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
151 CTCCGAGTGCAGACACACACAGCAGCGTGTGGGACTGTACAACAC 200
67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
201 TCTGAACCCCTGAAGCATCTGCCTCGCTTGTGCGTGCCTCCAGGACCTGG 250
84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
251 AGCCCTGACCATCTGTACTATGTTGGGAGGACCCCAAGTGGAGCAG 300
101 LeuSerAsnMetValValLysSerCysLysCysSer 112
301 CTCTCCAACTGGTGGTGAAGTCTTGTAAATGTAGC 336
seq_name: gb_pat1:A48569
seq_documentation_block: 336 bp DNA PAT 07-MAR-1997
LOCUS A48569
DEFINITION Sequence 7 from Patent WO9603433.
ACCESSION A48569
VERSION A48569.1 GI:2302339
KEYWORDS
SOURCE unidentified.
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 336)
AUTHORS Cerletti, N.
TITLE NEW PROCESS FOR THE PRODUCTION OF BIOLOGICALLY ACTIVE PROTEIN
JOURNAL Patent: WO 9603433-A 7 08-FEB-1996;
COMMENT CIBA GEIGY AG (CH)
FEATURES
source Location/Qualifiers
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/note="Protein sequence is in conflict with the conceptual translation"
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/product="HYBRID TGF-BETA NAMED TGF-BETA1-3"
/protein_id="CAA03123.1"
/db_xref="GI:2302340"
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BASE COUNT 75 a 109 c 86 g 66 t
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alignment_scores:

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Percent Similarity: 98.214  Percent Identity: 91.071

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1 GCTTTGGATGGCGCTATTGCTTTAGAAATGTCAGGATAATTGCTGCCT 50

17 largProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
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51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
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151 CTCCGCGATGCGACACAAACCCACAGCAGCGTGTGGGAGACCTTGG 200

67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
201 TCTGAACCTTGAAACATCTGCCTCGCCTTGTGGTGGCCCGAGACCTGG 250

84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
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251 AGCCCCTGACCATCTGACTATGTTGGAGGAGCCCCCAAGTGGAGCAG 300

101 LeuSerAsnMetValValLysSerCysLysCysSer 112
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seq_documentation_block:
LOCUS A48571 336 bp DNA PAT 07-MAR-1997
DEFINITION Sequence 9 from Patent WO9603433.
ACCESSION A48571
VERSION A48571.1 GI:2302341
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 336)
AUTHORS Cerletti,N.
TITLE NEW PROCESS FOR THE PRODUCTION OF BIOLOGICALLY ACTIVE PROTEIN
JOURNAL Patent: WO 9603433-A 9 08-FEB-1996;
CIBA GEIGY AG (CH)
COMMENT Other publication AU 3109695 960222.
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Ratio: 5.373 Gaps: 0
Percent Similarity: 98.214 Percent Identity: 91.071

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1 GCTTTGGATGGCGCTATTGCTTTAGAAATGTCAGGATAATTGCTGCCT 50

17 largProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
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84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
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seq_documentation_block:
LOCUS A23759 336 bp mRNA PAT
DEFINITION TGF-beta3(44/45)beta2 hybrid coding region.
ACCESSION A23759
VERSION A23759.1 GI:825593
KEYWORDS human.
SOURCE
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 336)
AUTHORS McMaster,G.K., Cox,D., Cerletti,N. and Kuhla,J.
TITLE Novel hybrid transforming growth factors
JOURNAL Patent: EP 0542679-A 9 19-MAY-1993;
CIBA-GEIGY AG
FEATURES
source
location/Qualifiers
1..336
/organism="Homo sapiens"
/db_xref="taxon:9606"

BASE COUNT 88 a 87 c 71 g 90 t
ORIGIN

alignment_scores:
Quality: 577.00 Length: 112
Ratio: 5.393 Gaps: 0
Percent Similarity: 95.536 Percent Identity: 88.393

alignment_block:
TGFB3P x A23759
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17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTTrpLysTrpValH 34
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34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
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67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
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seq_name: gb_pat1:A48559

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seq_documentation_block: 336 bp DNA PAT 07-MAR-1997
LOCUS A48559
DEFINITION Sequence 11 from Patent WO9603432.
ACCESSION A48559
VERSION A48559.1 GI:2302329
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 336)
AUTHORS Cerletti,N.
TITLE NOVEL PROCESS FOR THE PRODUCTION OF BIOLOGICALLY ACTIVE DIMERIC
JOURNAL PROTEI
PATENT: WO 9603432-A 11 08-FEB-1996;
CIBA GEIGY AG (CH)
Other publication AU 3109595 960222.
FEATURES
Location/Qualifiers
1..336
/organism="unidentified"
/db_xref="taxon:32644"
/product="N-TERMINAL 44 AMINO ACIDS OF HUMAN TGF-BETA3"
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1..336
/translation="Protein sequence is in conflict with the conceptual translation"
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/product="HYBRID TGF-BETA3-2"
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/db_xref="GI:2302330"
/translational="ALDNYCFRNLNENCCVRPLYIDFRODLGKWKVHEPKGYANFC
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133..336
/product="C-TERMINAL 68 AMINO ACIDS OF HUMAN TGF-BETA2"
BASE COUNT 88 a 87 c 71 g 90 t
ORIGIN
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alignment_scores:
Quality: 577.00 Length: 112
Ratio: 5.393 Gaps: 0

Percent Similarity: 95.536 Percent Identity: 88.393

alignment_block:
TGFB3P x A48559

Align seg 1/1 to: A48559 from: 1 to: 336

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1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
|||||
1 GCTTTGGACACCAATTAAGTCTCCGCAACTTGGAGGAGAACTGCTGTGT 50
|||||
17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTTrpLysTrpValH 34
|||||
51 GCGCCCCCTCTACATTGACTTCCGACAGGATCTGGGCTGGAAGTGGGTCC 100
|||||
34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
|||||
101 ATGAACCTAAGGCTACTATGCCAACTTCTGCTGGAGCATGCCCGTAT 150
|||||
51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
||| |:::|||||
151 TTATGGAGTTCAGACACTCAGCACAGCAGGTCCTGAGCTTATATAATAC 200
|||||
67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
||| |:::|||||
201 CATAAATCCAGAGCATCTGCTTCTCTGCTGCGTGTCCCAAGATTAG 250
|||||
84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
|||||
251 AACCTTAACCATCTCTACTACATTGGCAAAACACCCCAAGATTGAACAG 300
|||||
101 LeuSerAsnMetValValLysSerCysLysCysSer 112
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301 CTTTCTAATATGATTGTAAGCTTTCGAATGCAGC 336
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seq_name: gb_pat1:A48573

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seq_documentation_block: 336 bp DNA PAT 07-MAR-1997
LOCUS A48573
DEFINITION Sequence 11 from Patent WO9603433.
ACCESSION A48573
VERSION A48573.1 GI:2302343
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 336)
AUTHORS Cerletti,N.
TITLE NEW PROCESS FOR THE PRODUCTION OF BIOLOGICALLY ACTIVE PROTEIN
JOURNAL
PATENT: WO 9603433-A 11 08-FEB-1996;
CIBA GEIGY AG (CH)
Other publication AU 3109695 960222.
FEATURES
Location/Qualifiers
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/product="N-TERMINAL 44 AMINO ACIDS OF HUMAN TGF-BETA3"
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/db_xref="GI:2302344"
/translational="ALDNYCFRNLNENCCVRPLYIDFRODLGKWKVHEPKGYANFC
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NMIVSKCKS"
mat_peptide
133..336
/product="C-TERMINAL 68 AMINO ACIDS OF HUMAN TGF-BETA2"
BASE COUNT 88 a 87 c 71 g 90 t
ORIGIN
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alignment_scores:
  Quality: 577.00      Length: 112
  Ratio: 5.393        Gaps: 0
  Percent Similarity: 95.536      Percent Identity: 88.393

alignment_block:
  TGFB3P x A48573  ..

Align seg 1/1 to: A48573 from: 1 to: 336

1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluAsnCysCysVa 17
|||||
1 GCCTTGGACACCAATATTGCTTCCGCAACTGGAGGAGAACTGCTGTGT 50
|||||
17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
|||||
51 GCGGCCCTCTACATTGACTTCCGACAGGATCTGGGCTGGAGTGGTCC 100
|||||
34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
|||||
101 ACAGGCCCAAGGGCTACCATGCAATCTTCTGCTGGAGCATGCCCGTAT 150
|||||
51 LeuArgSerAlaAspThrHisSerThrValLeuGlyTrpLysTrpValH 67
|||||
151 TTATGGAGTTCAGACACTCAGCACAGGATCTGGGCTGGAGTGGTCC 200
|||||
67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
|||||
201 ATGAACCTAAGGGTACTATGCCAACTCTGCTGGAGCATGCCCGTAT 150
|||||
51 LeuArgSerAlaAspThrHisSerThrValLeuGlyLeuTyrAsnTh 67
|||||
151 TTATGGAGTTCAGACACTCAGCACAGGATCTGCTGGAGCATGCCCGTAT 200
|||||
67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
|||||
201 CATAAATCCAGAGCATCTGCTTCTCTGCTGGAGCATGCCCGTAT 250
|||||
84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
|||||
251 AACCTCTAACCATTTCTACTACATTGGCAAAACACCCAAAGATTGACAG 300
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101 LeuSerAsnMetValValLysSerCysLysCysSer 112
|||||
301 CTTTCTAATATGATTGTAAGTCTTGCNAATGCAGC 336
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seq_name: gb_pat1:A23754

seq_documentation_block:
LOCUS A23754 336 bp mRNA PAT 25-JAN-1995
DEFINITION TGF-beta1(44/45)beta2 hybrid coding region.
ACCESSION A23754
VERSION A23754.1 GI:825588
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS McMaster,G.K., Cox,D., Cerletti,N. and Kuhla,J.
TITLE Novel hybrid transforming growth factors
JOURNAL Patent: EP 0542679-A 4 19-MAY-1993;
CIBA-GEIGY AG
FEATURES
source
1..336
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 90 a 92 c 72 g 82 t
ORIGIN

alignment_scores:
  Quality: 539.00      Length: 112
  Ratio: 5.183        Gaps: 0
  Percent Similarity: 92.857      Percent Identity: 81.250

alignment_block:
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Align seg 1/1 to: A23754 from: 1 to: 336
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1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluAsnCysCysVa 17
|||||
1 GCCTTGGACACCAATATTGCTTCCGCTCCACGAGAGAACTGCTCGGT 50
|||||
17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
|||||
51 GCGGCAGCTGTACATTGACTTCCGCAAGGACCTCGGCTGGAGTGGATCC 100
|||||
34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
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101 ACAGGCCCAAGGGCTACCATGCAATCTTCTGCTGGAGCATGCCCGTAT 150
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51 LeuArgSerAlaAspThrHisSerThrValLeuGlyLeuTyrAsnTh 67
|||||
151 TTATGGAGTTCAGACACTCAGCACAGGATCTGCTGGAGCATTATATAATAC 200
|||||
67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
|||||
201 CATAAATCCAGAGCATCTGCTTCTCTGCTGGAGCATGCCAAAGATTGACAG 250
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84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
|||||
251 AACCTCTAACCATTTCTACTACATTGGCAAAACACCCAAAGATTGACAG 300
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101 LeuSerAsnMetValValLysSerCysLysCysSer 112
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301 CTTTCTAATATGATTGTAAGTCTTGCNAATGCAGC 336
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seq_name: gb_pat1:A23758

seq_documentation_block:
LOCUS A23758 336 bp mRNA PAT 25-JAN-1995
DEFINITION TGF-beta3(44/45)beta1 hybrid coding region.
ACCESSION A23758
VERSION A23758.1 GI:825592
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS McMaster,G.K., Cox,D., Cerletti,N. and Kuhla,J.
TITLE Novel hybrid transforming growth factors
JOURNAL Patent: EP 0542679-A 8 19-MAY-1993;
CIBA-GEIGY AG
FEATURES
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BASE COUNT 63 a 109 c 98 g 56 t
ORIGIN

alignment_scores:
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  Ratio: 5.327        Gaps: 0
  Percent Similarity: 90.179      Percent Identity: 83.929

alignment_block:
  TGFB3P x A23758  ..

Align seg 1/1 to: A23758 from: 1 to: 336

1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluAsnCysCysVa 17
|||||
1 GCCTTGGACACCAATATTGCTTCCGCAACTGGAGGAGAACTGCTGTGT 50
|||||
17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
|||||
51 GCGGCCCTCTACATTGACTTCCGACAGGATCTGGGCTGGAGTGGGTC 100
|||||
34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
|||||
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|||||
101 ATCAACCTAAGGCTACTATGCCAACTTCTGCGCTCGGCCCTGCCCTAC 150
51 LeuArgSerAlaAspThrHisSerThrValLeuGlyLeuTyrAsnTh 67
:: ||| |||| ::||| |||| ::||| ||||
151 ATTTGGAGCTGCACACGACGACAGCAAGGCTCTGGCCCTGTACAACCA 200
67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
201 GCATAACCCGGGCGCTCGCGCGCGCGTCTGCTGCGCGCAGCGCTGG 250
84 luProLeuThrIleLeuTyrValGlyArgThrProLysValGluGln 100
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
251 AGCCGCTGCCCATCGTACTAGTGGCGCGCAAGCCCAAGGTGGAGCAG 300
101 LeuSerAsnMetValValLysSerCysLysCysSer 112
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301 CTGTCCAACATGATCGTGGCTCTGCAAGTGCAGC 336
seq_name: gb_pat1:A18279
seq_documentation_block:
LOCUS A18279 339 bp mRNA PAT 17-MAY-1994
DEFINITION H.sapiens TGF-beta 2 peptide seq ID No:2.
ACCESSION A18279
VERSION A18279.1 GI:513239
KEYWORDS
SOURCE
ORGANISM
synthetic construct.
synthetic construct.
artificial sequence.
REFERENCE
1 (bases 1 to 339)
AUTHORS Cerletti,N., McMaster,G.K., Cox,D., Schmitz,A. and Meyhack,B.
TITLE Process for the production of biologically active protein (e.g.
TGF)
JOURNAL Patent: EP 0433225-A 3 19-JUN-1991;
CIBA-GEIGY AG
FEATURES
Location/Qualifiers
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/protein_id="CAA01386.1"
/db_xref="GI:4529904"
/translation="ALDAAYCFRNVDNCCRLPLYPIDPKRLDGLGWKWIHEPKGYNANFC
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NMIVKSKCS"
BASE COUNT 98 a 77 c 70 g 94 t
ORIGIN
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alignment_scores:
Quality: 535.00 Length: 112
Ratio: 5.095 Gaps: 0
Percent Similarity: 93.750 Percent Identity: 79.464
alignment_block:
TGFB3P x A18279 ..
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1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluAsnCysCysVa 17
||||| ::||| |||| ::||| |||| ::||| ||||
1 GCCTTGGATCGCGCTATTCCTTTAGAAATGTCAGGATAATTGCTGCCT 50
17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
::||| ||||| ||||| ||||| ||||| ||||| |||||
51 ACGTCCACTTACATTGATTTCAAGAGGGATCTAGGGTGGAAATGGATAC 100
..
alignment_scores:
Quality: 535.00 Length: 112
Ratio: 5.095 Gaps: 0
Percent Similarity: 93.750 Percent Identity: 79.464
alignment_block:
TGFB3P x A18279 ..
Align seg 1/1 to: A18279 from: 1 to: 339
1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluAsnCysCysVa 17
||||| ::||| |||| ::||| |||| ::||| ||||
1 GCCTTGGATCGCGCTATTCCTTTAGAAATGTCAGGATAATTGCTGCCT 50
17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
::||| ||||| ||||| ||||| ||||| ||||| |||||
51 ACGTCCACTTACATTGATTTCAAGAGGGATCTAGGGTGGAAATGGATAC 100
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34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
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51 LeuArgSerAlaAspThrHisSerThrValLeuGlyLeuTyrAsnTh 67
||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
151 TTATGGAGTTCAGACACTCAGCACAGAGGTCCTGAGCTTATATAATAC 200
67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
201 CATAATCCAGAACATCTGCTTCTCTGCTGCTGCCAGGATTAG 250
84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
251 AACCTCTAAGCATCTCTACTACATTTGGCAAAACACCAAGATTGAACAG 300
101 LeuSerAsnMetValValLysSerCysLysCysSer 112
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seq_name: gb_pat1:A23752
seq_documentation_block:
LOCUS A23752 339 bp mRNA PAT 25-JAN-1995
DEFINITION TGF-beta2 coding region.
ACCESSION A23752
VERSION A23752.1 GI:825586
KEYWORDS
SOURCE
ORGANISM
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 339)
AUTHORS McMaster,G.K., Cox,D., Cerletti,N. and Kuhla,J.
TITLE Novel hybrid transforming growth factors
JOURNAL Patent: EP 0542679-A 2 19-MAY-1993;
CIBA-GEIGY AG
FEATURES
Location/Qualifiers
source
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/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 98 a 77 c 70 g 94 t
ORIGIN
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alignment_scores:
Quality: 535.00 Length: 112
Ratio: 5.095 Gaps: 0
Percent Similarity: 93.750 Percent Identity: 79.464
alignment_block:
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||||| ::||| |||| ::||| |||| ::||| ||||
1 GCCTTGGATCGCGCTATTCCTTTAGAAATGTCAGGATAATTGCTGCCT 50
17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
::||| ||||| ||||| ||||| ||||| ||||| |||||
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..
alignment_scores:
Quality: 535.00 Length: 112
Ratio: 5.095 Gaps: 0
Percent Similarity: 93.750 Percent Identity: 79.464
alignment_block:
TGFB3P x A23752 ..
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1 GCCTTGGATCGCGCTATTCCTTTAGAAATGTCAGGATAATTGCTGCCT 50
17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
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51 ACGTCCACTTACATTGATTTCAAGAGGGATCTAGGGTGGAAATGGATAC 100
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201 CATAAATCCAGAGCATCTGCTTCTCTCTGCTGCGTGTCCCAAGATTAG 250
84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
251 AACCTCTAACCATCTCTACTACATTTGGCAAAACACCCCAAGATTGAACAG 300
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301 CTTTCTAATATGATTGTAAGTCTTGCAAAATGCAGC 336

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seq_name: gb_pat1:A48551

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seq_documentation_block: 339 bp DNA PAT 07-MAR-1997
LOCUS A48551
DEFINITION Sequence 3 from Patent WO9603432.
ACCESSION A48551
VERSION A48551.1 GI:2302321
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 339)
AUTHORS Cerletti,N.
TITLE NOVEL PROCESS FOR THE PRODUCTION OF BIOLOGICALLY ACTIVE DIMERIC
JOURNAL
COMMENT Patent: WO 9603432-A 3 08-FEB-1996;
CIBA GEIGY AG (CH)
FEATURES
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/db_xref="taxon:32644"
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/note="Protein sequence is in conflict with the conceptual
translation"
/codon_start=1
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/protein_id="CAA03114.1"
/db_xref="GI:2302322"
/translation="ALDAAYCFRNVDNCCLRPYLIDFKRDLGKWKWIHEPKGYNANFC
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NMIVKSKCS"
BASE COUNT 98 a 77 c 70 g 94 t
ORIGIN

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alignment_scores:
Quality: 535.00 Length: 112
Ratio: 5.095 Gaps: 0
Percent Similarity: 93.750 Percent Identity: 79.464

alignment_block:
TGFB3P x A48551 ..
Align seg 1/1 to: A48551 from: 1 to: 339

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1 GCTTGGATGGCGCTATTGCTTTAGAAATGTCAGGATAATTGCTGCT 50
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51 ACGTCCACTTTACATTGATTTCAGAGGGGATCTAGGGTGGAAATGGATAC 100
34 lsGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
101 ACGAACCAAGGGTACAAATGCCCACTCTGCTGCGGATGCCCGTAT 150
51 LeuArgSerAlaAspThrHisSerThrValLeuGlyLeuTyrAsnTh 67
151 TTATGGAGTTTCAGACATCAGCAGCAGGGTCTCTGAGCTTATATAATAC 200
67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84

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1:::|||||
201 CATAAATCCAGAGCATCTGCTTCTCTCTGCTGCGTGTCCCAAGATTAG 250
84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
251 AACCTCTAACCATCTCTACTACATTTGGCAAAACACCCCAAGATTGAACAG 300
101 LeuSerAsnMetValValLysSerCysLysCysSer 112
301 CTTTCTAATATGATTGTAAGTCTTGCAAAATGCAGC 336

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seq_name: gb_pat1:A48565

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seq_documentation_block:
LOCUS A48565 339 bp DNA PAT 07-MAR-1997
DEFINITION Sequence 3 from Patent WO9603433.
ACCESSION A48565
VERSION A48565.1 GI:2302335
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 339)
AUTHORS Cerletti,N.
TITLE NEW PROCESS FOR THE PRODUCTION OF BIOLOGICALLY ACTIVE PROTEIN
JOURNAL
COMMENT Patent: WO 9603433-A 3 08-FEB-1996;
CIBA GEIGY AG (CH)
FEATURES
source
1..339
/organism="unidentified"
/db_xref="taxon:32644"
CDS
1..336
/note="Protein sequence is in conflict with the conceptual
translation"
/codon_start=1
/product="HUMAN TGF-BETA2"
/protein_id="CAA03121.1"
/db_xref="GI:2302336"
/translation="ALDAAYCFRNVDNCCLRPYLIDFKRDLGKWKWIHEPKGYNANFC
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NMIVKSKCS"
BASE COUNT 98 a 77 c 70 g 94 t
ORIGIN

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alignment_scores:
Quality: 535.00 Length: 112
Ratio: 5.095 Gaps: 0
Percent Similarity: 93.750 Percent Identity: 79.464

alignment_block:
TGFB3P x A48565 ..
Align seg 1/1 to: A48565 from: 1 to: 339

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1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluAsnCysCysVa 17
1 GCTTGGATGGCGCTATTGCTTTAGAAATGTCAGGATAATTGCTGCT 50
17 largProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
51 ACGTCCACTTTACATTGATTTCAGAGGGGATCTAGGGTGGAAATGGATAC 100
34 lsGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
101 ACGAACCAAGGGTACAAATGCCCACTCTGCTGCGGATGCCCGTAT 150
51 LeuArgSerAlaAspThrHisSerThrValLeuGlyLeuTyrAsnTh 67
151 TTATGGAGTTTCAGACATCAGCAGCAGGGTCTCTGAGCTTATATAATAC 200
67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84

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101 CATAAATCCAGAGCATCTGCTTCTCTCTGCTGCTGCCAAGATTAG 250
84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
251 AACCTCTAACCATTTCTCTACTACATTGGCAAAACACCCCAAGATTGAACAG 300
101 LeuSerAsnMetValValLysSerCysLysCysSer 112
301 CTTTCTAAATGATGTTAAAGTCTTGCAAAATGCAGC 336

seq_name: gb_pat1:AR036687

seq_documentation_block:
LOCUS AR036687 339 bp DNA PAT 29-SEP-1999
DEFINITION Sequence 31 from patent US 5800811.
ACCESSION AR036687
VERSION AR036687.1 GI:5954543
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 339)
AUTHORS Hall,F.L., Nimmi,M.E., Tuan,T., Wu,L. and Cheung,D.T.
TITLE Artificial skin prepared from collagen matrix containing transforming growth factor-.beta. having a collagen binding site
JOURNAL Patent: US 5800811-A 31 01-SEP-1998;
FEATURES Location/Qualifiers
source 1..339
/organism="unknown"
BASE COUNT 98 a 77 c 70 g 94 t
ORIGIN

alignment_scores:
Quality: 535.00 Length: 112
Ratio: 5.095 Gaps: 0
Percent Similarity: 93.750 Percent Identity: 79.464

alignment_block:

TGFB3P x AR036687 ..

Align seg 1/1 to: AR036687 from: 1 to: 339

1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
1 GCCTTGATCGCGCCTATTGCTTTAGAAATGTCAGGATAATTGCTGCC 50
17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
51 ACCTCCACTTTACATTGATTTCAGAGGGATCTAGGGTGGAAATGGATAC 100
34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
101 ACGAACCCAAAGGGTACAATGCCAACTTCTGTCTGGAGCATGCCCGTAT 150
51 LeuArgSerAlaAspThrHisSerThrValLeuGlyLeuTyrAsnTh 67
151 TTATGGAGTTACAGACTCAGCAGCAGGCTCTGAGCTTATATAATAC 200
67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
201 CATAAATCCAGAGCATCTGCTTCTCTGCTGGGTGCCAAGATTAG 250
84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
251 AACCTCTAACCATTTCTCTACTACATTGGCAAAACACCCCAAGATTGAACAG 300
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seq_name: gb_pat2:I56855

seq_documentation_block:
LOCUS I56855 339 bp DNA PAT 07-OCT-1997
DEFINITION Sequence 2 from patent US 5650494.
ACCESSION I56855
VERSION I56855.1 GI:2477268
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 339)
AUTHORS Cerletti,N., McMaster,G.Kent, Cox,D., Schmitz,A. and Meyhack,B.
TITLE Process for refolding recombinantly produced TGF-.beta.-like proteins
JOURNAL Patent: US 5650494-A 2 22-JUL-1997;
FEATURES Location/Qualifiers
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Ratio: 5.095 Gaps: 0
Percent Similarity: 93.750 Percent Identity: 79.464

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17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
51 ACCTCCACTTTACATTGATTTCAGAGGGATCTAGGGTGGAAATGGATAC 100
34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
101 ACGAACCCAAAGGGTACAATGCCAACTTCTGTCTGGAGCATGCCCGTAT 150
51 LeuArgSerAlaAspThrHisSerThrValLeuGlyLeuTyrAsnTh 67
151 TTATGGAGTTACAGACTCAGCAGCAGGCTCTGAGCTTATATAATAC 200
67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
201 CATAAATCCAGAGCATCTGCTTCTCTGCTGGGTGCCAAGATTAG 250
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251 AACCTCTAACCATTTCTCTACTACATTGGCAAAACACCCCAAGATTGAACAG 300
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seq_name: gb_pat1:A05306

seq_documentation_block:
LOCUS A05306 342 bp DNA PAT 07-MAY-1993
DEFINITION Complete nucleotide sequence of mature human G-Tsf.
ACCESSION A05306
VERSION A05306.1 GI:345049
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 342)
AUTHORS

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JOURNAL Patent: WO 8803807-A 10 02-JUN-1988;
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BASE COUNT      98 a   78 c   71 g   95 t
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Ratio:         5.095           Gaps:         0
Percent Similarity: 93.750 Percent Identity: 79.464
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17 lArGProlEuTYrIleasPheARgGlInASPLeUGlyTrpLySrPrValH 34
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seq_name: gb_pat1:A11707
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LOCUS All1707 342 bp DNA PAT 26-NOV-1993
DEFINITION mature H.sapiens G-Tsf gene.
ACCESSION All1707
VERSION All1707.1 GI:490099
KEYWORDS .
SOURCE human.
ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelestomi;
REFERENCE Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
AUTHORS De Martin,R., Fontana,A., Hofer,E., Hofer-Warbinek,R. and Wrann,M.
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17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTyrPlystrpValH 34
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51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
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seq_documentation_block:
LOCUS AGMGBSC1 1585 bp mRNA PRI 27-APR-1993
DEFINITION African green monkey BSC-1 cell growth inhibitor, complete cds.
ACCESSION J03585
VERSION J03585.1 GI:176495
KEYWORDS BSC-1 cell growth inhibitor; cartilage-inducing factor B;
polyargin; transforming growth factor-beta 2.
SOURCE African green monkey kidney epithelium, cDNA to mRNA.
ORGANISM Cercopithecus aethiops

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Cercopithecus.
REFERENCE
  1 (bases 1 to 1585)
AUTHORS
  Hanks, S., Armour, R., Baldwin, J.H., Maldonado, F., Spiess, J. and
  Holley, R.W.
TITLE
  Amino acid sequence of the BSC-1 cell growth inhibitor (polyargin)
  deduced from the nucleotide sequence of the cDNA
JOURNAL
  proc. Natl. Acad. Sci. U.S.A. 85, 79-82 (1988)
MEDLINE
  88124824
COMMENT
  Draft entry and computer-readable sequence for [1] kindly provided
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DEFINITION Nucleotide sequence for the human G-Tsf precursor.
ACCESSION  A05308
VERSION    A05308.1  GI:345051
KEYWORDS   .
SOURCE     synthetic construct.
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ORGANISM   1 (bases 1 to 1695)
REFERENCE  Patent: WO 8803807-A 12 02-JUN-1988;
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seq_name: gb_pat1:A11709

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DEFINITION H sapiens G-Tsf gene precursor.
ACCESSION  A11709
VERSION    A11709.1  GI:490100
KEYWORDS   .
SOURCE     human.
ORGANISM   Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 1695)
AUTHORS   De Martin,R., Fontana,A., Hofer,E., Hofer-Warbinek,R. and Wrann,M.
TITLE     Production and use of a novel T-cell suppressor factor
JOURNAL   Patent: EP 0268561-A 8 25-MAY-1988;
           SANDOZ AG; SANDOZ-PATENT-GMBH; SANDOZ-ERFINDUNGEN
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  Ratio: 5.095        Gaps: 0
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DEFINITION H sapiens G-Tsf gene precursor.
ACCESSION  A11709
VERSION    A11709.1  GI:490100
KEYWORDS   .
SOURCE     human.
ORGANISM   Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 1695)
AUTHORS   De Martin,R., Fontana,A., Hofer,E., Hofer-Warbinek,R. and Wrann,M.
TITLE     Production and use of a novel T-cell suppressor factor
JOURNAL   Patent: EP 0268561-A 8 25-MAY-1988;
           SANDOZ AG; SANDOZ-PATENT-GMBH; SANDOZ-ERFINDUNGEN
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  Ratio: 5.095        Gaps: 0
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alignment_block:
TGFB3P x A11709
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Align seg 1/1 to: A11709 from: 1 to: 1695

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1088 GCTTTGGATCGGCCTATTGCTTTAGAAATGTCAGGATAATGTCGCT 1137

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67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1288 CATAAATCCAGAGCATCTGCTTCTCTGCTGCGTGTCCCAAGATTAG 1337

84 lUpProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
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1338 AACCTCTAACCATCTCTACTACATGGCAAAACACCAAGATTGAACAG 1387

101 LeuSerAsnMetValLysSerCysLysCysSer 112
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1388 CTTCTAATATGATTGAAGTCTTCAAAATGCAGC 1423
seq_name: gb_pr9:HSRTSF

seq_documentation_block:
LOCUS      HSGTSF      1695 bp      mRNA      PRI      27-MAR-1995
DEFINITION Human mRNA for glioblastoma-derived T-cell suppressor factor G-Tsf
            (transforming growth factor-beta2, tgfb-beta2).
ACCESSION  Y00083
VERSION    Y00083.1 GI:31959
KEYWORDS   T-cell suppressor factor; transforming growth factor-beta2.
SOURCE     human
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
            1 (bases 1 to 1695)
AUTHORS    Hofer, E.
TITLE      Direct Submission
JOURNAL    Submitted (02-NOV-1987) Hofer, E., Sandoz AG, Department for
            Biotechnology, Preclinical Research, Building 386/328, Sandoz AG,
            CH-4002 Basel
REFERENCE   2 (bases 1 to 1695)
AUTHORS    de Martin, R., Haendler, B., Hofer-Warbinek, R., Gaugitsch, H.,
            Wrann, M., Schlusener, H., Seifert, J.M., Bodmer, S., Fontana, A. and
            Hofer, E.
TITLE      Complementary DNA for human glioblastoma-derived T cell suppressor
            factor, a novel member of the transforming growth factor-beta gene
            family
JOURNAL    EMBO J. 6 (12), 3673-3677 (1987)
MEDLINE    8811555
FEATURES   Location/Qualifiers
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              /clone="lambda SUP25, lambda SUP40, lambda SUP42"
              182..1426
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              /db_xref="GI:31960"
              /db_xref="SWISS-PROT:P08112"
              /translation="MHYCVLSAFLILHVTVALSITGCTLDMQDFMBKRIETRGQI
              LSKLKLSPDPEDYPEPEVPPEVISIYNSTRDLQEKASRAACERERSDEEYAKE
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              VPEQRIELYQLKSKDLTSPQRYIDSKVVRABGEWLSDFTDADVHEWLHDKRNL
              GFKISLHCPCCTFVPSNNYIIIPNKSEELAEAFAGIDGTSTVSGDQKTIKSTRKNSG
              KTHPLLMLPLSRLSQQTRKRRKRALDAAYCFRNVDNCLRLPLYIDFKRDLGKW
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              /note="put. protease cleavage site"
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              /product="put. mature G-Tsf"
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              523 a 386 c 354 g 432 t
            BASE COUNT      523 a 386 c 354 g 432 t
            ORIGIN

alignment_scores:
Quality: 535.00      Length: 112
Ratio: 5.095        Gaps: 0
Percent Similarity: 93.750      Percent Identity: 79.464

alignment_block:
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Align seg 1/1 to: HSGTSF from: 1 to: 1695

1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
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34 iGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
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1188 ACGAACCAAGGGTACAAATGCCAACTTCTGTGCTGGAGCATGCCGTAT 1237

51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
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1238 TTATGGAGTTCAGACACTCAGCAGCAGGCTCTGAGCTTATATAATAC 1287

67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
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1288 CATAAATCCAGAACATCTGCTCTCTGCTGCTGCTGCCCAAGATTAG 1337

84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
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1338 AACCTCTAACCATTTCTACTACATTGGCAAAACACCAAGATTGAACAG 1387

101 LeuSerAsnMetValValLysSerCysLysCysSer 112
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1388 CTTTCTAATATGATTGAAGTCTTGCAAAATGCAGC 1423

seq_name: gb_pat2:108281
seq_documentation_block:
LOCUS      I08281      2569 bp      PAT      02-DEC-1994
DEFINITION Sequence 3 from Patent EP 0376785.
ACCESSION  I08281
VERSION    I08281.1 GI:589009
KEYWORDS
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE   1 (bases 1 to 2569)
AUTHORS    Purchio, A.F., Madisen, L. and Webb, N.
TITLE      Cloning and expression of transforming growth factor beta 2
JOURNAL    Patent: EP 0376785-A2 3 04-JUL-1990;
FEATURES   Location/Qualifiers
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              /organism="unknown"
            BASE COUNT      772 a 599 c 512 g 686 t
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alignment_scores:
Quality: 535.00      Length: 112
Ratio: 5.095        Gaps: 0
Percent Similarity: 93.750      Percent Identity: 79.464

alignment_block:
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Align seg 1/1 to: I08281 from: 1 to: 2569

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17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
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1507 ACGTCCACTTTACATTGATTTCAGAGGGATCTAGGGTGGAAATGGATAC 1556

34 iGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
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1557 ACGAACCAAGGGTACAAATGCCAACTTCTGCTGGAGCATGCCGTAT 1606

51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
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1364 CTGTGGAGTTCAGACACACACACACCAAGTCTCTCAGCCTGTACACAC 1413
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1414 CATAAACCCGGAAGCTTCTGCTCCCTGTGTGTGTGTCGCCAGGATCGG 1463
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84 luProLeuThrIleLeuTyrrValGlyArgThrProLysValGluGln 100
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1464 AACCACTGACCATCTCTACTACATTTGGCAATAGCCCAAGATGCAACAG 1513
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1514 CTTTCCACATGATCGTCAAGCTCTGTAAATGCAGC 1549
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seq_name: gb_rol:AF153012

seq_documentation_block:
LOCUS AF153012 2880 bp mRNA ROD 24-JUL-2000
DEFINITION Rattus norvegicus TGF-beta 2 long form precursor (TGF-beta2) mRNA,
complete cds.
ACCESSION AF153012
VERSION AF153012.2 GI:4980482
KEYWORDS Norway rat.
SOURCE Rattus norvegicus
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 2880)
AUTHORS Koishi,K., Dalzell,K.G. and McLennan,I.S.
TITLE The expression and structure of TGF-beta2 transcripts in rat
muscles
JOURNAL Biochim. Biophys. Acta 1492 (2-3), 311-319 (2000)
MEDLINE 20461836
REFERENCE 2 (bases 1 to 2880)
AUTHORS Koishi,K., Dalzell,K.G.B. and McLennan,I.S.
TITLE Direct Submission
JOURNAL Submitted (18-MAY-1999) Anatomy & Structural Biology, University of
Otago, Dunedin PO Box 913, New Zealand
COMMENT On Jun 3, 1999 this sequence version replaced gi:4929795.
FEATURES
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/strain="Wistar"
/db_xref="taxon:10116"
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308..1636
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/feature="minor variant"
/codon_start=1
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/protein_id="AAD34159.1"
/db_xref="GI:4929796"
/translation="MHYCVLRTFLHLVLPVALSLSTCTLDMDQPMKRIRAIKQI
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DYSTMEKNALNVKAEFRFLQNPKARVAEQRIELYQLKSKDLTSPQRYIDSKV
KTRAGEWLSFDVTDVHFWLHKDNLGFKISLHCPCCFTIPSNVYIIPNKSOELEA
RFAGIDGSTYASGDKQTIKTRKSSGKTPHLLMLPSYRESQSSRRRRKRALDA
AFCFRNQDNCCLRLPYIDFKRDGLGWKIHEPKGNANFCAGCPYLWSSDSTQHTKVL
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/feature="putative"
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2836..2842
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/feature="putative"
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BASE COUNT 824 a 684 c 604 g 768 t
ORIGIN

alignment_scores:
Quality: 530.00 Length: 112
Ratio: 5.048 Gaps: 0
Percent Similarity: 93.750 Percent Identity: 78.571

alignment_block:
TGFBP3 x AF153012 ..
Align seg 1/1 to: AF153012 from: 1 to: 2880

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1298 GCTTTGGATGCCGCTTATTGCTTTAGGAATGTGAGGATAATTGCTGCT 1347
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17 lArgProLeuTyrrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
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1348 TCGCCCTCTTACATTTGATTTTAAAGAGGATCTTGGATGGAATGGATCC 1397
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1398 ATGAACCCAAAGGATACAAATGCTAACTTCTGTGGGGCATGCCCTTAT 1447
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51 LeuArgSerAlaAspThrHisSerThrValLeuGlyLeuTyrrAsnTh 67
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1448 CTGTGGAGTTCAGACACACACACCAAGTCTCTCAGCCTGTACACAC 1497
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1498 CATAAACCCGGAAGCTTCTGCTCCCTGTGTGTGTGTCGCCAGGATCGG 1547
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84 luProLeuThrIleLeuTyrrValGlyArgThrProLysValGluGln 100
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1548 AACCACTGACCATCTCTACTACATTTGGCAATAGCCCAAGATGCAACAG 1597
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1598 CTTTCCACATGATCGTCAAGCTCTGTAAATGCAGC 1633
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seq_name: gb_rol:MMTGFB2

seq_documentation_block:
LOCUS MMTGFB2 4267 bp mRNA ROD 14-JUN-1991
DEFINITION Mouse mRNA for transforming growth factor-beta2.
ACCESSION X57413
VERSION X57413.1 GI:54772
KEYWORDS cell proliferation; transforming growth factor-beta2.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 4267)
AUTHORS Miller,D.A., Lee,A., Pelton,R.W., Chen,E.Y., Moses,H.L. and
Derynck,R.
TITLE Murine transforming growth factor-beta 2 cDNA sequence and
expression in adult tissues and embryos
JOURNAL Mol. Endocrinol. 3 (7), 1108-1114 (1989)
MEDLINE 90014832
FEATURES
source
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1222 CTTTCCAAATGATGCGCAAGTCTGTAAATGCAGC 1257
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seq_name: gb_ov:SSTGFB2

seq_documentation_block:
LOCUS SSTGFB2 477 bp mRNA MAM 30-JUN-1993
DEFINITION S. scrofa mRNA for transforming growth factor beta 2.
ACCESSION X70142 S48994
VERSION X70142.1 GI:312949
KEYWORDS TGF-beta 2; transforming growth factor-beta2.
SOURCE pig.
ORGANISM Sus scrofa

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactylia; Suina; Suidae; Sus.

REFERENCE 1 (bases 1 to 477)
AUTHORS Mulheron,G.W., Mulheron,J.G., Danielpour,D. and Schomberg,D.W.
TITLE porcine granulosa cells do not express transforming growth
factor-beta 2 (TGF-beta 2) messenger ribonucleic acid: molecular
basis for their inability to produce TGF-beta activity comparable
to that of rat granulosa cells
JOURNAL Endocrinology 131 (6), 2609-2614 (1992)
MEDLINE 93076683

FEATURES
Location/Qualifiers
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1..477
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/product="Transforming Growth Factor-beta 2"
primer_bind 1..20
primer_bind 458..477
BASE COUNT 129 a 124 c 108 g 116 t
ORIGIN

alignment_scores:
Quality: 523.00 Length: 112
Ratio: 5.078 Gaps: 0
Percent Similarity: 91.964 Percent Identity: 77.679

alignment_block:

TGFB3P x SSTGFB2

Align seg 1/1 to: SSTGFB2 from: 1 to: 477

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142 GCTTTGGATGCAGCCATTGCTTTAGAAATGTGCAGGATAATGCTGCCT 191
17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpIysTrpValH 34
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192 GCGTCACCTTACATTGATTCAAGAGGATCTGGGTGGAATGGATAC 241
34 isGluProLysGlyTyrTrValAlaAsnPheCysSerGlyProCysProTyr 50
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242 ATGAGCCTAAAGGTACATGCCAATCTGTGCGGGGGCTGCCGCTAC 291
51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
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292 CTGTGGAGCTTGGCACCAGCATAGCAGGGTCTCAGCTTATATAACAC 341
67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
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342 CATAAACCCAGAGCTTCGCTTCCCTTGTCCGCTGCTCCAGGATTAG 391
84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
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392 ACCCGCTCACTACTCTACTACATCGGCAAAACGCCAAGATCGAGCAG 441
101 LeuSerAsnMetValValLysSerCysLysCysSer 112
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442 CTTTCTAACATGATGCTCAAGTGTGTTGTAATGCAGC 477

seq_name: gb_ov:XLTGFB2

seq_documentation_block:

LOCUS XLTGFB2 2724 bp mRNA VRT 08-NOV-1993
DEFINITION Xenopus laevis TGF-beta2 mRNA for transforming growth factor-beta2.
ACCESSION X51817
VERSION X51817.1 GI:414789
KEYWORDS growth factor; transforming growth factor.
SOURCE African clawed frog.
ORGANISM Xenopus laevis

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
Xenopodinae; Xenopus.

REFERENCE 1 (bases 1 to 2724)
AUTHORS Rebbert,M.L.
TITLE Direct Submission

JOURNAL Submitted (07-FEB-1990) Rebbert M.L., Laboratory of Molecular
Genetics, National Institute of Child, Health and Human
Development, Bldg 6 Rm 324, Bethesda MD 20892, U S A

REMARK sequence revised by [3]

REFERENCE 2 (bases 1 to 2724)

AUTHORS Rebbert,M.L., Bhatia-Dey,N. and Dawid,I.B.

TITLE The sequence of TGF-beta 2 from Xenopus laevis

JOURNAL Nucleic Acids Res. 18 (8), 2185 (1990)

MEDLINE 90245678

REFERENCE 3 (bases 1 to 2724)

AUTHORS Rebbert,M.L.

TITLE Direct Submission

JOURNAL Submitted (08-NOV-1993) Rebbert M.L., Laboratory of Molecular
Genetics, National Institute of Child, Health and Human
Development, Bldg 6 Rm 324, Bethesda MD 20892, U S A

COMMENT On Nov 9, 1993 this sequence version replaced gi:651136.

FEATURES Data kindly reviewed (16-AUG-1990) by Rebbert .M.L.

Location/Qualifiers

source

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/organism="Xenopus laevis"

/db_xref="taxon:8355"

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/clone_lib="lambda ZAP"

79..1320

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/protein_id="CAA36116.1"

/db_xref="GI:65137"

/db_xref="SWISS-PROT:P17247"

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VSPQRIELYOILKSKDLASPTORYIDSKVVKTRAEGEWLSPDVTAEVNEWLHKDRNL
GFKLSLHCPCCTPTPSNNYIIPNKSSELETRPFAGIDDAYWYAGGDSKSKTKRKHGTGR
TPHLLMLLPYSYRLESQSSRRKRALDAAYCFRNQDNCCLRPYIDFKKDLGKWKWI
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79..135

/product="signal peptide"

136..1317

/note="Protein sequence is in conflict with the conceptual
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/codon_start=1

/product="pro-TGF-beta2"

/protein_id="CAA36117.1"

/db_xref="GI:1334690"

/db_xref="SWISS-PROT:P17247"

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PTQRYIDSKVVKTRAEGEWLSPDVTAEVNEWLHKDRNLGFKLSLHCPCCTPTPSNNY
IIPNKSSELETRPFAGIDDAYWYAGGDSKSKTKRKHGTGRPHLLMLLPYSYRLESQSS
SRKRALDAAYCFRNQDNCCLRPYIDFKKDLGKWKWIHEPKYNANFCAGACPYLW
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Percent Similarity:		91.964	Percent Identity:		76.786
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TGFB3P x XLTFB2					
Align seg 1/1 to: XLTFB2 from: 1 to: 2724					
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17	lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTyrLysTrpValH	34			
1032	ACGTCCCTTATACATTGACTTTAAAGAGACCTTGGTTGGAAGTGGATAC	1081			
34	isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr	50			
1082	ATGAACCAAGGTTACAAATGCAAAATTTCTGTGCTGGAGCTTGTCCGTAT	1131			
51	LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh	67			
1132	CTGTGGAGCTCAGATCTCAACATAGCCGGTGCTAAGCCTGTACACAC	1181			
67	rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG	84			
1182	CATTAAATCCGGAAGCATCTGCCTCCCGTGTTCGCTCTCAAGATTAG	1231			
84	luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln	100			
1232	ACTCTTGACCATCTGTACTACATCGGAATAAGCCAAATAATGAACAG	1281			
101	LeuSerAsnMetValValLysSerCysLysCysSer	112			
1282	CTTTCAAAATGATTGTAATAATCATGCAAGTCAGC	1317			
seq_name: gb_pat2:I08275					
seq_documentation_block:					
LOCUS	I08275	1561 bp	PAT	02-DEC-1994	
DEFINITION	Sequence 3 from Patent EP 0374044.				
ACCESSION	I08275				
VERSION	I08275.1 GI:589015				
KEYWORDS	Unknown.				
SOURCE	Unknown.				
ORGANISM	Unclassified.				
REFERENCE	1 (bases 1 to 1561)				
AUTHORS	Purchio,A.F. and Madisen,L.				
TITLE	TGF - beta 1 / beta 2 : a novel chimeric transforming growth factor-beta				
JOURNAL	Patent: EP 0374044-A2 3 20-JUN-1990;				
FEATURES	Location/Qualifiers				
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BASE COUNT	304 a	544 c	442 g	271 t	
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alignment_scores:					
Quality:		503.00	Length:		112
Ratio:		5.030	Gaps:		0
Percent Similarity:		89.286	Percent Identity:		75.893
alignment_block:					
TGFB3P x I08275					
Align seg 1/1 to: I08275 from: 1 to: 1561					
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1096	GCCCTGGACACCAACTACTGCTTCAGAAATGTGAGGATAATTGCTGCT	1145			
17	lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTyrLysTrpValH	34			
1146	ACGTCCGCTTTACATTGACTTCAAGAGGACCTCGGCTGGAAGTGGATCC	1195			
34	isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr	50			
1196	ACGAGCCCAAGGGCTACCATGCCCAACTTCTGCTGGGGCCCTGTCCTAC	1245			
51	LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh	67			
1246	ATTTGGAGCCTGGACACGACGACGACGAGTCTGGCCCTGTACACCA	1295			
67	rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG	84			
1296	GCATAACCCGGGCGCTCGGGCGCGCTGCTGCTGCCGACGCGCTGG	1345			
84	luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln	100			
1346	AGCCACTGCCCATCGTGTACTACGTGGCGCGCAAGCCCAAGGTGGAGCAG	1395			
101	LeuSerAsnMetValValLysSerCysLysCysSer	112			
1396	CTGTCCAAACATGATCGTGGCTCGCTCCGTCAAATGCAGC	1431			
seq_name: gb_rol:MUSTGFRNA					
seq_documentation_block:					
LOCUS	MUSTGFRNA	1579 bp	mRNA	ROD	27-APR-1993
DEFINITION	Mouse transforming growth factor beta mRNA (TGF-beta), complete cds.				
ACCESSION	M13177				
VERSION	M13177.1 GI:201952				
KEYWORDS	growth factor.				
SOURCE	Mouse monocytic cell, cDNA to mRNA.				
ORGANISM	Mus musculus				
REFERENCE	1 (bases 1 to 1579)				
AUTHORS	Derynck,R., Jarrett,J.A., Chen,E.Y. and Goeddel,D.V.				
TITLE	The murine transforming growth factor-beta precursor				
JOURNAL	J. Biol. Chem. 261, 4377-4379 (1986)				
MEDLINE	86168129				
FEATURES	Location/Qualifiers				
source	1. .1579				
/organism="Mus musculus"					
/db_xref="taxon:10090"					
1. .1579					
/note="TGF-beta mRNA"					
353. .1525					
/note="TGF-beta precursor"					
/codon_start=1					
/protein_id="AAA0423.1"					
/db_xref="GI:201953"					
/translation="MPPSGRLPLLLPLPMLVLTGPRPAAGLSTCKTIDMELVKRR					
RIEARGQILSKRLASPPGQEVPPGLPEAVLALYNSTRDRVAGESADPEPEAD					
YYAEVTVLWDRNNAIYEKTKDISHIYFFNTSDIREAVPEPPLLSRAELRLQRL					
KSSVEQHVELYQKYSNNSRWYLTGTPWELSDVTGVVROWLNQGGIGQGR					
FSAHSCDSKDNKLHVEINGISPRKRGDGTIDHNNRPFLLMATPLERAQHLHSRR					
RRALDTNYCFSTKNCVQRLYIDFRKDLGKWKIHPKGYHANFCLGPCPIWISLDT					
QYSKVLALYNQHNPGASAPCCVQALPELPVIVYVGRKPKVQELSNMIVRSKCS"					
BASE COUNT	330 a	540 c	410 g	299 t	
ORIGIN					
alignment_scores:					
Quality:		503.00	Length:		112

AUTHORS Poiriot,L., Benoist,C. and Mathis,D.
TITLE Transforming growth factor-beta 1 sequence and expression: no
JOURNAL difference between NOD/Lt and C57Bl/6 mouse strains
JOURNAL Unpublished
FEATURES Location/Qualifiers
source 1..2094
/organism="Mus musculus"
/strain="NOD/Lt"
/strain="C57Bl/6"
/db_xref="taxon:10090"
/tissue_type="spleen"
868..2040
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/gene="tgfb beta 1"
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/product="transforming growth factor-beta 1"
/protein_id="CAA08900.1"
/db_xref="GI:3688424"
/translation="MPPSGLRLPLLLPLPVLVTPGRPAAGLSTCKTIDMELVYRK
RIEAIKRGILSKLRASPSQGEVPPGLPEAVLALYNSTRDRVAGESADPEPEAD
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KSSVEQHVLYQKYSNNRWYLGNRLTPTDTPWLSFDVTGVVROWLNOGDGIGER
FSAHSCSDSKNKLHVEINGTSPKRGDLGTIDMNRPLLLMATPLERAQHLHSSRH
BRALDNTYCFSTENKCCVRQLYIDFRKDLGKWKIHEPKGYHANFCLGCPYIWSLDT
QYSKVLALYNQHNPGASAPCCVPQALEPLPIVYVGRKPKVEQLSNMIVRSCKCS"
1702..2037
mat_peptide /gene="tgfb beta 1"
/product="transforming growth factor-beta 1"
BASE COUNT 421 a 734 c 574 g 365 t
ORIGIN
alignment_scores:
Quality: 503.00 Length: 112
Ratio: 5.133 Gaps: 0
Percent Similarity: 87.500 Percent Identity: 77.679
alignment_block:
TGFB3P x MMU009862 ..
Align seg 1/1 to: MMU009862 from: 1 to: 2094
1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
1702 GCCCTGGATACCAACTATGCTTCAGCTCCACAGAGAAGAACTGCTGT 1751
17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
1752 GCGGCAGCTGTACATTGACTTTAGGAGGACCTTGGTGGAGTGGATCC 1801
34 iSGluProLysGlyTyrTyrAlaAspPheCysSerGlyProCysProTyr 50
1802 ACAGAGCCAAAGGCTACCAAGTCCCACTTCTGCTGGAGACCTGCCCTAT 1851
51 LeuArgSerAlaAspThrHisSerThrValLeuGlyLeuTyrAsnTh 67
1852 ATTTGGAGCTGGACACAGTACAGCAAGTCTTGCCTCTACAAACCA 1901
67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
1902 ACACAACCCGGCGCTTCGCGGTCCACCGTGTGCTGCGCGAGGCTTTGG 1951
84 lUpProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluIn 100
1952 AGCCATGCCATGCTGCTACTACGTGGGTGCGAAGCCCAAGGTGGAGCAG 2001
101 LeuSerAsnMetValValLysSerCysLysCysSer 112
2002 TTGTCAACATGATTGTGGCTCTCTCAAGTGCAGC 2037
seq_name: gb_om:OCAF000133

seq documentation_block:
LOCUS OCAF000133 339 bp mRNA MAM 06-MAY-1997
DEFINITION Oryctolagus cuniculus transforming growth factor beta-1 mRNA,
partial cds.
ACCESSION AF000133
VERSION AF000133.1 GI:2072531
KEYWORDS rabbit.
SOURCE
ORGANISM Oryctolagus cuniculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
REFERENCE 1 (bases 1 to 339)
AUTHORS Taylor,T.K., James,E.R., McGonigle,S. and Yoho,E.R.
TITLE Rabbit transforming growth factor beta-1 active region
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 339)
AUTHORS Taylor,T.K., James,E.R., McGonigle,S. and Yoho,E.R.
TITLE Direct Submission
JOURNAL Submitted (16-APR-1997) Ophthalmology, Med.Univ. S.C., 171 Ashley
Avenue, Charleston, SC 29464, USA
FEATURES
source 1..339
/organism="Oryctolagus cuniculus"
/db_xref="taxon:9986"
<1..339
/note="encodes active region"
/codon_start=1
/product="transforming growth factor beta-1"
/protein_id="AAB53806.1"
/db_xref="GI:2072532"
/translation="ALDNTYCFSTENKCCVRQLYIDFRKDLGKWKIHEPKGYHANFC
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NMIVRSCKCS"
BASE COUNT 71 a 114 c 97 g 57 t
ORIGIN
alignment_scores:
Quality: 500.00 Length: 112
Ratio: 5.102 Gaps: 0
Percent Similarity: 87.500 Percent Identity: 76.786
alignment_block:
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Align seg 1/1 to: OCAF000133 from: 1 to: 339
1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
1 GCCCTGGACACCAACTACTGCTTCAGCTCCACAGAGAAGAACTGCTGTGT 50
17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
1752 GCGGCAGCTGTACATTGACTTCCGCAAGGACCTGGGCTGGAGTGGATCC 100
34 iSGluProLysGlyTyrTyrAlaAspPheCysSerGlyProCysProTyr 50
101 ACAGAGCCAAAGGCTACCAAGTCCCACTTCTGCTGGAGACCTGCCCTTAC 150
51 LeuArgSerAlaAspThrHisSerThrValLeuGlyLeuTyrAsnTh 67
151 ATCTGGAGCTGGACACCCAGTACAGCAAGTCTCTGGCCCTGTACAACCA 200
67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
201 GCACAACCCGGCGCTTCGCGAGCGCGTGTGTGTGTCACACAGGCGTGG 250
84 lUpProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluIn 100
251 AGCCATGCCATGCTGCTACTACGTGGGTGCGAAGCCCAAGGTGGAGCAG 300
101 LeuSerAsnMetValValLysSerCysLysCysSer 112
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301 CTGTCCACATGATCGTGGCTCTCTGCAAGTGCAGC 336
seq_name: gb_pat1:A18277

seq_documentation_block:
LOCUS   A18277             339 bp    mRNA           PAT       17-MAY-1994
DEFINITION   H.sapiens TGF-beta 1 gene seq ID No:1.
ACCESSION   A18277
VERSION     A18277.1   GI:513237
KEYWORDS    .
SOURCE      synthetic construct.
            artificial sequence.
ORGANISM    1 (bases 1 to 339)
REFERENCE   Cerletti,N., McMaster,G.K., Cox,D., Schmitz,A. and Meyhack,B.
AUTHORS    Cerletti,N., McMaster,G.K., Cox,D., Schmitz,A. and Meyhack,B.
TITLE      Process for the production of biologically active protein (e.g.
            TGF)
JOURNAL     Patent: EP 0433225-A 1 19-JUN-1991;
CIBA-GEIGY AG
FEATURES    Location/Qualifiers
            source          1..339
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                        /db_xref="taxon:32630"
            CDS             1..339
                        /note="Protein sequence is in conflict with the conceptual
                        translation"
                        /codon_start=1
                        /transl_table=11
                        /product="TGF-beta 1"
                        /protein_id="CAA01385.1"
                        /db_xref="GI:4529903"
                        /translation="ALDNYCFSTSEKNCVRLYIDFKDLGKWKIHPKGYHANFC
                        LGPCPYIWSLDTQYSKVLALYNQHNPGASAPCCVPPQALEPLPIVYVYGRKKPKVEQLS
                        NMIVRSCKCS"
BASE COUNT  66 a 114 c 100 g 59 t
ORIGIN
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alignment_scores:
    Quality: 500.00      Length: 112
    Ratio: 5.102        Gaps: 0
    Percent Similarity: 87.500      Percent Identity: 76.786

alignment_block:
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Align seg 1/1 to: A18277 from: 1 to: 339
1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
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1 GCCCTGGACACCAACTATTGCTTCAGCTCCACGGAGAGAACTGCTCGGT 50
|||||
17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
|||||
51 GCGGCAGCTGTACATTGACTTCCGCAAGGACCTCGGCTGGAAGTGGATCC 100
|||||
34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
|||||
101 ACGAGCCCAAGGGCTACCATGCAACTTCTGCTCGGGCCCTGCCCTAC 150
|||||
51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
::: |||
151 ATTTGGAGCGCTGGACACGACGACGTACACGAAGTCTGCGCTGTACAACCA 200
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67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
|||||
201 GCATAACCCGGCGCTCGGCGCGCGCTGCTGCGCTGCGCGCGCTGG 250
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84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
|||||
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|||||
101 LeuSerAsnMetValValLysSerCysLysCysSer 112
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301 CTGTCCACATGATCGTGGCTCTCTGCAAGTGCAGC 336

seq_name: gb_pat1:A48549

seq_documentation_block:
LOCUS   A48549             339 bp    DNA           PAT       07-MAR-1997
DEFINITION   Sequence 1 from Patent WO9603432.
ACCESSION   A48549
VERSION     A48549.1   GI:2302319
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301 CTGTCCACATGATCGTGGCTCTCTGCAAGTGCAGC 336
seq_name: gb_pat1:A23751

seq_documentation_block:
LOCUS   A23751             339 bp    mRNA           PAT       25-JAN-1995
DEFINITION   TGF-beta1 coding region.
ACCESSION   A23751
VERSION     A23751.1   GI:825585
KEYWORDS    .
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 339)
AUTHORS    McMaster,G.K., Cox,D., Cerletti,N. and Kuhla,J.
TITLE      Novel hybrid transforming growth factors
JOURNAL     Patent: EP 0542679-A 1 19-MAY-1993;
CIBA-GEIGY AG
FEATURES    Location/Qualifiers
            source          1..339
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                        /db_xref="taxon:9606"
            BASE COUNT      66 a 114 c 100 g 59 t
            ORIGIN
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alignment_scores:
    Quality: 500.00      Length: 112
    Ratio: 5.102        Gaps: 0
    Percent Similarity: 87.500      Percent Identity: 76.786

alignment_block:
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Align seg 1/1 to: A23751 from: 1 to: 339
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1 GCCCTGGACACCAACTATTGCTTCAGCTCCACGGAGAGAACTGCTCGGT 50
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17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
|||||
51 GCGGCAGCTGTACATTGACTTCCGCAAGGACCTCGGCTGGAAGTGGATCC 100
|||||
34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
|||||
101 ACGAGCCCAAGGGCTACCATGCAACTTCTGCTCGGGCCCTGCCCTAC 150
|||||
51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
::: |||
151 ATTTGGAGCGCTGGACACGACGACGTACACGAAGTCTGCGCTGTACAACCA 200
::: |||
67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
|||||
201 GCATAACCCGGCGCTCGGCGCGCGCTGCTGCGCTGCGCGCGCTGG 250
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84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
|||||
251 AGCGCGTCCCATCGTGTACTACGTGGGCGGCAAGCCCAAGGTGGAGCAG 300
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seq_name: gb_pat1:A48549

seq_documentation_block:
LOCUS   A48549             339 bp    DNA           PAT       07-MAR-1997
DEFINITION   Sequence 1 from Patent WO9603432.
ACCESSION   A48549
VERSION     A48549.1   GI:2302319
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KEYWORDS      unidentified.
SOURCE        unidentified
ORGANISM      unclassified.
REFERENCE     1 (bases 1 to 339)
AUTHORS       Cerletti,N.
TITLE        NOVEL PROCESS FOR THE PRODUCTION OF BIOLOGICALLY ACTIVE DIMERIC
JOURNAL       PROTEI
PATENT       Patent: WO 9603432-A 1 08-FEB-1996;
COMMENT       CIBA GEIGY AG (CH)
FEATURES     Other publication AU 3109595 960222.
SOURCE       Location/Qualifiers
             1..339
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             /protein_id="CAA03113.1"
             /db_xref="GI:2302320"
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BASE COUNT   66 a 114 c 100 g 59 t
ORIGIN

alignment_scores:
  Quality: 500.00      Length: 112
  Ratio: 5.102        Gaps: 0
  Percent Similarity: 87.500 Percent Identity: 76.786

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17 largProLeuTyrIleAspPheArgGlnAspLeuGlyTyrLysTrpValH 34
|||||
51 GCGGCAGCTGTACATTGACTTCGCAAGGACCTCGGCTGGAAGTGGATCC 100
|||||
34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
|||||
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51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
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151 ATTTGGAGCTGGACACGACAGTACAGCAAGTCTTGGCCCTGTACAACCA 200
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67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
|||||
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84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
|||||
251 AGCCCGTGCCTCGTGTACTACGTGGCGCGCAAGCCCAAGGTGGAGCAG 300
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101 LeuSerAsnMetValValLysSerCysLysCysSer 112
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seq_documentation_block:
LOCUS      A48563      339 bp      DNA
DEFINITION Sequence 1 from Patent WO9603433.
ACCESSION A48563
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VERSION      A48563.1 GI:2302333
KEYWORDS     unidentified.
SOURCE       unclassified.
ORGANISM     unclassified.
REFERENCE    1 (bases 1 to 339)
AUTHORS      Cerletti,N.
TITLE        NEW PROCESS FOR THE PRODUCTION OF BIOLOGICALLY ACTIVE PROTEIN
JOURNAL      Patent: WO 9603433-A 1 08-FEB-1996;
COMMENT      CIBA GEIGY AG (CH)
FEATURES     Other publication AU 3109695 960222.
SOURCE       Location/Qualifiers
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             /db_xref="GI:2302334"
             /translation="ALDYNCFSTSEKNCVRLQYIDFRKDLGKWKIHEPKGYHANFC
             LGPCPYIWSLDTQYSKVLALYNQHNPGASAPCCVPALEPLPIVYIVGRRPKRVEQLS
             NMIVRSCKCS"
BASE COUNT   66 a 114 c 100 g 59 t
ORIGIN

alignment_scores:
  Quality: 500.00      Length: 112
  Ratio: 5.102        Gaps: 0
  Percent Similarity: 87.500 Percent Identity: 76.786

alignment_block:
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Align seg 1/1 to: A48563 from: 1 to: 339
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1  GCCCTGGACACCAACTATTGCTTACGCTCCACGGAGAACTGCTGCGT 50
|||||
17 largProLeuTyrIleAspPheArgGlnAspLeuGlyTyrLysTrpValH 34
|||||
51 GCGGCAGCTGTACATTGACTTCGCAAGGACCTCGGCTGGAAGTGGATCC 100
|||||
34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
|||||
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|||||
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151 ATTTGGAGCTGGACACGACAGTACAGCAAGTCTTGGCCCTGTACAACCA 200
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67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
|||||
201 GCATAACCCGGCGCCTCGCGCGCGCGTGTGCTGCGCGCAGGCGCTGG 250
|||||
84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
|||||
251 AGCCCGTGCCTCGTGTACTACGTGGCGCGCAAGCCCAAGGTGGAGCAG 300
|||||
101 LeuSerAsnMetValValLysSerCysLysCysSer 112
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301 CTGTCCAAACATGATGCTGCGCTCTCTCAAGTGCAGC 336
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seq_documentation_block:
LOCUS      AR036686      339 bp      DNA
DEFINITION Sequence 29 from patent US 5800811.
ACCESSION AR036686
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VERSION      AR036686.1  GI:5954542
KEYWORDS
SOURCE       Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 339)
AUTHORS      Hall, F.L., Nimmi, M.E., Tuan, T., Wu, L. and Cheung, D.T.
TITLE        Artificial skin prepared from coclrogen matrix containing
              transforming growth factor-beta. having a collagen binding site
JOURNAL      Patent: US 5800811-A 29 01-SEP-1998;
FEATURES     Location/Qualifiers
             source
               1..339
               /organism="unknown"
BASE COUNT   66 a 113 c 100 g 60 t
ORIGIN

alignment_scores:
  Quality: 500.00      Length: 112
  Ratio: 5.102         Gaps: 0
  Percent Similarity: 87.500  Percent Identity: 76.786

alignment_block:
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  Align seg 1/1 to: AR036686 from: 1 to: 339
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  1 GCCCTGGACACCACTATTGCTTCAGCTCCACGGAGAAGAACTGCTGCGT 50
    |||||
  17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTyrLysTrpValH 34
    |||||
  51 GCGGCAGCTGTACATTGACTTCCGCAAGGACCTCGGCTGGAGTGGATCC 100
    |||||
  34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
    |||||
  101 ATGAGCCCAAGGGCTAGCATGCCAACTTCTGCCCTCGGGCCCTGCCCTAC 150
    |||||
  51 LeuArgSerAlaAspThrHisSerThrValLeuGlyLeuTyrAsnTh 67
    |||||
  151 ATTTGGAGCTGGACACGACGATACAGCAAGGTCTGCGCTGCAAGTGCACCA 200
    |||||
  67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
    |||||
  201 GCATAACCCGGCGCCCTCGCGCGCGCGCTGCTGCTGCGCGCAGGCGCTGG 250
    |||||
  84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
    |||||
  251 AGCGCGTGGCCCATCGTGTACTACGTGGCGCGCAAGCCCAAGGTGGAGCAG 300
    |||||
  101 LeuSerAsnMetValValLysSerCysLysCysSer 112
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  301 CTGTCCCAACATGATCGTGGCGCTCTGCAAGTGCAGC 336
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seq_name: gb_pat2:156854

seq_documentation_block:
LOCUS      HUMTGFBA 650 bp mRNA PRI 03-AUG-1993
DEFINITION Human transforming growth factor-beta mRNA, complete cds, clone
            pTGF-beta-trp114.
ACCESSION  M38449 M55656
VERSION    M38449.1 GI:339557
KEYWORDS   transforming growth factor-beta.
SOURCE     Human nasopharyngeal carcinoma cell line KB, cDNA to mRNA.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 650)
AUTHORS    Koshizaki, Y., Niitsu, Y., Terui, T., Koshida, Y., Mahara, K.,
            Kohgo, Y., Urushizaki, I., Takahashi, Y. and Ito, H.
TITLE      Cloning and expression of the gene for human transforming growth
            factor-beta in Escherichia coli
JOURNAL    Tumor Res. 22, 41-55 (1987)
FEATURES   Location/Qualifiers
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              1..650
              /organism="Homo sapiens"
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VERSION      AR036686.1  GI:5954542
KEYWORDS
SOURCE       Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 339)
AUTHORS      Hall, F.L., Nimmi, M.E., Tuan, T., Wu, L. and Cheung, D.T.
TITLE        Artificial skin prepared from coclrogen matrix containing
              transforming growth factor-beta. having a collagen binding site
JOURNAL      Patent: US 5800811-A 29 01-SEP-1998;
FEATURES     Location/Qualifiers
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BASE COUNT   66 a 113 c 100 g 60 t
ORIGIN

alignment_scores:
  Quality: 500.00      Length: 112
  Ratio: 5.102         Gaps: 0
  Percent Similarity: 87.500  Percent Identity: 76.786

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  Align seg 1/1 to: AR036686 from: 1 to: 339
  1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluAsnCysCysVa 17
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  1 GCCCTGGACACCACTATTGCTTCAGCTCCACGGAGAAGAACTGCTGCGT 50
    |||||
  17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTyrLysTrpValH 34
    |||||
  51 GCGGCAGCTGTACATTGACTTCCGCAAGGACCTCGGCTGGAGTGGATCC 100
    |||||
  34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
    |||||
  101 ATGAGCCCAAGGGCTAGCATGCCAACTTCTGCCCTCGGGCCCTGCCCTAC 150
    |||||
  51 LeuArgSerAlaAspThrHisSerThrValLeuGlyLeuTyrAsnTh 67
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  151 ATTTGGAGCTGGACACGACGATACAGCAAGGTCTGCGCTGCAAGTGCACCA 200
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  67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
    |||||
  201 GCATAACCCGGCGCCCTCGCGCGCGCGCTGCTGCTGCGCGCAGGCGCTGG 250
    |||||
  84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
    |||||
  251 AGCGCGTGGCCCATCGTGTACTACGTGGCGCGCAAGCCCAAGGTGGAGCAG 300
    |||||
  101 LeuSerAsnMetValValLysSerCysLysCysSer 112
    |||||
  301 CTGTCCCAACATGATCGTGGCGCTCTGCAAGTGCAGC 336
    |||||
seq_name: gb_pat2:156854

seq_documentation_block:
LOCUS      I56854 339 bp DNA PAT 07-OCT-1997
DEFINITION Sequence 1 from patent US 5650494.
ACCESSION  I56854
VERSION    I56854.1 GI:2477267
KEYWORDS
SOURCE     Unknown.
ORGANISM   Unknown.
            Unclassified.
REFERENCE  1 (bases 1 to 339)
AUTHORS    Cerletti, N., McMaster, G. Kent, Cox, D., Schmitz, A. and Meyhack, B.
TITLE      Process for refeeding recombinantly produced TGF-beta-like
            proteins
JOURNAL    Patent: US 5650494-A 1 22-JUL-1997;
FEATURES   Location/Qualifiers
            source
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/product="transforming growth factor-beta"
/protein_id="AAA36735.1"
/db_xref="GI:339558"
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LGPCPYIWSLDIQTYSKVLALYNQHPGASAPCCVPQALEPLPIVYVGRPKVEQLS
NMIVRSCKCS"
BASE COUNT 108 a 244 c 179 g 119 t
ORIGIN

alignment_scores:
Quality: 500.00 Length: 112
Ratio: 5.102 Gaps: 0
Percent Similarity: 87.500 Percent Identity: 76.786

alignment_block:

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Align seg 1/1 to: HUMTGFA from: 1 to: 650

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1 GCCTGGACACCAACTATTGCTTCAGCTCCACGGAGAAGAACTGCTGCGT 50
17 largProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
|||||
51 GCGGACGCTGTACATTGACTTCGCGAAGGACCTCGGCTGGAAGTGGATCC 100
34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
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101 ACGAGCCCAAGGGCTACCATGCCAACTTCTGCTCGGGCCCTGCCCTAC 150
51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
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151 ATTTGGAGCTGGACACGACGATACAGCAAGTCTCTGCCCTGTACAACCA 200
67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
|||||
201 GCATAACCCGGCGCCTCGCGGCGCGTGTGCTGCGTGGCGAGCGCTGG 250
84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
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251 AGCCGCTGCCCATCGTGTACTAGTGGCGCGCAAGCCCAAGGTGGAGCAG 300

101 LeuSerAsnMetValValLysSerCysLysCysSer 112
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seq_name: gb_pat2:I05434

seq_documentation_block:
LOCUS I05434 699 bp PAT 02-DEC-1994
DEFINITION Sequence 4 from Patent EP 0267463.
ACCESSION I05434
VERSION I05434.1 GI:590975

KEYWORDS

SOURCE

ORGANISM

Unclassified.

REFERENCE

1 (bases 1 to 699)

Iwata,K.K., Gold,L.I. and Stephenson,J.R.

Tissue-derived tumor growth inhibitors, methods of preparation and

uses thereof

JOURNAL Patent: EP 0267463-A2 4 18-MAY-1988;

FEATURES

Location/Qualifiers

1..699

/organism="unknown"

BASE COUNT 146 a 221 c 204 g 128 t

ORIGIN

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Quality: 500.00 Length: 112

Ratio: 5.102 Gaps: 0
Percent Similarity: 87.500 Percent Identity: 76.786
alignment_block:
TGFB3P x I05434 ..

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361 GCCTGGACACCAACTATTGCTTCAGCTCCACGGAGAAGAACTGCTGCGT 410
17 largProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
|||||
411 GCGGACGCTGTACATTGACTTCGCGAAGGACCTCGGCTGGAAGTGGATCC 460
34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
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461 ACGAGCCCAAGGGCTACCATGCCAACTTCTGCTCGGGCCCTGCCCTAC 510
51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
::: |||
511 ATTTGGAGCTGGACACGACGATACAGCAAGTCTCTGCCCTGTACAACCA 560
67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
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561 GCATAACCCGGCGCCTCGCGGCGCGTGTGCTGCGTGGCGAGCGCTGG 610
84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
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611 AGCGCTGCCCATCGTGTACTAGTGGCGCGCAAGCCCAAGGTGGAGCAG 660
101 LeuSerAsnMetValValLysSerCysLysCysSer 112
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661 CTGTCCACATGATGCTGCGCTCTCTCAAGTGACGC 696

seq_name: gb_pat2:I03312

seq_documentation_block:

LOCUS I03312 862 bp ss-DNA PAT 21-MAY-1993

DEFINITION Sequence 3 from Patent US 4886747.

ACCESSION I03312

VERSION I03312.1 GI:270706

KEYWORDS

SOURCE

Unknown.

ORGANISM

Unclassified.

REFERENCE

1 (bases 1 to 862)

Derynck,R.M.A. and Goeddel,D.V.

TITLE Nucleic acid encoding TGF-beta, and its uses

JOURNAL Patent: US 4886747-A 3 12-DEC-1989;

Genentech, Inc.;

South San Francisco, CA

FEATURES

Location/Qualifiers

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/organism="unknown"

BASE COUNT 177 a 284 c 231 g 170 t

ORIGIN

alignment_scores:

Quality: 500.00 Length: 112

Ratio: 5.102 Gaps: 0

Percent Similarity: 87.500 Percent Identity: 76.786

alignment_block:

TGFB3P x I03312 ..

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1 GCCTGGACACCAACTATTGCTTCAGCTCCACGGAGAAGAACTGCTGCGT 50

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17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
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34 isGluProLysGlyTyrTyrAlaAspPheCysSerGlyProCysProTyr 50
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
101 ACAGGCCAAGGCTACCATGCCAATCTTCGCTCGGCGCCCTGCCCCCTAC 150
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
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151 ATTGGAGCGCTGCACAGCAGTACAGCAAGTCTCGCCCTGTACACCA 200
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67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
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201 GCATAACCCGGCGGCGCTCGGCGCGCGTCTCGTGCAGCGCGCTGG 250
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251 AGCCGCTGCCCATCGTGTACTACGTGGCGCGCAAGCCCAAGGTGGAGCAG 300
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101 LeuSerAsnMetValValLysSerCysLysCysSer 112
301 CTGTCCCAACATGATCGTGCCTCTCGCAAGTGCAGC 336
seq_name: gb_om:BOVTGFB

seq_documentation_block:
LOCUS BOVTGFB 1117 bp mRNA MAM 27-APR-1993
DEFINITION Bovine transforming growth factor-beta-1 (TGF beta-1) mRNA, 3' end.
ACCESSION M36271
VERSION M36271.1 GI:163747
KEYWORDS transforming growth factor-beta 1.
SOURCE Bovine fibropapilloma, cDNA to mRNA, (library of Okayama and Berg).
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
REFERENCE 1 (bases 1 to 1117)
AUTHORS Van Obberghen-Schilling, E., Kondaiah, P., Ludwig, R.L., Sporn, M.B.
and Baker, C.C.
TITLE Complementary deoxyribonucleic acid cloning of bovine transforming
growth factor-beta-1
JOURNAL Mol. Endocrinol. 1, 693-698 (1987)
MEDLINE 91042552
FEATURES
source Location/Qualifiers
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/organism="Bos taurus"
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IYDKMKSSHSIYWFNTSELREAVPEPVLISRADVRLRLKLVKEQHVLYQKYSNN
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INGFSSGRGLDATHGMNRPFLLLMATPLERAQHLHSRRHALDTNYCFSSTEKNC
CVRQLYIDFRDLQMGWKHPKGYHANFCLGPPYIWSLDTQYSKVLALYNQHNPFGAS
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BASE COUNT 244 a 379 c 301 g 193 t
ORIGIN

alignment_scores:
Quality: 500.00 Length: 112
Ratio: 5.102 Gaps: 0
Percent Similarity: 87.500 Percent Identity: 76.786

alignment_block:
TGFB3P x BOVTGFB
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Align seg 1/1 to: BOVTGFB from: 1 to: 1117

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17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
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662 TCGTCAGCTCTACATTGACTTCGCGAAGGACCTGGGCTGGAAGTGGATTC 711
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
34 isGluProLysGlyTyrTyrAlaAspPheCysSerGlyProCysProTyr 50
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712 ATGAACCCCAAGGGTACCACGCCAATTTCTGCCTGGGGCCCTGCCCTTAC 761
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51 LeuArgSerAlaAspThrHisSerThrValLeuGlyLeuTyrAsnTh 67
::: ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
762 ATCTGGAGCCTGGATACACAGTACAGCAAGTCTCGGCCCTGTACACCA 811
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67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
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812 GCACAACCCGGCGGCTTCGGCGGCGCGTGTGCTGCTGCCTCAGGCGCTGG 861
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84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
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862 AGCCCTCGCCCATCGTGTACTACGTGGCGCGCAAGCCCAAGGTGGAGCAG 911
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101 LeuSerAsnMetValValLysSerCysLysCysSer 112
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912 TTGTCCCAACATGATCGTGCCTCTCGCAAGTGCAGC 947
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seq_name: gb_om:OATGFB1

seq_documentation_block:
LOCUS OATGFB1 1173 bp mRNA MAM 18-APR-1995
DEFINITION O.aries mRNA for transforming growth factor-beta 1.
ACCESSION X76916
VERSION X76916.1 GI:496648
KEYWORDS TGF-beta 1; transforming growth factor-beta 1.
SOURCE sheep.
ORGANISM Ovis aries
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Caprinae; Ovis.
REFERENCE 1 (bases 1 to 1173)
AUTHORS Woodall, C.J., McLaren, L.J. and Watt, N.J.
TITLE Sequence and chromosomal localisation of the gene encoding ovine
latent transforming growth factor-beta 1
JOURNAL Gene 150 (2), 371-373 (1994)
MEDLINE 95121932
REFERENCE 2 (bases 1 to 1173)
AUTHORS Woodall, C.
TITLE Direct Submission
JOURNAL Submitted (24-DEC-1993) C. Woodall, Univ. of Edinburgh, Dept. of
Veterinary Pathology, Sc. of Vet. Studies, Univ. of Edinburgh,
Edinburgh EH9 1QH, UK
FEATURES
source Location/Qualifiers
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SWRILNRLAPSPSEWLSFDVTGVVQWLTREIEIGFRLSAHCSCKSDKNTLQVD
INGFSSGRGLDATHGMNRPFLLLMATPLERAQHLHSRRHALDTNYCFSSTEKNC
CVRQLYIDFRDLQMGWKHPKGYHANFCLGPPYIWSLDTQYSKVLALYNQHNPFGAS
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BASE COUNT 244 a 379 c 301 g 193 t
ORIGIN
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ORIGIN
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  Ratio: 5.102        Gaps: 0
  Percent Similarity: 87.500      Percent Identity: 76.786
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835 GCCCTGGACACCACTACTGCTTACAGCTCCACAGAAAGAACTGCTGTG 884
17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTyrIleValH 34
|||||
885 TCGTCAGCTCTACATGTACTCCGGAAGACCTGGCTGGAGTGGATTC 934
34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
|||||
935 ACGAACCAAGGCTACCAAGGCAATTTCTGCTGGGGCCCTGTCCCTAC 984
51 LeuArgSerAlaAspThrHisSerThrValLeuGlyLeuTyrAsnTh 57
::: ||| ||||| ::||| ||||| ::||| |||||
985 ATCTGGAGCGCTGGACACAGTACAGCAAGGTCCTGGCCCTGTACAACCA 1034
67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
|||||
1035 GCACAAACCCGGCGCATCGGGCGCCGCTGCTGCTGCTCAGGCGCTGG 1084
84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
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1085 AACCCCTGCCATCGTGTACTACGTGGCGCAAGCCCAAGGTGGAGCAG 1134
101 LeuSerAsnMetValValLysSerCysLysSer 112
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seq_name: gb_om:DOGTGFB1A

seq_documentation_block:
LOCUS      DOGTGFB1A      1369 bp      mRNA      MAM      30-OCT-1994
DEFINITION Canine transforming growth factor-beta 1 (TGFb1) mRNA, complete cds.
ACCESSION L34956
VERSION L34956.1 GI:516071
KEYWORDS  homologue; transforming growth factor-beta 1.
SOURCE     Canis familiaris adult jugular vein endothelial cDNA to mRNA.
ORGANISM   Canis familiaris
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE  1 (bases 1 to 1369)
AUTHORS   Manning,A.M., Auchampach,J.A., Drong,R.F. and Slightom,J.L.
TITLE     Cloning of a canine cDNA homologous to human transforming growth
factor-beta 1 (TGFbeta1)
JOURNAL   Unpublished (1994)
FEATURES   Location/Qualifiers
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5'UTR
gene
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Cercopithecinae; Cercopithecus.
1 (bases 1 to 1561)
Sharples, K., Ploeman, G.D., Rose, T.M., Twardzik, D.R. and Purchio, A.F.
Cloning and sequence analysis of simian transforming growth factor-beta cDNA
factor-beta cDNA
JOURNAL DNA 6, 239-244 (1987)
MEDLINE 87246074
FEATURES
Location/Qualifiers
1..1561
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262..1095
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262..1434
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/protein_id="AAA35369.1"
/db_xref="GI:176553"
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BASE COUNT 301 a 547 c 446 g 267 t
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Quality: 500.00 Length: 112
Ratio: 5.102 Gaps: 0
Percent Similarity: 87.500 Percent Identity: 76.786
alignment_block:
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1096 GCCTGGACCACTACTCTTCACTCCAGGAGAACTGCTGCGT 1145
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17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTyrLysTyrValH 34
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1146 CGGCAGCTGTATATTGACTTCGCGAAGGACCTGCGTGGAAAGTGGATCC 1195
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34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
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1196 ACGAGCCCAAGGCTACCATGCCAATTCCTGCTGGGGCCCTGTCCTAC 1245
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67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
|||||
1296 GCATAACCGGCGCTGCGCGCGCGTCTGCGTGGCGCGCGCTGG 1345
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84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
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1346 AGCCATGCGCATCGTACTAGTGGCGCGCAAGCCCAAGTGGAGCAG 1395
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101 LeuSerAsnMetValValLysSerCysLysCysSer 112
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1396 CTGTCCAACATGATCTGGCGCTCCTCCAAATGCAGC 1431
seq_name: gb_on:SSTGFB

seq_documentation_block:
LOCUS SSTGFB 1605 bp mRNA MAM 27-MAR-1995
DEFINITION Porcine mRNA for transforming growth factor-beta (TFG) precursor.
ACCESSION Y00111
VERSION Y00111.1 GI:2129
KEYWORDS transforming growth factor-beta.
SOURCE pig.
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
1 (bases 1 to 1605)
Derynck, R. and Rhee, L.
Sequence of the porcine transforming growth factor-beta precursor
Nucleic Acids Res. 15 (7), 3187 (1987)
MEDLINE 87174844
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Location/Qualifiers
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809..817
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1238 GCCTGGATACCACTACTGCTTCACTCCAGGAGAACTGCTGCGT 1287
|||
17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTyrLysTyrValH 34
|||
1288 CGCGAGCTCTACATGACTTCCGGAAGGACCTGGCTGGAAGTGGATTTC 1337
|||
34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
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51 LeuArgSerAlaAspThrHisSerThrValLeuGlyLeuTyrAsnTh 67
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1388 ATCTGGAGCGCTAGACACTCAGTACAGCAAGGTCCTGGCTCTGTACAACCA 1437
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67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
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through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAL Plate: 6 Row: e Column: 11.

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1331 GGGGCGAGCTGATGACTTACCTCCGCAAGGACCTCGGCTGGAAGTGATCC 1380
34 iScLupProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
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51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
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67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
1481 GCATAACCCGGCGCTCGCGGGCGCGCTGCTGCGGCGCAGCGCTG 1530
84 lUpProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
1531 AGCCGCTGCCATCGTGTACTACGTGGCGCGCAAGCCCAAGGTGGAGCAG 1580
101 LeuSerAsnMetValValLysSerCysLysCysSer 112
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seq_documentation_block:

LOCUS BC001180 1780 bp mRNA PRI 16-MAR-2001
DEFINITION Homo sapiens, Similar to transforming growth factor, beta 1, clone
MGC:2323, mRNA, complete cds.
ACCESSION BC001180
VERSION BC001180.1 GI:12654682

KEYWORDS
SOURCE
ORGANISM

human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1780)

REFERENCE
AUTHORS
TITLE
JOURNAL

Strausberg,R.
Direct Submission
Submitted (11-DEC-2000) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA

REMARK
COMMENT

NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@bcgsc.bc.ca

Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,
Leticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo
Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven
Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saedi, Jacqueline
Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott,
Michael Thorne, Miranada Tsai, Natasha van den Bosch, Jill Vardy,
George Yang, Scott Zuyderduyn, Marco Marra.

Clone distribution: MGC clone distribution information can be found
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CDS

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LOCUS E03028
DEFINITION DNA encoding human prepro TGF-beta1.
ACCESSION E03028
VERSION E03028.1 GI:2171250
KEYWORDS JP 1991180192-A/1.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Ohashi,H., Ishii,Y., Miyata,Y., Miyazono,K., Miyagawa,K. and
Takaku,F.
PRODUCTION OF HUMAN PRO-TGF-BETA1 BY GENETIC RECOMBINATION
Patent: JP 1991180192-A 1 06-AUG-1991;
KIRIN BREWERY CO LTD
OS Homo sapiens (human)
PN JP 1991180192-A/1
PD 06-AUG-1991
PF 07-DEC-1989 JP 1989318243
PI OHASHI HIDEYA, ISHII YASUYUKI, MIYATA YOSHINORI, PI MIYAZONO KOHEI,
PI MIYAGAWA KIYOSHI, TAKAKU FUMIMARO
PC C12P21/00,C07K13/00,C12N5/10,C12N15/18//C12Q1/68,(C12P21/00,
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CC topology: Linear;
CC hypothetical: No;
CC anti-sense: No;
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FH CDS 511..1683
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seq_documentation_block: 2537 bp mRNA PAT 29-JUL-1993
LOCUS A06669
DEFINITION Synthetic mRNA for preTGF-beta1.
ACCESSION A06669
VERSION A06669.1 GI:412940
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 2537)
AUTHORS
TITLE NUCLEIC ACID CODING TGF- beta 3 AND ITS USE
JOURNAL Patent: WO 8912101-A 4 14-DEC-1989;
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DEFINITION Sus scrofa transforming growth factor beta-1 mRNA, complete cds.
ACCESSION M23703
VERSION M23703.1 GI:755044
KEYWORDS transforming growth factor-beta-1.
SOURCE Sus scrofa (strain miniature swine) cDNA to mRNA.
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE 1 (bases 1 to 3206)
AUTHORS Kondiah,P., Van Obberghen-Schilling,E., Ludwig,R.L., Dhar,R.,
Sporn,M.B. and Roberts,A.B.
TITLE cDNA cloning of porcine transforming growth factor-beta 1 mRNAs.
Evidence for alternate splicing and polyadenylation
J. Biol. Chem. 263 (34), 18313-18317 (1988)
JOURNAL
MEDLINE 89054010
COMMENT On Apr 1, 1995 this sequence version replaced gi:341017.
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DEFINITION E. caballus mRNA for transforming growth factor beta 1.
ACCESSION X99438
VERSION X99438.1 GI:2598418
KEYWORDS TGF-beta 1; transforming growth factor-beta 1.
SOURCE horse.
ORGANISM Equus caballus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
REFERENCE 1 (bases 1 to 1173)
AUTHORS Penha-Goncalves,M.N., Onions,D.E. and Nicolson,L.
TITLE Cloning and sequencing of equine transforming growth factor-beta 1
(TGF beta-1) cDNA
JOURNAL DNA Seq. 7 (6), 375-378 (1997)
MEDLINE 9818507
REFERENCE 2 (bases 1 to 1173)
AUTHORS Penha-Goncalves,M.N.
TITLE Direct Submision
JOURNAL Submitted (18-JUL-1996) M.N. Penha-Goncalves, University of
Glasgow, Veterinary Pathology Department, Veterinary School,
Bearsden Road, Glasgow G61 1QH Scotland, UK
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1085 AGCGCGTGCCTGCTGTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1134
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LOCUS E00973 2527 bp RNA PAT 29-SEP-1997
DEFINITION cDNA encoding human TGF-beta.
ACCESSION E00973
VERSION E00973.1 GI:2169234
KEYWORDS JP 1986219395-A/1.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2527)
Riku,M.A.D.D. and Debitsudo,B.G.
NUCLEIC ACID CODED WITH TGF-BETA AND ITS USE
Patent: JP 1986219395-A 1 29-SEP-1986;
GENENTECH INC
OS human
PN JP 1986219395-A/1
PD 29-SEP-1986
PF 20-MAR-1986 JP 1986064661
PR 22-MAR-1985 US 85 715142
PI RIKU MAIKERU ANDORE DERINKU, DEBITSUDO BANNOOMAN GETSUDERU PC
C12P21/00,C12N1/00,C12N5/00,C12N15/00,C12Q1/68,(C12P21/00, PC
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PC (C12N1/00,C12R1:19),(C12N5/00,C12R1:91),(C12N15/00,C12R1:91);
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CC anti-sense: No;
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1676 GCCTGGACACCACTACTGCTTCAGCTCCACGAGAAAGAACTGCTGCGT 1725
17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
1726 GCGGCGCTGTACATTGACTTTCGCAAGGACCTCGGCTGGAAGTGGATCC 1775
34 lsgluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
1776 ACGAGCCCAAGGGGTACCATGCCAAGTCTGCTGCGGGCCCTGCCCTAC 1825
51 LeuArgSerAlaAspThrHisSerThrValLeuGlyLeuTyrAsnTh 67
1826 ATTTGGAGCTGGACACGACGACGACGACGACGACGACGACGACGACG 1875
67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
1876 GCATAACCCGGCGCGCTCGGCGGCGCGTGTGCTGCTGCTGCTGCTGCTG 1925
84 lUpProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGln 100
1926 AGCGCGTGCCTGCTGTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1975
101 LeuSerAsnMetValValLysSerCysLysCysSer 112
1976 CTGTCCACATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2011
seq_name: gb_pat1:A23756
seq_documentation_block:
LOCUS A23756 336 bp mRNA PAT 25-JAN-1995
DEFINITION TGF-beta2(44/45)beta1 hybrid coding region.
ACCESSION A23756
VERSION A23756.1 GI:825590
KEYWORDS human.
SOURCE Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 336)
McMaster,G.K., Cox,D., Cerletti,N. and Kuhla,J.
Novel hybrid transforming growth factors
Patent: EP 0542679-A 6 19-MAY-1993;
CIBA-GEIGY AG
Location/Qualifiers
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BASE COUNT      230 a  395 c  361 g  201 t
ORIGIN

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Align seg 1/1 to: AF175709 from: 1 to: 1187

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17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
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899 AGCGGAGCTGTACATGTACTTTCGCAAGGATCTGGCTGGAAAGTGGATCC 948

34 lsgluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
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51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
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999 ATTTGGAGCTGGACACGACGATACAGAGGTCCTGGCCCTGTACACCA 1048

67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
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1049 GCACAACCGCGGCGGCTGCGCGCGCGCTGCTGCGTGGCGCAGGTGCTGG 1098

84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
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1099 AGCCCTGCTCCATCGTGTACTACGTGGGTGGCAAGCCCAAGGTGGAGCAG 1148

101 LeuSerAsnMetValLysSerCysLysCysSer 112
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1149 CTGTCCACATGATCGTGGCTCTCTGCAAGTGCAGC 1184

seq_name: gb_ov:CCU66874
seq_documentation_block:
LOCUS      CCU66874      1083 bp      mRNA      VRT      14-JUL-1997
DEFINITION Cyprinus carpio transforming growth factor-beta 2 mRNA, partial
cds.
ACCESSION U66874
VERSION   U66874.1 GI:1519488
KEYWORDS .
SOURCE    common carp.
ORGANISM Cyprinus carpio
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
            Cypriniformes; Cyprinidae; Cyprininae; Cyprinus.
REFERENCE 1 (bases 1 to 1083)
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AUTHORS      Sumathy,K., Desai,K.V. and Kondaiah,P.
TITLE        Isolation of transforming growth factor-beta2 cDNA from a fish,
              Cyprinus carpio by RT-PCR
JOURNAL      Gene 191 (1), 103-107 (1997)
MEDLINE      97354301
REFERENCE    2 (bases 1 to 1083)
AUTHORS      Sumathy,K., Desai,K.V. and Kondaiah,P.
TITLE        Direct Submission
JOURNAL      Submitted (14-AUG-1996) Center for Reproductive Biology and
              Molecular Endocrinology, Indian Institute of Science, Bangalore,
              Karnataka 560 012, India
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BASE COUNT   282 a  310 c  281 g  210 t
ORIGIN

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  Ratio: 5.041        Gaps: 0
Percent Similarity: 93.269 Percent Identity: 77.885

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17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
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822 ACCTCTCTCTACATCGACTTCAAGAAGGATCTGGGTGGAGTGGATCC 871

34 lsgluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
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872 ACGAACCAAGGATATACGCCCACTTCTGTGGGGAGCTGCTCCGTAT 921

51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
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67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
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84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
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1072 CTGTCCAACATG 1083

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seq_documentation_block:
LOCUS      MATGFB1      469 bp      mRNA      ROD      02-AUG-1993
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DEFINITION M.aureatus mRNA for transforming growth factor beta-1.
ACCESSION X60296
VERSION X60296.1 GI:396177
KEYWORDS transforming growth factor-beta-1.
SOURCE golden hamster.
ORGANISM Mesocricetus auratus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
Mesocricetus.
REFERENCE 1 (bases 1 to 469)
AUTHORS Yang, J.T.
TITLE Direct Submission
JOURNAL Submitted (18-SEP-1991) J.T. Yang, Harvard School of Dental
Medicine, Laboratory of Molecular Carcinogenesis, Rm 122,
188 Longwood Avenue, Boston, MA 02115, USA
REFERENCE 2 (bases 1 to 469)
AUTHORS Wong, D.T., Donoff, R.B., Yang, J., Song, B.Z., Matossian, K.,
Nagura, N., Elovic, A., McBride, J., Gallagher, G., Todd, R., et.al.
TITLE Sequential expression of transforming growth factors alpha and beta
1 by eosinophils during cutaneous wound healing in the hamster
JOURNAL Am. J. Pathol. 143 (1), 130-142 (1993)
MEDLINE 93304479
FEATURES
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                |||||
                128 GCGGACGCTGTACATGACTTCCGACAGGACCTCGGCTGGAGTGGATCC 177
                |||||
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67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
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278 GCATAACCCGGGCGCTCGCGGGCCCGTGCCTGCGCGCAGGCGCTGG 327
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84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
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328 AGCCGCTCCCATCGTGTACTACGTGGCCGCAAGCCCAAGGTGGAGCAG 377
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101 LeuSerAsnMetValValLysSerCysLysCysSer 112
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378 CTGTCACACATGATCGTGCCTGCTCTACAAAGTCAGC 413
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seq_name: gb_rol:AF191297

seq_documentation_block:
LOCUS AF191297 1597 bp mRNA ROD 16-OCT-1999
DEFINITION Cavia porcellus transforming growth factor-beta (TGF-beta) mRNA,
complete cds.
ACCESSION AF191297
VERSION AF191297.1 GI:6049850
KEYWORDS domestic guinea pig.
ORGANISM Cavia porcellus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Hystricognathi; Cavidae; Cavia.
REFERENCE 1 (bases 1 to 1597)
AUTHORS Jeevan, A., McMurray, D.N. and Yoshimura, T.
TITLE Guinea pig transforming growth factor-beta in peritoneal exudates
after BCG vaccination
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1597)
AUTHORS Jeevan, A., McMurray, D.N. and Yoshimura, T.
TITLE Direct Submission
JOURNAL Submitted (01-OCT-1999) Medical Microbiology & Immunology, Texas
A&M Univ. System Hlth. Sci. Ctr., 407 Reynolds Medical Building,
College Station, TX 77843-1114, USA
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            KLNVEQHEVDYQYISNNWRYLSNQLTSPDPEWLSFDVTGVVQWLSEGLEGER
            FSAHCSDKNDTLRVEINGIGPKRGDLAAIHGMNRPFLLLMATPLRQAHLHSSRH
            RRGLDNTYCFSTSEKNCVRLYIDFRKDLGKWIHPKGYHANFCLGPGPYIWSLDT
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886 GCCTTGGATGCTCCCTATTGCTTTAGAAATGTGAGGATAAATTGCTGCCT 935

17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTyrLysTrpValH 34
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67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
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84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
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seq_documentation_block: 1560 bp PAT 02-DEC-1994
LOCUS I06216 Sequence 2 from Patent EP 0293785.
ACCESSION I06216
VERSION I06216.1 GI:590649
KEYWORDS
SOURCE
ORGANISM
REFERENCE
Unclassified.
AUTHORS Purchio,A.F., Gentry,L. and Twardzik,D.
TITLE Cloning and expression of simian transforming growth factor-SS1
JOURNAL Patent: EP 0293785-A2 2 07-DEC-1988;
FEATURES
Location/Qualifiers
source 1. 1560
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BASE COUNT 301 a 547 c 442 g 267 t 3 others
ORIGIN

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Percent Similarity: 85.714 Percent Identity: 75.000

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17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTyrLysTrpValH 34
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1145 CGGGCAGCTGTATATTGACTTCCGCAAGGACCTCGGCTGGAAGTGGATCC 1194

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1195 ACGAGCCCAAGGGCTACCATGCCAACTTCTGCTGGGGCCCTCTGCCCTAC 1244

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51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
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67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
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seq_name: gb_pat2:106221

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seq_documentation_block: 1569 bp PAT 02-DEC-1994
LOCUS I06221 Sequence 3 from Patent EP 0293785.
ACCESSION I06221
VERSION I06221.1 GI:590650
KEYWORDS
SOURCE
ORGANISM
REFERENCE
Unclassified.
AUTHORS Purchio,A.F., Gentry,L. and Twardzik,D.
TITLE Cloning and expression of simian transforming growth factor-SS1
JOURNAL Patent: EP 0293785-A2 3 07-DEC-1988;
FEATURES
Location/Qualifiers
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Ratio: 4.958 Gaps: 0
Percent Similarity: 85.714 Percent Identity: 75.000

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Align seg 1/1 to: I06221 from: 1 to: 1569

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17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTyrLysTrpValH 34
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101 LeuSerAsnMetValValLysSerCysLysCysSer 112

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LOCUS AF152592
DEFINITION Capreolus capreolus transforming growth factor beta 3 (TGF-b3)
mRNA, partial cds.
ACCESSION AF152592
VERSION AF152592.1 GI:8132130
SOURCE roe deer.
ORGANISM Capreolus capreolus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidae;
Cervidae; Odocoileinae; Capreolus.

REFERENCE 1 (bases 1 to 244)
Wagener,A., Blottner,S., Goeritz,F. and Fickel,J.
TITLE Detection of growth factors in the testis of roe deer (Capreolus capreolus)
JOURNAL Anim. Reprod. Sci. 64 (1-2), 65-75 (2000)
MEDLINE 20532861
PUBMED 11078967

REFERENCE 2 (bases 1 to 244)
Wagener,A. and Fickel,J.
AUTHORS Direct Submission
TITLE Submitted (19-MAY-1999) Evolutionary Genetics, Institute for Zoo
Biology and Wildlife Research, Alfred-Kowalke-Str. 17, Berlin
JOURNAL D-10315, Germany
MEDLINE 89112198
PUBMED 92357039

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28 uGlyTrpLysTrpValHisGluProLysGlyTyrTyrAlaAsnPheCysS 45
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45 erglyProCysProTyrLeuArgSerAlaAspThrHisSerThrVal 61
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101 CAGGCCCATGCCATACCTCCGCACTCAGACACACCCACAGCAGGTG 150
|||||

62 LeuGlyLeuTyrAsnThrLeuAsnProGluAlaSerAlaSerProCysCy 78
|||||

151 CTGGGCGCTGTACAAACACCCCTGAACCCCTGAGCCTCAGCCTCCCTTGCTG 200
78 sValProGlnAspLeuGluProLeuThrIleLeuTyrTyrVal 92
|||||

201 CGTACCCAGGACTTGAGCCCTGACCATCTGTACTATGTC 243
|||||

seq_name: gb_ov:CHKTGFB4

seq_documentation_block: 1256 bp mRNA VRT 05-AUG-1996
LOCUS CHKTGFB4
DEFINITION Chicken transforming growth factor beta 4 (TGF-beta 4) mRNA,
partial cds.

ACCESSION M31160 X08012 S41706
VERSION M31160.1 GI:1262437
KEYWORDS growth factor; transforming growth factor-beta 4.
SOURCE Chicken cDNA to mRNA.
ORGANISM Gallus gallus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
REFERENCE 1 (bases 1 to 1256)
Jaworski,S.B., Dillard,P.J., Sporn,M.B. and Roberts,A.B.

TITLE Complementary deoxyribonucleic acid cloning of a messenger
ribonucleic acid encoding transforming growth factor beta 4 from
chicken embryo chondrocytes
JOURNAL Mol. Endocrinol. 2 (12), 1186-1195 (1988)
MEDLINE 89112198
PUBMED 92357039

REFERENCE 2 (bases 1 to 1256)
Burt,D.W. and Jakowlew,S.B.
AUTHORS Correction: a new interpretation of a chicken transforming growth
factor-beta 4 complementary DNA
JOURNAL Mol. Endocrinol. 6 (6), 989-992 (1992)
MEDLINE 92357039
COMMENT On Apr 12, 1996 this sequence version replaced gi:212760.

The sequence overlaps with that reported by Derynck et al. in
Nature 316:701-705(1985), X02812, and Derynck et al. in Nucl. Acids
Res.15:3187-3187(1987) Y00111, and Van Oberghen et al. in Mol.
Endocrin. 1:693-698(1987).

FEATURES
Location/Qualifiers
1..1256
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/strain="white leghorn"
/db_xref="taxon:9031"
/dev_stage="embryo"
/clone="pTGFb-Chx63"
/tissue_type="chondrocyte"
<1..1256
/note="TGF-beta 4 mRNA"
CDS <1..1124
/codon_start=3
/product="transforming growth factor beta 4 precursor"
/protein_id="AAB05637.1"
/db_xref="GI:1262438"

/translation="ALSTCRDLLEAAKKRIEAVRGQILSLRLTAPPASPTPPRP
LPDDVRLYNSTQELLKQARLRPPDPDEYWAELRIPMETTWDGMEHQPSH
SIFVFNVSRAHGGRTLLHRAELRLKQAADASGTEQLRLTYGYNASWRYLH
GRSVRATADDELSFDVDAHOWLSGSELLGVFKLSVHCPCMGPGHAEMLIEG
FEQQRDMQSIATKHRRVYVLAMALPAERANELHSAARRRDLDTYCFGPGTDEKNC
CVRLYIDFRKDLQWKIHEPKGYANFCSGPCPYIWSADTYTKVLALYNQHNPGAS
AAPCCVPQTLDPPLIYYVGRNVRVQLSNMVRACKS"
mat_peptide 780..1121
/product="transforming growth factor beta 4"

BASE COUNT 231 a 450 c 379 g 196 t
ORIGIN

alignment_scores:
Quality: 461.00 Length: 113
Ratio: 4.753 Gaps: 1
Percent Similarity: 85.841 Percent Identity: 71.681

alignment_block:
TGFb3P x CHKTGFB4 ..


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/organism="Capra hircus"
/db_xref="taxon:9925"
/tissue_type="ovarian follicle"
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/codon_start=1
/product="TGF beta 2"
/protein_id="AAF87742.1"
/db_xref="GI:9454283"
/translation="RNQDNCCLRPYLIDFKRDLGKWIHEPKGYHANFCLGPCPY
SADTQHSRVLSLYNTINPEASASCCVQDLEPLTILYIGNTPKIE"
BASE COUNT      73 a   67 c   63 g   70 t
ORIGIN

alignment_scores:
  Quality: 435.00      Length: 91
  Ratio: 5.118        Gaps: 0
Percent Similarity: 93.407 Percent Identity: 79.121

alignment_block:
  TGFb3P x AF276986 ..
  Align seg 1/1 to: AF276986 from: 1 to: 273

9 ArgAsnLeuGluGluAsnCysCysValArgProLeuTyrlleAspPhear 25
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1 AGAAATGTCAGGAAATGCTGCGCTACGCCCACTTACATTGATTCAA 50
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
25 gGlnAspLeuGlyTrpLysTrpValHisGluProLysGlyTyTrAlaa 42
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
51 GAGGGATCTGGGTGGAATGATTATCATGAGCCTAAAGGTACAAATGCCA 100
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
42 snPheCysSerGlyProCysProTyTrLeuArgSerAlaAspThrHis 58
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
101 ACTTCTGTGCTGGAGCGTGCCGTATCTGTGGAGCGCACACTCAGCAC 150
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
59 SerThrValLeuGlyLeuTyTrAsnThrLeuAsnProGluAlaSerAla 75
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
151 AGTAGGGTCTCAGCTTATATAATACCAATAAATCCAGAGCGTCTGCTTC 200
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
75 rProcCysValProGlnAspLeuGluProLeuThrIleLeuTyTrV 92
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
201 CCCTTGTCTGCTGCCAGATTAGAGCGCTCACCATTCTCTACTAGA 250
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
92 alGlyArgThrProLysValGlu 99
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251 TTGGAATACGCCCAAGATCGAA 273

seq_name: gb_rol:AF161218

seq_documentation_block: 302 bp mRNA ROD 28-JUL-1999
LOCUS AF161218 Meriones unguiculatus transforming growth factor beta mRNA, partial
DEFINITION cds.
ACCESSION AF161218
VERSION AF161218.1 GI:5616326
KEYWORDS Mongolian gerbil.
SOURCE Meriones unguiculatus
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Gerbillinae;
Meriones.
REFERENCE 1 (bases 1 to 302)
Rao,U.R. and Klei,T.R.
TITLE cDNA Cloning of Gerbil Transforming Growth Factor-beta by PCR
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 302)
Rao,U.R. and Klei,T.R.
TITLE Direct Submission
JOURNAL Submitted (21-JUN-1999) Microbiology and Parasitology, School of
Veterinary Medicine, South Stadium Drive, Baton Rouge, LA 70803,
USA Location/Qualifiers

FEATURES
seq_documentation_block: 358 bp DNA ROD 09-DEC-1998
LOCUS AF097509 Cavia porcellus interleukin TGF beta gene, partial cds.
DEFINITION AF097509
ACCESSION AF097509
VERSION AF097509.1 GI:3983112
KEYWORDS domestic guinea pig.
SOURCE

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ORGANISM  Cavia porcellus
REFERENCE  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS    Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
TITLE      Wicher, V., Scarozza, A.M., Ramsingh, A.I. and Wicher, K.
           Cytokine gene expression in skin of susceptible guinea-pig infected
           with Treponema pallidum
JOURNAL    Immunology 95 (2), 242-247 (1998)
MEDLINE    99069279
REFERENCE  2 (bases 1 to 358)
AUTHORS    Scarozza, A.M., Ramsingh, A.I., Wicher, V. and Wicher, K.
TITLE      Spontaneous cytokine gene expression in normal guinea pig blood and
           tissues
JOURNAL    Cytokine 10 (11), 851-859 (1998)
MEDLINE    99144670
REFERENCE  3 (bases 1 to 358)
AUTHORS    Scarozza, A.M., Ramsingh, A.I., Wicher, V. and Wicher, K.
TITLE      Direct Submission
JOURNAL    Submitted (05-OCT-1998) New York State Dept of Health, David
           Axelrod Institute, Wadsworth Center for Laboratories & Research,
           120 New Scotland Ave, Albany, NY 12208, USA
FEATURES   Location/Qualifiers
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              VYVVGKAKVEQLSNM"
BASE COUNT 76 a 120 c 103 g 59 t
ORIGIN
alignment_scores
  Quality: 420.00      Length: 103
  Ratio: 4.884        Gaps: 0
Percent Similarity: 83.495 Percent Identity: 71.845
alignment_block
TGFB3P x AF097509 ..
Align seg 1/1 to: AF097509 from: 1 to: 358
2 LeuAspThrAsnTyrCysPheArgAsnLeuGluAsnCysValArg 18
|||||
48 CTGGACACCAACTATTGCTCCAGCTCCACGAGAGAAGAACTGCTGTGCG 97
18 qProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValHisG 35
| |||||
98 GCAGCTCTACATTGACATTCGCGAAGGACCTAGGATGGAGTGACCG 147
35 luProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyrLeu 51
|||||
148 AGCCACAGGCTACATGCCAACTTCGCCCTGGGGCCCTGCCCTACATT 197
52 ArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnThrLe 68
||| |||||
198 TGGAGCTGGACACACAGTACAGCAAGTCTCGCCCTGTACACACGCA 247
68 uAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuGluP 85
|||||
248 CAACCCCGGGGTTTCGGGGCGGCTTGCTGTGTCGCGCAGGCGTTGGAGC 297
85 roLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGlnLeu 101
|||||
298 CACTGCCCATCGTGACTACGTGGGCGCGAAAGCAAGGTGGAGCAGCTC 347
102 SerAsnMet 104
|||||

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348 TCAACATG 356
seq_name: gb_on:CEU62111
seq_documentation_block:
LOCUS      CEU62111      259 bp      mRNA      MAM      31-JUL-1996
DEFINITION Cervus elaphus transforming growth factor-beta-2 (TGF beta-2) mRNA,
partial cds.
ACCESSION U62111
VERSION    U62111.1 GI:1470104
KEYWORDS   red deer.
SOURCE     Cervus elaphus
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervioidea;
           Cervidae; Cervinae; Cervus.
REFERENCE  1 (bases 1 to 259)
AUTHORS    Francis, S.M. and Suttie, J.M.
TITLE      Reverse-Transcriptase Polymerase Chain Reaction (RT-PCR) to measure
           the expression of growth factors and proto-oncogenes in the tip of
           the growing deer antler
JOURNAL    Unpublished
REFERENCE  2 (bases 1 to 259)
AUTHORS    Francis, S.M. and Suttie, J.M.
TITLE      Direct Submission
JOURNAL    Submitted (26-JUN-1996) AgResearch, Invermay Agricultural Centre,
           Puddle Alley, Mosgiel, New Zealand
FEATURES   Location/Qualifiers
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              /db_xref="taxon:9860"
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            gene
              1..259
              /gene="TGF beta-2"
              <!.>.259
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              /codon_start=2
              /product="transforming growth factor-beta-2"
              /protein_id="AAB05257.1"
              /db_xref="GI:1470105"
              /translation="QDNCCCLRPYIDFKRDLGWKWIHEPKGYNANFCACPYLWSSD
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BASE COUNT 68 a 65 c 58 g 68 t
ORIGIN
alignment_scores
  Quality: 412.00      Length: 86
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Percent Similarity: 93.023 Percent Identity: 79.070
alignment_block
TGFB3P x CEU62111 ..
Align seg 1/1 to: CEU62111 from: 1 to: 259
12 GluGluAsnCysCysValArgProLeuTyrIleAspPheArgGlnAspLe 28
|||||
2 CAGGATAATTGTTGGCTAGCCGCACTTTACATTGATTTCAAGAGGATCT 51
28 uGlyTrpLysTrpValHisGluProLysGlyTyrTyrAlaAsnPheCys 45
|||||
52 TGGGTGGAAATGGATTGATGACCTAAAGGGTACAATGCCACTTCTGTG 101
45 exGlyProCysProTyrLeuArgSerAlaAspThrThrHisSerThrVal 61
|||||
102 CTGGAGCGTGGCCCATATCTGTGAGCTCAGACACTCAGCAGCAGTAGGTT 151
62 LeuGlyLeuTyrAsnThrLeuAsnProGluAlaSerAlaSerProCysCy 78
|||||
152 CTCAGCTTATATAATACCATAAATCCAGAGCGTCTGCTTCCCTTGCTG 201
78 svalProGlnAspLeuGluProLeuThrIleLeuTyrTyrValGlyArgT 95

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|||||
202 TGTGTCCCAAGATTAGAGCGCTACACATCTCTACTACATGGCAAAA 251
95 hrProLys 97
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252 CACCCAAG 259
seq_name: gb_rol:AF169347
seq_documentation_block:
LOCUS AF169347 278 bp mRNA ROD 15-AUG-1999
DEFINITION Cavia porcellus transforming growth factor-beta mRNA, partial cds.
ACCESSION AF169347
VERSION AF169347.1 GI:5732935
KEYWORDS
SOURCE domestic guinea pig.
ORGANISM Cavia porcellus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
Morishima,Y., Uchida,Y., Nomura,A., Ishii,Y., Sakamoto,T. and
Sekizawa,K.
TITLE Guinea-pig transforming growth factor-beta expression in injured
tracheal epithelium
JOURNAL Unpublished
REFERENCE 1 (bases 1 to 278)
AUTHORS Morishima,Y., Uchida,Y., Nomura,A., Ishii,Y., Sakamoto,T. and
Sekizawa,K.
TITLE Direct Submission
JOURNAL Submitted (16-JUL-1999) Department of Pulmonary Medicine, Institute
of Clinical Medicine, University of Tsukuba, 1-1-1 Tennoudai,
Tsukuba, Ibaraki 305-8575, Japan
FEATURES
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/strain="Hartley"
/db_xref="taxon:10141"
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/tissue_type="trachea"
/notes="obtained from injured tissue"
<L>..>278
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/translation="ELDTNYCSSTKKNCCVRLQYIDFRKDLGKWKIHPKGYHANFC
LGPCPYIWSLDTQYSKVLALYNQHNPGASAPCCVPQALEPLPIVYVG"
BASE COUNT 56 a 92 c 77 g 53 t
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alignment_scores:
Quality: 401.00 Length: 91
Ratio: 5.141 Gaps: 0
Percent Similarity: 85.714 Percent Identity: 74.725
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TGFB3P x AF169347 ..
Align seg 1/1 to: AF169347 from: 1 to: 278
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|||||
4 CTGGACACCAACATATTCCTTTCAGCTCCACGAGAGAAGACTGCTGTGCG 53
18 qProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValHisG 35
| |||||
54 GCAGCTCTACATTGACATTCGCGAAGGACCTAGGATGGAAGTGGATCCACG 103
35 luProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyrLeu 51
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104 AGCCCAAGGCTACCATGCCCACTTCGTGCTGGGCGCCCTGCGCCCTACATT 153
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52 ArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnThrLe 68
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154 TGGAGCGCTGGACACACAGTACAGCAAGGTCTGTGCCCTGTACAACACGCA 203
68 uAsnProGluAlaSerAlaSerProCysValProGlnAspLeuGluP 85
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204 CAACCCCGCGCTCGCGCGCCTTGTCTGTGTGCCGCGCGGTGGAGC 253
85 roLeuThrIleLeuTyrTyrVal 92
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254 CACTGCCCATCGTGACTACGTG 276
seq_name: gb_htg17:AC079432
seq_documentation_block:
LOCUS AC079432 215287 bp DNA HTG 01-SEP-2000
DEFINITION Mus musculus chromosome 16 clone RP23-235H2, WORKING DRAFT
SEQUENCE, 43 unordered pieces.
ACCESSION AC079432
VERSION AC079432.1 GI:9958044
KEYWORDS HTG: HTGS_PHASE1; HTGS_DRAFT.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 215287)
AUTHORS DOE Joint Genome Institute.
TITLE Sequencing of Mouse
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 215287)
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (01-SEP-2000) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
COMMENT
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov
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Project Information
Center Project Name: 0
Center clone name: RPCI-23_235H2
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Summary Statistics
Consensus quality: 130929 bases at least Q40
Consensus quality: 155193 bases at least Q30
Consensus quality: 166143 bases at least Q20
Estimated insert size: 123300; agarose-fp estimation
Estimated insert size: 211087; sum-of-contigs estimation
Quality coverage: 4.98 in Q20 bases; agarose-fp estimation
Quality coverage: 2.91 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 43 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 1221: contig of 1221 bp in length
* 1222 1321: gap of unknown length
* 1322 2450: contig of 1129 bp in length
* 2451 2550: gap of unknown length
* 2551 3734: contig of 1184 bp in length
* 3735 3834: gap of unknown length
* 3835 5248: contig of 1414 bp in length
* 5249 5348: gap of unknown length
* 5349 6444: contig of 1096 bp in length
* 6445 7871: gap of unknown length
* 7872 7971: contig of 1327 bp in length
* 7972 9199: contig of 1228 bp in length
* 9199 9200: gap of unknown length
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* 9300 10379: contig of 1080 bp in length
* 10380 10479: gap of unknown length
* 10480 11597: contig of 1118 bp in length
* 11598 11697: gap of unknown length
* 11698 12849: contig of 1152 bp in length
* 12850 12950: gap of unknown length
* 12950 14153: contig of 1203 bp in length
* 14153 14252: gap of unknown length
* 14252 15426: contig of 1174 bp in length
* 15426 15527: gap of unknown length
* 15527 16631: contig of 1105 bp in length
* 16631 16732: gap of unknown length
* 16732 17804: contig of 1073 bp in length
* 17804 17904: gap of unknown length
* 17904 19077: contig of 1173 bp in length
* 19077 19177: gap of unknown length
* 19177 20507: contig of 1330 bp in length
* 20507 20607: gap of unknown length
* 20607 21763: contig of 1156 bp in length
* 21763 21863: gap of unknown length
* 21863 23109: contig of 1246 bp in length
* 23109 23209: gap of unknown length
* 23209 24447: contig of 1238 bp in length
* 24447 24547: gap of unknown length
* 24547 25812: contig of 1265 bp in length
* 25812 25912: gap of unknown length
* 25912 27151: contig of 1239 bp in length
* 27151 27251: gap of unknown length
* 27251 28293: contig of 1042 bp in length
* 28293 28393: gap of unknown length
* 28393 29910: contig of 1517 bp in length
* 29910 30010: gap of unknown length
* 30010 31518: contig of 1508 bp in length
* 31518 31618: gap of unknown length
* 31618 32733: contig of 1115 bp in length
* 32733 32833: gap of unknown length
* 32833 34632: contig of 1799 bp in length
* 34632 34732: gap of unknown length
* 34732 37157: contig of 2425 bp in length
* 37157 37257: gap of unknown length
* 37257 40264: contig of 3007 bp in length
* 40264 40364: gap of unknown length
* 40364 43087: contig of 2723 bp in length
* 43087 43187: gap of unknown length
* 43187 46514: contig of 3327 bp in length
* 46514 46614: gap of unknown length
* 46614 48688: contig of 2074 bp in length
* 48688 48788: gap of unknown length
* 48788 54008: contig of 5220 bp in length
* 54008 54108: gap of unknown length
* 54108 59084: contig of 4976 bp in length
* 59084 59184: gap of unknown length
* 59184 62589: contig of 3405 bp in length
* 62589 62690: gap of unknown length
* 62690 67662: contig of 4973 bp in length
* 67662 67762: gap of unknown length
* 67762 73470: contig of 5708 bp in length
* 73470 73570: gap of unknown length
* 73570 80059: contig of 6489 bp in length
* 80059 80159: gap of unknown length
* 80159 80606: contig of 5906 bp in length
* 80606 86165: gap of unknown length
* 86165 95152: contig of 8987 bp in length
* 95152 95252: gap of unknown length
* 95252 107209: contig of 11957 bp in length
* 107209 107309: gap of unknown length
* 107309 124400: contig of 17091 bp in length
* 124400 124500: gap of unknown length
* 124500 154709: contig of 30209 bp in length
* 154709 154809: gap of unknown length
* 154809 215287: contig of 60478 bp in length.
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Location/Qualifiers

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alignment_scores:  
Quality: 401.00 Length: 429  
Ratio: 3.819 Gaps: 3  
Percent Similarity: 24.476 Percent Identity: 24.476  
  
alignment_block:  
TGFB3P x AC079432/rev ..  
  
Align seg 1/1 to reverse of: AC079432 from: 1 to: 215287  
  
7 CysPhe.....ArgAsnLeuGluAsnCysCysValArgProLeuTy 21  
||||| ||||||||||||||||||||||||||||||||||||  
121718 TGTTCCTTCATAGCAACCTGGAGGAGAACTGCTGTGTACGCCCTTTA 121669  
  
21 rIleAspPheArgGlnAspLeuGlyTrpLysTrpValHisGluProLysG 38  
||||| ||||||||||||||||||||||||||||||||||||  
121668 TATTGACTTCGGCAGGATCTAGGCTGGAATGGTCCACGAACCTAAGG 121619  
  
38 lYTrpTrpAlaAsnPheCysSerGlyProCysProTyrLeuArgSerAla 54  
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121618 GTTACTATGCCAACTTCTGCTCAGGCCCTTGCCCATACCTCCGCGAGCCA 121569  
  
55 AspThrThrHisSer..... 59  
||||| ||||||||||||  
121568 GACACAACCCATAGCACGGTATGAGCTAGCGCATGCTCTTTGGATACTG 121519  
  
59 ..... 59  
121518 GGGCTCCCTGGCCGGACTACTTCCAGTGTGAGTGAATGAAGATTGAA 121469  
  
59 ..... 59  
121468 TGTGTAATGAATGGTAATCTTGGATGAGAAATCCCTGTAAACAGTTCT 121419  
  
59 ..... 59  
121418 GATCTGGCAGCGTGGTCCACTGCTACTCAGCTGCACCTCTGCAATTTAAA 121369  
  
59 ..... 59  
121368 TCCTACCGCGGAGCTAGCACATGGGTAAACATGCTTGTAGTGTGTC 121319  
  
59 ..... 59  
121318 CATGCTCTGGATTAGTCTCTAGCAAAACACACTTACCTGAACATGCACAC 121269  
  
59 ..... 59  
121268 AGCATGTGCACACACATGCAGAGTTCACCACCATAGTTTCAAGCATCCTT 121219  
  
59 ..... 59  
121218 TTTATTGTCTAAAGCTTCTGTACTATGAAAGTTATTTCAGCTGTGCGCATG 121169  
  
59 ..... 59  
121168 TCACCTCTGTGTACAGATGATGACCTGGTGGTGAAGATGTGGGGCCCA 121119  
  
59 ..... 59  
121118 GAGNAGTTTCTACCTCCGTTAAGACAGAAATGACGCATCTAGGAAGGAAT 121069  
  
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63 GlyTyrAsnThrLeuAsnProGluAlaSerProCysCysVa 79
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1085 GCCGTGTATAGCATCAACACGAGCCTCTGCCAGCCTCGTGT 1134

79 lProGlnAspLeuGluProLeuThrIleLeuTyrTrpValGlyArgThrP 96
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1135 TCCCAGGCACCTGGAGCCACTGCCAATCTCTACTATGTGGCAGGCAC 1184

96 roLysValGluGlnLeuSerAsnMetValLysSerCysLysCysSer 112
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1185 ACAAGTGGAGCAGCTGCCAATATGATTGTGAAGTCCTGCAAGTGTAGC 1234

seq_name: gb_rol:AF046214

seq_documentation_block:
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DEFINITION Mesocricetus auratus transforming growth factor-beta mRNA, partial cds.
ACCESSION AF046214 GI:3005106
VERSION 98234044
KEYWORDS golden hamster.
SOURCE Mesocricetus auratus
ORGANISM Mesocricetus auratus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
Mesocricetus.
REFERENCE 1 (bases 1 to 270)
AUTHORS Melby,P.C., Tryon,V.V., Chandrasekar,B. and Freeman,G.L.
TITLE Cloning of Syrian hamster (Mesocricetus auratus) cytokine cDNAs and analysis of cytokine mRNA expression in experimental visceral leishmaniasis
JOURNAL Infect. Immun. 66 (5), 2135-2142 (1998)
MEDLINE 98234044
REFERENCE 2 (bases 1 to 270)
AUTHORS Melby,P.C. and Tryon,V.V.
TITLE Direct Submission
JOURNAL Submitted (06-FEB-1998) Medicine, UTHSCSA, 7703 Floyd Curl Drive, San Antonio, TX 78284, USA
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BASE COUNT 53 a 86 c 76 g 55 t
ORIGIN

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Ratio: 5.118 Gaps: 0
Percent Similarity: 84.444 Percent Identity: 74.444

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24 eArgGlnAspLeuGlyTrpLysTrpValHisGluProLysGlyTyrA 41
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58 HisSerThrValLeuGlyLeuTyrAsnThrLeuAsnProGluAlaSerAl 74
   ::::::::::::::::::::|
151 TAGAGTAAGGTCTCTTGGCCCTCTACACCAACACACACCCGGGTGCTTGGC 200

74 asrProCysCysValProGlnAspLeuGluProLeuThrIleLeuTyrT 91
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201 GTCTCCGTGCTGTGTGCCCCAGCGCTGGAGCGCTGCCCATCGTGTACT 250

91 yrValGlyArgThrProLys 97
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251 ACGTGGGTGCAAGCCCAAG 270

seq_name: gb_ov:OMTGFb

seq_documentation_block:
LOCUS OMTGFb 1152 bp mRNA VRT 17-JUL-1998
DEFINITION O.mykiss mRNA for transforming growth factor beta.
ACCESSION X99303
VERSION X99303.1 GI:1478246
KEYWORDS tgf-beta; transforming growth factor beta.
SOURCE rainbow trout.
ORGANISM Oncorhynchus mykiss
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
REFERENCE 1 (bases 1 to 1152)
AUTHORS Hardie,L.J., Laing,K.J., Daniels,G.D., Grabowski,P.S., Cunningham,C. and Secombes,C.J.
TITLE Isolation of the first piscine transforming growth factor B gene: analysis reveals tissue specific expression and a potential regulatory sequence in rainbow trout (Oncorhynchus mykiss)
JOURNAL Cytokine in press
REFERENCE 2 (bases 1 to 1152)
AUTHORS Secombes,C.J.
TITLE Direct Submission
JOURNAL Submitted (11-JUL-1996) C.J. Secombes, Univ. of Aberdeen, Dept. of Zoology and Medicine, Therapeutics,, Tillydrone Avenue, Aberdeen AB24 2Tz, UK
REMARK revised by [3]
REFERENCE 3 (bases 1 to 1152)
AUTHORS Secombes,C.J.
TITLE Direct Submission
JOURNAL Submitted (30-JUL-1996) C.J. Secombes, Univ. of Aberdeen, Dept. of Zoology and Medicine, Therapeutics,, Tillydrone Avenue, Aberdeen AB24 2Tz, UK
COMMENT On Aug 2, 1996 this sequence version replaced gi:1438515.
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  Quality: 389.00      Length: 100
  Ratio: 4.687         Gaps: 0
  Percent Similarity: 83.000  Percent Identity: 66.000

alignment_block:
TGFB3P x OMTGFB ..

Align seg 1/1 to: OMTGFB from: 1 to: 1152

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308 GAGAGTGTCTGTGGAAACATTACATTGACTCCGTAAGGACCTGGG 357

29 yTrpLysTrpValHisGluProLysGlyTyrTyrAlaAsnPheCysSerG 46
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
358 CTGGAAGTGGATCCATGACCCACTGGCTACTTGTCTAAGTACTGCAATCG 407

46 lyProCysProTyrLeuArgSerAlaAspThrThrHisSerThrValLeu 62
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408 GCCCTGACCTATATATGGAACACACAGAAACAAAGTATTCCTCCAGGTACTG 457

63 GlyLeuTyrAsnThrLeuAsnProGluAlaSerAlaSerProCysCysVa 79
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458 GCTCTGTATAAGCACACACACCCCGGAGCCTCTGCCACCCCTGCTGTGT 507

79 lProGlnAspLeuGluProLeuThrIleLeuTyrTyrValGlyArgThrp 96
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508 TCCACAGGTCTTGGAGCCCTCCCCATTATCTATTATGTGGGGAGACAC 557

96 roLysValGluGlnLeuSerAsnMetValValLysSerCysLysCysSer 112
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OM of: TGFB3P To: N_Geneseq_0601:* out_format : pfs

Date: Oct 30, 2001 9:13 AM

About: Results were produced by the GenCore software, version 4.5,
Copyright (c) 1993-2000 CompuGen Ltd.

Command line parameters:

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-GAPEXT=4.000 -MINMATCH=0.100 -LOOPCL=0.000 -LOPOPT=0.000
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-DELOP=6.000 -DELEXT=7.000 -START=1 -MATRIX=blotsum62
-TRANS=human40.cdi -LIST=100 -DOCCALIGN=200 -THR_SCORE=pct
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-NORM=ext -MINLEN=0 -MAXLEN=200000000
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Search information block:

Query: TGFB3P

Query length: 113

Database: N_Geneseq_0601.*

Database sequences: 730101

Database length: 313950809

Search time (sec): 76.040000

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seq_documentation_block:

ID AAQ11995 standard; DNA; 339 BP.

XX AAQ11995;

AC AAQ11995;

DT 29-AUG-1991 (first entry)

DE Encodes Transforming Growth Factor beta 3.

XX TGF-beta3; biologically active protein production; ss.

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XX OS Homo sapiens.
XX PN EP433225-A.
XX PD 19-JUN-1991.
XX PF 27-NOV-1990; 90EP-0810922.
XX PR 06-DEC-1989; 89GB-0027546.
XX PS (CIBA ) CIBA GEIGY AG.
XX PI Cerletti N, McMaster GK, Cox D, Schmitz A, Meyhack B;
XX WPI; 1991-180005/25.
XX DR P-PSDB; AAR12404.
XX PT Prodn. of Transforming Growth Factor type-beta-like proteins - by
XX subjecting denaturated monomeric form to refolding conditions
XX PS Example; Page 27; 35pp; English.
XX CC This coding sequence was isolated from the CI-215 human glioma cell
XX line. It was incorporated into an appropriate vector to transform
XX Saccharomyces cerevisiae or E.coli. Monomeric TGF-beta1 was purified,
XX denatured and dissolved in 140ml 50mM Tris/HCl pH8, 1M NaCl, 5mM EDTA,
XX 2mM reduced glutathione, 1mM oxidised glutathione and 33mM Chaps.
XX After 72 hrs at 4 deg C, pH was adjusted to 2.5 and the mixture was
XX conc. 10 times. The conc. soln was diluted to the original vol. with
XX 10mM HCl and conc to a final vol of 10 ml. The supernatant from
XX centrifugation at 5000g for 30 min contained disulphide-linked dimeric
XX TGF-beta3.
XX SQ Sequence 339 BP; 74 A; 104 C; 86 G; 75 T; 0 other;

alignment_scores:
    Quality: 633.00      Length: 112
    Ratio: 5.652        Gaps: 0
    Percent Similarity: 100.000    Percent Identity: 100.000

alignment_block:
TGFB3P x AAQ11995 ..
Align seg 1/1 to: AAQ11995 from: 1 to: 339
1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluAsnCysCysVa 17
|||||
1 GCTTTGGACACCAATTAAGTCTTCCGCAACTTGGAGGAGAACTGCTGTG 50
17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
|||||
51 GCGCCCCCTCTACATVTGACTTCCGACAGGATCTGGGCTGGAAAGTGGTCC 100
34 lSgLuProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
|||||
101 ATGAACCTTAAGGCTACTATGCTGCTAGGCTTCCCATAC 150
51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
|||||
151 CTCGCGAGTGCAGACACACACACAGCAGCGTGTGGGACTGTACAACAC 200
67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
201 TCTGAACCTTGAAGCATCTGCTCGCTGCTGCTGCTGCTGCTGCTGCTG 250
84 LuProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
|||||
251 AGCCCCCTGACCATCTGTACTATGTGTGGAGAGGACCCCAAGAGTGGAGCAG 300
101 LeuSerAsnMetValValLysSerCysLysCysSer 112
|||||
```

```
301 CTCCTCAACATGGTGGTGAAGTCTTGTAAATGTAGC 336
seq_name: /SIDS1/gcgdata/geneseq/NA1993.DAT:AAQ41601
seq_documentation_block:
ID_AAQ41601 standard; cDNA; 339 BP.
XX AC AAQ41601;
XX DT 26-AUG-1993 (first entry)
XX DE Mature human Transforming Growth Factor-beta3.
XX KW hTGF-beta3; hybrid protein; wound healing; cancer treatment;
XX bone repair; growth regulation; ss.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT mat_peptide 1..336
XX FT /*tag= a
XX PN EP542679-A.
XX PD 19-MAY-1993.
XX PF 03-NOV-1992; 92EP-0810845.
XX PR 11-NOV-1991; 91EP-0810870.
XX PA (CIBA ) CIBA GEIGY AG.
XX PI McMaster GK, Cox D, Cerletti N, Kuhla J;
XX WPI; 1993-161126/20.
XX DR P-PSDB; AAR39640.
XX PT New hybrid transforming growth factor-beta molecules - comprise
XX portions of mature TGF-beta isoforms; useful as wound healants,
XX cardioprotective, antiinflammatory and immunosuppressive agents etc.
XX PS Claim 4; Page 24; 48pp; English.
XX CC The invention covers hybrid TGF-beta molecules consisting of parts
XX of the human isoforms TGF-beta1, TGF-beta2 and TGF-beta3 (see AAQ41599,
XX AAQ41600 and AAQ41601, respectively). The hinge points between parts
XX derived from different parent isoforms are pref. between amino acids
XX 44 and 45, 56 and 57, 79 and 80, 90 and 91, or 22 and 23. The hybrid
XX molecules promote cell migration, inhibit the growth of A375
XX melanoma cells, accelerate the healing of partial-thickness burn
XX wounds and full-thickness incisional wounds and increase formation
XX of fibrous granular tissue. See e.g. AAQ41602-Q41607 for pref. hybrids.
XX SQ Sequence 339 BP; 74 A; 104 C; 86 G; 75 T; 0 other;
```

```
alignment_scores:
    Quality: 633.00      Length: 112
    Ratio: 5.652        Gaps: 0
    Percent Similarity: 100.000    Percent Identity: 100.000

alignment_block:
TGFB3P x AAQ41601 ..
Align seg 1/1 to: AAQ41601 from: 1 to: 339
1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluAsnCysCysVa 17
|||||
1 GCTTTGGACACCAATTAAGTCTTCCGCAACTTGGAGGAGAACTGCTGTG 50
17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
|||||
51 GCGCCCCCTCTACATVTGACTTCCGACAGGATCTGGGCTGGAAAGTGGTCC 100
```

```

34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
|||||
101 ATGAACCTAAGGCTACTATGCCAACTTCTGCTCAGGCCCTTGCCCATAC 150
|||||
51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
|||||
151 CTCGGCAGTGCAGACACACACCCACAGCAGGCTGGGACTGTACAACAC 200
|||||
67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
|||||
201 TCTGAACCTGAAGCATCTGCCTGCCTTGCCTGCGTGGCCAGACCTGG 250
|||||
84 luProLeuThrLeuLeuTyrTyrValGlyArgThrProLysValGluGln 100
|||||
251 AGCCCTTGACCTCCCTGCTACTATGTTGGGAGGACCCCAAGTGGAGCAG 300
|||||
101 LeuSerAsnMetValValLysSerCysLysCysSer 112
|||||
301 CTCCTCAACATGGTGGTGAAGTCTTCTGAATGTAGC 336
|||||

```

seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1996.DAT:AAT17234

seq_documentation_block:

ID AAT17234 standard; cDNA to mRNA; 339 BP.

AC AAT17234;

DT 17-JUL-1996 (first entry)

XX Human TGF-beta 3 cDNA.

XX Transforming growth factor type beta; TGF-beta 3;
XX protein renaturation; protein folding; ds.

OS Homo sapiens.

XX WO9603433-A1.

XX 08-FEB-1996.

XX 12-JUL-1995; 95WO-EP02719.

XX 25-JUL-1994; 94EP-0810439.

XX (CIBA) CIBA GEIGY AG.

XX Cerletti N;

XX WPI: 1996-117000/12.

DR P-PSDB; AAR92772.

XX Prodn. of dimeric biologically active transforming growth factor
PT by refolding denatured monomer in detergent-free folding buffer
PT contg. specific organic solvent to improve yield

PS Example 1B; Page 34; 54pp; English.

XX The coding sequence (AAT17234) of human transforming growth factor
CC TGF-beta 3 (AAR92772) was cloned into plasmid pGEM-52E(+) (Promega)
CC and the construct used to transform E. coli Y1090. Subcloning in
CC pPLMu yielded plasmid pPLMu.hTGF-beta 3. Non-soluble, monomeric
CC TGF-beta 3 was recovered from E. coli LC 137/pPLMu.hTGF-beta 3 (DSM
CC 5658) transformants. A biologically active, dimeric form of
CC TGF-beta 3 was obtd. by refolding this monomer in detergent-free
CC buffer contg. DMSO and/or DMF. Dimers of TGF-beta 1 (AAR92773) and
CC TGF-beta 2 (AAR92774), and hybrid dimers (see also AAR92775-77), were
CC also produced.

SQ Sequence 339 BP; 74 A; 104 C; 86 G; 75 T; 0 other;

alignment_scores:

Quality: 633.00 Length: 112
Ratio: 5.652 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
TGFB3P x AAT17234 ..

Align seg 1/1 to: AAT17234 from: 1 to: 339

```

1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluAsnCysCysVa 17
|||||
1 GCTTTGGACACCAATTAATCTGCTTCCGCAACTTGGAGGAGAACTGCTGTGT 50
|||||
17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTyrLysTrpValH 34
|||||
51 GCGCCCTCTCTACATTGACTTCCGACAGATCTGGCTGGAAAGTGGTCC 100
|||||
34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
|||||
101 ATGAACCTAAGGCTACTATGCCAACTTCTGCTCAGGCCCTTGCCCATAC 150
|||||
51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
|||||
151 CTCGGCAGTGCAGACACACACCCACAGCAGGCTGGGACTGTACAACAC 200
|||||
67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
|||||
201 TCTGAACCTGAAGCATCTGCCTGCCTTGCCTGCGTGGCCAGACCTGG 250
|||||
84 luProLeuThrLeuLeuTyrTyrValGlyArgThrProLysValGluGln 100
|||||
251 AGCCCTTGACCTCCCTGCTACTATGTTGGGAGGACCCCAAGTGGAGCAG 300
|||||
101 LeuSerAsnMetValValLysSerCysLysCysSer 112
|||||
301 CTCCTCAACATGGTGGTGAAGTCTTCTGAATGTAGC 336
|||||

```

seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1996.DAT:AAT15464

seq_documentation_block:

ID AAT15464 standard; cDNA to mRNA; 339 BP.

XX AAT15464;

DT 10-JUN-1996 (first entry)

XX Human transforming growth factor beta 3 encoding cDNA.

XX Transforming growth factor beta; TGF; regulator; method;
XX proliferation; differentiation; wound healing; solvent; ds.

OS Homo sapiens.

XX Key Location/Qualifiers

FT CDS 1..339

FT /*tag= a

FT /product= human_TGF-beta-3

XX WO9603432-A1.

XX 08-FEB-1996.

XX 12-JUL-1995; 95WO-EP02718.

XX 25-JUL-1994; 94EP-0810438.

XX (CIBA) CIBA GEIGY AG.

XX Cerletti N;

XX WPI: 1996-116999/12.

DR P-PSDB; AAR91958.

XX

PT Prodn. of dimeric, biologically active transforming growth factor
 PT beta - by refolding denatured monomer in buffer contg. mild
 detergent and specific organic solvents to improve yields
 XX
 PS Example 1; Page 36-37; 59pp; English.
 XX
 CC AAT15462-T15464 encode transforming growth factor (TGF) beta-1,
 CC TGF beta-2 and TGF beta-3 which are produced using recombinant
 CC DNA technology and used to produce TGF beta-like proteins in
 CC dimeric form. The TGF beta-like proteins produced are hybrids of
 CC 2 different types of TGF beta e.g. TGF beta-1-3, TGF beta-2-3, etc,
 CC or bone morphogenic proteins e.g. BMP-2. The TGF beta hybrids were
 CC made using a new process of producing dimeric, biologically active
 CC TGF beta-like proteins. The new process involves treating denatured
 CC TGF beta monomers with folding buffer contg. a mild detergent (CHAPS,
 CC CHAPS0 or digitonin) and at least one of the solvents DMSO (dimethyl
 CC sulphoxide), DMSO2 (dimethylsulphone) and DMF (dimethyl formamide).
 CC The detergent allows folding of the monomer such that, after
 CC dimerisation, the TGF beta-like protein retains biological activity
 CC and remains in soluble form. The method allows relatively high yields
 CC of biologically active TGF beta-like proteins in their native dimeric
 CC form. TGF-beta like proteins are multifunctional regulators of
 CC cellular activity and a typical use is to stimulate wound healing.
 XX
 SQ Sequence 339 BP; 74 A; 104 C; 86 G; 75 T; 0 other;

alignment_scores:
 Quality: 633.00 Length: 112
 Ratio: 5.652 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
 TGF3P x AAT15464 ..

Align seg 1/1 to: AAT15464 from: 1 to: 339

1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluAsnCysCysVa 17
 |||||
 1 GCTTTGGACACCAATTACTGCTTCGCAACTTGGAGGAACTGCTGTGT 50
 17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
 |||||
 51 GCGCCCCCTCTACATTGACTTCCGACAGGATCTGGGCTGGAAGTGGGTCC 100
 34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
 |||||
 101 ATGAACTAAGGGCTACTATGCCAACTTCTGCTAGGCCCTTGCCCATAC 150
 51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
 |||||
 151 CTCCGCAGTCAGACACACACACACAGCAGCGTGTGGGACTGTACACAC 200
 67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
 |||||
 201 TCTGAACCTGAAGCATCTGCTCGCTTGTGCTGCGCCAGGACCTGG 250
 84 luProLeuThrIleLeuTyrValGlyArgThrProLysValGluGln 100
 |||||
 251 AGCCCCCTGACCATCTGTACTATGTGTGGAGGACCCCAAGGTGGAGCAG 300
 101 LeuSerAsnMetValValLysSerCysLysCysSer 112
 |||||
 301 CTCCTCCACATGGTGGTGAAGTCTGTAAATGTAGC 336

seq_name: /SIDS1/gcdata/geneseq/geneseq/NA197.DAT:AAT80110

seq_documentation_block:

ID AAT80110 standard; cDNA to mRNA; 339 BP.

XX
 AC AAT80110;

XX
 DT 28-NOV-1997 (first entry)

XX
 DE

XX Mature transforming growth factor beta3 coding sequence.

KW Transforming growth factor beta3; TGF-beta3; human; mature protein;
 KW acid-stable; heat-stable; homodimer; mitogenesis; cell proliferation;
 KW cell growth; wound; oral mucositis; intestinal mucositis; osteoarthritis;
 KW bone disease; bone repair; therapy; ds.

XX Homo sapiens.

XX W09705166-A1.

XX 13-FEB-1997.

PF 17-JUL-1996; 96WO-EP03140.

PR 25-JUL-1995; 95EP-0810484.

XX (CIBA) CIBA GEIGY AG.

PI Arvinde T, Grutter M, Mittl P;

DR WPI: 1997-145621/13.

XX P-PSDB; AAW26173.

PT Crystalline form of transforming growth factor beta-3 - useful in
 PT compns. as slow release form of TGF, e.g. for wound healing, and
 PT for structure determ. in rational drug design

XX Example 1; Page 25-26; 34pp; English.

CC This sequence represents the coding sequence for human transforming
 CC growth factor beta3 (TGF-beta3). TGF-beta3 is one of five distinct
 CC homodimeric TGF-beta's. TGF-beta3 is an acid-stable and heat-stable
 CC disulphide linked homodimer. All the TGF-beta's are produced as 390-412
 CC amino acid precursors, which undergo proteolytic cleavage to produce
 CC mature forms which consist of the C-terminal 112 amino acids. Depending
 CC upon cell and tissue type, and the presence of other growth factors,
 CC TGF-beta may either stimulate mitogenesis, cell proliferation and growth,
 CC or inhibit these processes. Many of the actions of TGF-beta are related
 CC to the response of cells or tissues to stress or injury, and to the
 CC repair of resultant damage. A crystalline form of TGF-beta3 can be
 CC produced by a method of the invention. Crystalline TGF-beta3 is useful in
 CC slow release compositions for treatment of conditions such as wounds,
 CC oral or intestinal mucositis, osteoarthritis, bone disease and repair,
 CC generally wherever TGF-beta3 is normally used. The crystalline form is
 CC also used for structure determination in rational drug design.
 CC Crystalline TGF-beta3 shows lower tendency than the dissolved protein to
 CC adsorb on the walls of vials and is more stable against oxidation.
 CC Variation of the properties, e.g. size, of the crystals allows control
 CC over the rate at which active TGF is released in vivo.

XX Sequence 339 BP; 74 A; 104 C; 86 G; 75 T; 0 other;

alignment_scores:

Quality: 633.00 Length: 112
 Ratio: 5.652 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

TGF3P x AAT80110 ..

Align seg 1/1 to: AAT80110 from: 1 to: 339

1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluAsnCysCysVa 17

|||||
 1 GCTTTGGACACCAATTACTGCTTCGCAACTTGGAGGAACTGCTGTGT 50

17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34

|||||
 51 GCGCCCCCTCTACATTGACTTCCGACAGGATCTGGGCTGGAAGTGGGTCC 100

```
34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
|||||
101 ATGAACTTAGGCTACTATGCCAACTTCGTCAGGCCCTTGCCCATAC 150
|||||
51 LeuArgSerAlaAspThrHisSerThrValLeuGlyLeuTyrAsnTh 67
|||||
151 CTCGGCAGTCAGACACACCAACCCAGCACGCGTGTGGACTGTACAACAC 200
|||||
67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
|||||
201 TCTGAACCCCTGAAGCACTCTGCGCTGCTGCGTGCCTGCCAGGACCTGG 250
|||||
84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
|||||
251 AGCCCTTGACCATCTCTACTATGTTGGAGGACCCCAAGTGGAGCAG 300
|||||
101 LeuSerAsnMetValValLysSerCysLysCysSer 112
|||||
301 CTCCTCAACATGGTGGTGAAGTCTGTAAATGTAGC 336
|||||
```

seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1997.DAT.AAT42773

seq_documentation_block:

ID AAT42773 standard; cDNA; 339 BP.

XX AC AAT42773;

XX DT 26-AUG-1997 (first entry)

XX DE TGF active fragment of a TGF-beta fusion protein encoding cDNA.

XX KW Transforming growth factor-beta fusion protein; wound healing;

XX KW artificial skin; surgery recovery time; ss.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT CDS 1..339

XX FT /*tag= a

XX FT /function= TGF active fragment

XX PN W09639430-A1.

XX PD 12-DEC-1996.

XX PF 05-JUN-1996; 96WO-US08973.

XX PR 06-JUN-1995; 95US-0470837.

XX PA (CHEU/) CHEUNG D T.

XX PA (HALL/) HALL F L.

XX PA (NIMN/) NIMNI M E.

XX PA (TUAN/) TUAN T.

XX PA (WULL/) WU L.

XX PI Cheung DT, Hall FL, Nimni ME, Tuan T, Wu L;

XX DR WPI; 1997-043065/04.

XX DR P-P5DB; AAW08175.

XX PT Prepn. of transforming growth factor-beta fusion protein - useful to

XX PT reduce surgery recovery time and to prepare artificial skin

XX PS Disclosure; Page 48; 59pp; English.

XX CC A novel transforming growth factor-beta (TGF-beta) fusion protein

XX CC comprises a purification tag and a TGF active fragment. The present

XX CC sequence encodes a specifically claimed TGF active fragment.

XX CC Additionally, the fusion protein may comprise proteinase-sensitive

XX CC linker sites and binding domain so the protein sequence may contain

XX CC some or all of the following elements: purification tag; proteinase

XX CC site; ECM binding site; proteinase site; TGF-beta. TGF-beta promotes

XX CC wound healing, and the fusion protein can be used to reduce surgery

CC recovery time and in the preparation of artificial skin. The inclusion

CC of a purification tag facilitates purification of the fusion protein.

CC The proteinase site is included to permit cleavage and release of the

CC purification tag after purification if desired. The extracellular

CC matrix binding site facilitates delivery of the fusion protein to the

CC desired site of action. Delivery of the TGF-beta to the site to be

CC treated reduces the amount of TGF-beta required to be administered to

CC be effective and reduces the concentration of circulating TGF-beta

CC which may result in undesirable effects.

XX

SQ Sequence 339 BP; 74 A; 104 C; 86 G; 75 T; 0 other;

alignment_scores:

Quality: 633.00 Length: 112

Ratio: 5.652 Gaps: 0

Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

TGFB3P x AAT42773 ..

Align seg 1/1 to: AAT42773 from: 1 to: 339

1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17

|||||

1 GCTTTGGACACCAATTACTGCTTCGCAACTTGGAGGAGAACTGCTGTGT 50

|||||

17 largProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34

|||||

51 GCGCCCTCTACATTGACTCCGACAGGATCTGGGCTGGAAGTGGGTCC 100

|||||

34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50

|||||

101 ATGAACCTAAGGGCTACTATGCCAACTTCTGCTCAGGCCCTTGCCCATAC 150

|||||

51 LeuArgSerAlaAspThrHisSerThrValLeuGlyLeuTyrAsnTh 67

|||||

151 CTCGCAGTCGACACACCAACCCAGCACGCGTGTGGGACTGTGTACAAACAC 200

|||||

67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84

|||||

201 TCTGAACCCCTGAAGCATCTGCGCTGCTGCGTGCCTGCCAGGACCTGG 250

|||||

84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100

|||||

251 AGCCCTGACCATCTCTACTATGTTGGAGGACCCCAAGTGGAGCAG 300

|||||

101 LeuSerAsnMetValValLysSerCysLysCysSer 112

|||||

301 CTCCTCAACATGGTGGTGAAGTCTGTAAATGTAGC 336

|||||

seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1999.DAT.AAX15247

seq_documentation_block:

ID AAX15247 standard; cDNA; 339 BP.

XX AC AAX15247;

XX XX 28-APR-1999 (first entry)

XX DT

XX DE cDNA encoding the mature form of transforming growth factor-beta-3.

XX KW Transforming growth factor-beta-3; TGF-beta-like protein;

XX KW S-sulphonated TGF-beta-like protein; wound treatment; cancer;

XX KW bone repair; tissue repair; bone marrow protective agent;

XX KW cardioprotection; anti-inflammatory; immunosuppressive;

XX KW ulcer; bed sore; ds.

XX OS Homo sapiens.

XX XX

XX PN EP891985-A1.

XX XX

XX XX 20-JAN-1999.

XX PD

```
XX PF 27-NOV-1990; 90EP-0810922.
XX PR 06-DEC-1989; 89GB-0027546.
XX XX (NOVS ) NOVARTIS AG.
XX XX Carletti N, Cox D, McMaster GK, Meyhack B, Schmitz A;
XX PI WPI; 1999-083520/08.
XX DR P-PSDB; AAW97093.
XX XX Producing biologically active dimeric Transforming Growth
XX PT Factor-beta - by refolding new monomeric Transforming Growth
XX PT Factor-beta, useful for treatment of wounds and cancer
XX PS Example 1; Page 30; 32pp; English.
XX CC The present sequence encodes the mature form of transforming growth
XX CC factor-beta-3. Dimeric, biologically active TGF-beta-like protein
XX CC can be produced by subjecting the denatured monomeric form to refolding
XX CC conditions. The new monomeric S-sulphonated TGF-beta-like protein is
XX CC useful for the production of the dimeric, biologically active
XX CC TGF-beta-like protein, which is useful for the treatment of wounds
XX CC (surface or internal) and cancer in a mammal, in bone and tissue
XX CC repair, as a bone marrow protective agent, a mediator of
XX CC cardioprotection, for the production of an anti-inflammatory or
XX CC immunosuppressive preparation. Treatment is useful for animals,
XX CC especially humans, and wound treatment (e.g. ulcers, bed sores etc.) is
XX CC particularly useful for the elderly.
XX SQ Sequence 339 BP; 74 A; 104 C; 86 G; 75 T; 0 other;

alignment_scores:
    Quality: 633.00    Length: 112
    Ratio: 5.652      Gaps: 0
    Percent Similarity: 100.000    Percent Identity: 100.000

alignment_block:
TGFB3P x AAX15247 ..

Align seg 1/1 to: AAX15247 from: 1 to: 339

1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
1 GCTTTGGACACCAACTACTGCTTCGCCCACTTGGAGGAACTGCTGTG 50
17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
51 GCGCCCTCTCTACATTGACTTCGACAGGATCTGGGCTGGAAGTGGGTCC 100
34 lGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
101 ATGAACCTTAAGGGCTACTATGCCAACTTCGTCTAGGCCCTTGCCCATAC 150
51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
151 CTCGCCAGTGCAGACACACACCCACAGCGGTCTGGGACTGTACAAACAC 200
67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
201 TCTGAACCTGAAGCATCTGCCTCGCTTGCCTGCGTGCCTCCAGGACCTGG 250
84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
251 AGCCCTCTGACCATCTGTACTATGTGGGAGGACCCCAAGTGGAGCAG 300
101 LeuSerAsnMetValValLysSerCysLysCysSer 112
301 CTCTCCACATGGTGGTGAAGTCTTGTAAATGTAGC 336

seq_name: /SIDSl/gcgdata/geneseq/geneseqn/NA1999.DAT:AAV99377
```

```
seq_documentation_block:
ID AAV99377 standard; cDNA; 339 BP.
XX AC AAV99377;
XX XX 25-MAR-1999 (first entry)
XX DE cDNA encoding a transforming growth factor beta active fragment.
XX KW Proteinase site; bone morphogenetic fusion protein; bone binding site;
XX KW bone morphogenetic protein; transforming growth factor beta;
XX KW active fragment; wound healing; bone growth; purification tag; ds.
XX OS Homo sapiens.
XX PN WO9855137-A1.
XX PD 10-DEC-1998.
XX PF 02-JUN-1998; 98WO-US11189.
XX PR 03-JUN-1997; 97US-0868452.
XX PA (HALL/) HALL F L.
XX PA (HANB/) HAN B.
XX PA (NIMN/) NIMNI M E.
XX PA (SHOR/) SHORS E C.
XX PA (WULL/) WU L.
XX PI Hall FL, Han B, Nimni ME, Shors EC, Wu L;
XX DR WPI; 1999-059875/05.
XX DR P-PSDB; AAW84209.
XX PT New bone morphogenetic fusion proteins - comprising a purification
XX PT tag and a bone morphogenetic active fragment, used for enhancing
XX PT wound healing or bone growth
XX PS Disclosure; Page 43; 64pp; English.
XX CC The present sequence encodes a transforming growth factor beta active
XX CC fragment. The protein can be used in place of a bone morphogenetic
XX CC active fragment to create the fusion proteins of the invention. When a
XX CC bone morphogenetic active fragment is used, the fusion proteins are
XX CC designated bone morphogenetic fusion proteins. The bone morphogenetic
XX CC fusion protein may contain some or all of the following elements: a
XX CC purification tag, a proteinase site, an ECM/bone binding site, a second
XX CC proteinase site, and a bone morphogenetic protein active fragment.
XX CC The bone morphogenetic fusion proteins can be used for enhancing wound
XX CC healing or bone growth.
XX SQ Sequence 339 BP; 74 A; 104 C; 86 G; 75 T; 0 other;

alignment_scores:
    Quality: 633.00    Length: 112
    Ratio: 5.652      Gaps: 0
    Percent Similarity: 100.000    Percent Identity: 100.000

alignment_block:
TGFB3P x AAV99377 ..

Align seg 1/1 to: AAV99377 from: 1 to: 339

1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluAsnCysCysVa 17
1 GCTTTGGACACCAACTACTGCTTCGCCCACTTGGAGGAACTGCTGTG 50
17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
51 GCGCCCTCTCTACATTGACTTCGACAGGATCTGGGCTGGAAGTGGGTCC 100
```

```

34  isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
|||||
101 ATGAACCACTAAGGGCTACTATGCCAACTTCTGCTCAGGCGCTTGCCCATAC 150
|||||
51  LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
|||||
151 CTCCGAGTCGACAGACACACCCAGCAGCGGTGCTGGGACTGTACAACAC 200
|||||
67  rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
|||||
201 TCTGAACCTGAAGCATCTGCTGCGCTTGTGCGTGCCCGAGGACCTGG 250
|||||
84  luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
|||||
251 AGCCCTGACCATCTCTACTATGTTGGGAGGACCCCAAGTGGAGCAG 300
|||||
101 LeuSerAsnMetValLysSerCysLysCysSer 112
|||||
301 CTCTCCCAACATGGTGGTGAAGTCTGTAAATGTAGC 336
|||||

```

seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1990.DAT:AAQ05774

seq_documentation_block:

ID_AAQ05774 standard; cDNA; 609 BP.

XX_AAQ05774;

DT_03-JAN-1991 (first entry)

XX Sequence encoding protein with tumour growth inhibitory activity.

DE Cancer; carcinoma; melanoma; leukaemia; arteriosclerosis; psoriasis;
KW TGF-alpha; ds;

XX Homo sapiens.

XX_EP384494-A.

PD_29-AUG-1990.

XX_20-OCT-1987; 87EP-0106772.

XX_01-JAN-1990; 90EP-0106772.

PR_20-OCT-1986; 86US-0922121.

XX (ONCO-) ONCOGENE SCI INC.

XX_Iwata KK, Stephenson JR, Gold LI;

DR_WPI; 1990-262507/35.

DR_P-PSDB; AAR06348.

XX Tissue-derived tumour growth inhibitors - used in diagnosis and
PT treatment of tumours and treatment of proliferative type
PT disorders, burns and wounds

XX_Disclosure; Fig 29; 81pp; English.

XX Gene product may be used to inhibit growth of tumour cells, to
CC treat proliferative type disorders, burns and other wounds, and may
CC also be used as an immune modulator. Detection of proteins and of
CC TGF-alpha can indicate presence of a tumour.

CC Proteins may be produced from a bacterial or eukaryotic expression
CC system.

XX Sequence 609 BP; 154 A; 172 C; 158 G; 125 T; 0 other;

alignment_scores:

Quality: 633.00 Length: 112

Ratio: 5.652 Gaps: 0

Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

TGFB3P x AAQ05774 ..

Align seg 1/1 to: AAQ05774 from: 1 to: 609

```

1  AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
|||||
271 GCTTTGGACACCAATTACTTCTCCCAACTTGGAGGAGAACTGCTGTGT 320
|||||
17  IArgProLeuTyrIleAspPheArgGlnAspLeuGlyTyrLysTrpValH 34
|||||
321 GGGCCCTCTCTACATGACTTCCGACAGGATCTGGGCTGGAAGTGGGTCC 370
|||||
34  isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
|||||
371 ATGAACCTAAGGGCTACTATGCCAACTTCTGCTCAGGCGCTTGCCCATAC 420
|||||
51  LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
|||||
421 CTCCGAGTCGACAGACACACCCAGCAGCGGTGCTGGGACTGTACAACAC 470
|||||
67  rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
|||||
471 TCTGAACCTGAAGCATCTGCTGCGCTTGTGCGTGCCCGAGGACCTGG 520
|||||
84  luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
|||||
521 AGCCCTGACCATCTCTACTATGTTGGGAGGACCCCAAGTGGAGCAG 570
|||||
101 LeuSerAsnMetValLysSerCysLysCysSer 112
|||||
571 CTCTCCCAACATGGTGGTGAAGTCTGTAAATGTAGC 606
|||||

```

seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1992.DAT:AAQ20576

seq_documentation_block:

ID_AAQ20576 standard; cDNA; 2529 BP.

XX_AAQ20576;

DT_05-MAY-1992 (first entry)

XX Transforming Growth Factor beta 3 coding sequence.

XX TGF-beta 3; homodimer; ss.

XX_Synthetic.

XX_WO9200318-A.

XX_09-JAN-1992.

XX_25-JUN-1991; 91WO-US04541.

XX_25-JUN-1990; 90US-0543348.

XX (ONCO-) ONCOGENE SCI INC.

XX_Iwata KK, Foulkes JG, Tendijke P, Haley JD;

DR_WPI; 1992-041510/05.

DR_P-PSDB; AAR20621.

XX Transforming growth factor beta 3 proteins, precursors and
PT mutants - obt'd. from polypeptide and antibodies, with optimal
PT therapeutic use due to genetic manipulation of coding sequence

XX Example 2; Fig 1; 107pp; English.

XX This 2529bp full-length TGF-beta3 gene sequence was obtained from
CC three shorter overlapping clones derived from human placental, human
CC umbilical cord and A673 cells cDNA libraries, respectively. The
CC predicted amino acid sequence of the gene encoding TGF-beta3 shows

CC	extensive homology to TGF-beta 1 and beta 2.
CC	See also AAQ22229 and AAR20622.
XX	
SQ	Sequence 2529 BP; 617 A; 670 C; 661 G; 581 T; 0 other;
alignment_scores:	
Quality: 633.00 Length: 112	
Ratio: 5.652 Gaps: 0	
Percent Similarity: 100.000 Percent Identity: 100.000	
 alignment_block:	
TGFβ3P x AAQ20576 ..	
 Align seg 1/1 to: AAQ20576 from: 1 to: 2529	
 1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluAsnCysCysVa 17	
1163	GCTTTGGACACCATTACTGCTTCGCCAACTTGGAGGAAGTGTCTGTGT 1212
17	l argProLeuTyrlleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
1213	GGCCCCCTCTACATTGACTTCCGACAGATCGGCTGGAGTGGGTCC 1262
34	isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
1263	ATGAACCTTAAGGCCTACTATGCAACTTCTGCTCAGGCCCTTGCCCATAC 1312
51	LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
1313	CPTCCGAGTGCAGACACAACCCACAGCAGGTGCTGGGACTGTACAACAC 1362
67	rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeu 84
1363	TCTGAACCTTGAGCATCTGCTCGCCCTTGCTGCTGCCCGCCAGGACCTGG 1412
84	luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
1413	AGCCCCCTGACCATCTGTACTATGTTGGAGAGACCCCAAGTGGAGCAG 1462
101	LeuSerAsnMetValValLysSerCysLysCysSer 112
1463	CFCTCCAACATGGTGGTGAAGTCTTGTAAATGTAGC 1498
 seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1998.DAT:AAV63209	
 seq_documentation_block:	
ID	AAV63209 standard; DNA: 2574 BP.
XX	
AC	AAV63209;
XX	
DT	14-JAN-1999 (first entry)
XX	
DE	Nucleic acid sequence of human transforming growth factor-beta 3.
XX	
KW	Human transforming growth factor-beta 3; TGF-beta3; oxygen tension;
KW	trophoblast invasion regulation; inhibitor; HIF-1 alpha;
KW	TGF-beta family cytokine receptor; hypoxia inducible factor 1 alpha;
KW	preeclampsia; pregnancy; choriocarcinoma; ss.
XX	
OS	Homo sapiens.
XX	
Key	Location/Qualifiers
FT	254..1492
FT	/tag= a
FT	/product= TGF-beta3
XX	
PN	WO9840747-A1.
PD	17-SEP-1998.
XX	
PF	05-MAR-1998; 98WO-CA00180.
XX	

PR 07-MAR-1997; 97US-0039919.
XX
PA (HOSP-) HOSPITAL FOR SICK CHILDREN.
PA (MOUN) MOUNT SINAI HOSPITAL CORP.
XX
Caniggia I, Lye S, Post M;
PI
XX
WPI; 1998-520837/44.
DR P-PSDB; AAW80417.
XX
Regulation of trophoblast invasion - by, e.g. transforming growth
factor-beta3 inhibitor, useful for detecting or treating
preeclampsia in pregnant women
PT
XX
Disclosure; Fig 1; 59pp; English.
XX
The present sequence encodes human transforming growth factor-beta 3
(TGF-beta3). The specification describes a composition for regulating
trophoblast invasion which comprises an inhibitor of TGF-beta3,
CC TGF-beta family cytokine receptors, hypoxia inducible factor 1 alpha
CC (HIF-1 alpha) or oxygen tension. The composition is used in methods of
diagnosing, monitoring, preventing or treating conditions requiring
CC regulation of trophoblast invasion, especially preeclampsia in pregnant
women or choriocarcinomas.
CC
SQ Sequence 2574 BP; 629 A; 680 C; 666 G; 599 T; 0 Other;

alignment_scores:
Quality: 633.00 Length: 112
Ratio: 5.652 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
TGFβ3P x AAV63209 ..

Align seg 1/1 to: AAV63209 from: 1 to: 2574

1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluAsnCysCysVa 17
|||||
1154 GCTTTGGACACCATTACTGCTTCGCCAACTTGGAGGAAGTGTCTGTGT 1203
|||||
17 l argProLeuTyrlleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
|||||
1204 GCGCCCCCTCTACATTGACTTCCGACAGGATCTGGGCTGGAGTGGGTCC 1253
|||||
34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
|||||
1254 ATGAACCTTAAGGCCTACTATGCCAATCTGCTCAGGCCCTTGCCCATAC 1303
|||||
51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
|||||
1304 CTCGCGAGTGCAGACACAACCCACAGCAGGTGCTGGGACTGTACAACAC 1353
|||||
67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
|||||
1354 TCTGAACCTTGAGCATCTGCTCGCCCTTGCTGCTGCCCGCCAGGACCTGG 1403
|||||
84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
|||||
1404 AGCCCCCTGACCATCTGTACTATGTTGGAGAGACCCCAAGTGGAGCAG 1453
|||||
101 LeuSerAsnMetValValLysSerCysLysCysSer 112
|||||
1454 CTCTCCAACATGGTGGTGAAGTCTTGTAAATGTAGC 1489
|||||
seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA2001.DAT:AAF55131

seq_documentation_block:
ID AAF55131 standard; DNA: 4382 BP.
XX
AC AAF55131;
XX

DT 29-MAY-2001 (first entry)
XX Nucleotide sequence of the vector puhld0-3-tgf.
DE
KW Stem cell; gene therapy; cell therapy; stem cell disorder; ss.
XX Synthetic.
OS
XX WO200114530-A2.
PN
XX 01-MAR-2001.
PD
XX 24-AUG-2000; 2000WO-EP08247.
PF
XX 24-AUG-1999; 99EP-0116533.
PR
XX (CHEN/) CHEN U.
PA
XX Chen U;
PI
XX WPI; 2001-218440/22.
DR
XX Growing stem cells useful as therapeutic, involves providing stem cells
PT with supporters which are genetically modified to provide externally
PT regulatable interactions, and applying an external signal -
XX
PS Disclosure; Fig 26; 92pp; English.
XX
XX The specification describes a method for growing stem cells. The method
CC involves providing stem cells with supporters which are genetically
CC modified in order to provide externally regulatable interactions between
CC the supporters and the stem cells, and applying an external signal for
CC starting or stopping the interactions. The cells are useful for curing
CC diseases by gene therapy and/or cell therapy in combination with tissue
CC engineering, when the functional expression of stem cells is helped
CC with engineered architecture of the tissue, which diseases are related
CC to insufficient and/or lack and/or disorders of stem cells. The present
CC sequence represents a vector, which is used in the method of the
CC invention.
XX
SQ Sequence 4382 BP; 1153 A; 1120 C; 1091 G; 1018 T; 0 other;

alignment_scores:
Quality: 633.00 Length: 112
Ratio: 5.652 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
TGFB3P x AAF55131 ..

Align seg 1/1 to: AAF55131 from: 1 to: 4382

1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
1358 GCCCTGGACACCAATTAATCTCCGCAACCTGGAGGAGAACTGCTGT 1407
17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpPlyTrpValH 34
1408 ACGCCCCCTTTATATTACTTCGCGCAGGATCTAGGCTGGAAATGGGTCC 1457
34 lSGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
1458 ACCAACTTAAAGGTGTTACTATGCGCAACTTCGCTCAGGCCCTTGCCTCATC 1507
51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
1508 CTCGGCAGCGCACACACACCCATAGCAGCGGTGCTTGGACTATACACAC 1557
67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
1558 CCTGAACCCAGAGCGCTCTGCTCGCATCTGCTGCTCCCGCCAGACCTGG 1607

84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
1608 AGCCCTTACCATCTGTACTATGTGGCAGAACCCCAAGGTGGAGCAG 1657
101 LeuSerAsnMetValLysSerCysLysCysSer 112
1658 CTGTCCACATGGTGTGAAGTCGTGTAAAGTCGAGC 1693
seq_name: /SIDS1/gcdata/geneseq/geneseq/NA1994.DAT:AAQ56926
seq_documentation_block:
ID_AAQ56926 standard; cDNA; 2157 BP.
XX
AC_AAQ56926;
XX
DT 09-JUL-1994 (first entry)
XX
XX Human TGF-beta-3.
DE
XX TGF-beta-1; TGF-beta-2; transforming growth factor beta-1;
KW transforming growth factor beta-3; recombinant; wound healing;
KW vulnerary; ss.
XX
XX Homo sapiens.
OS
XX US284763-A.
PN
XX 08-FEB-1994.
PD
XX 22-MAR-1985; 85US-0715142.
PF
XX 22-MAR-1985; 85US-0715142.
PR 13-MAR-1987; 87US-0025423.
PR 04-AUG-1989; 89US-0389929.
PR 04-MAR-1992; 92US-0845893.
XX
XX (GETH) GENENTECH INC.
PA
XX Derynk RMA, Goeddel DV;
XX
XX WPI; 1994-056343/07.
DR P-PSDB; AAR46229.
XX
XX Nucleic acid sequences encoding transforming growth factor-beta -
PT diagnostic probes, and for use in therapeutics
PT
XX Disclosure; Fig 4a-c; 25pp; English.
PS
XX cDNA sequences were determined for human pre-TGF-beta-1 (AAQ56923),
CC pig TGF-beta-3 (AAQ56925) and human TGF-beta-3 (AAQ56926), and the
CC corresponding amino acid sequences were determined (AAR46227-29,
CC respectively). A genomic fragment corresponding to a human TGF-
CC beta-1 exon (AAQ56924) was also isolated and its amino acid sequence
CC determined (AAR46230). The sequences have been used in the
CC construction of vectors for the expression of recombinant TGF-
CC beta.
XX
SQ Sequence 2157 BP; 621 A; 462 C; 492 G; 582 T; 0 other;

alignment_scores:
Quality: 630.00 Length: 112
Ratio: 5.625 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 99.107

alignment_block:
TGFB3P x AAQ56926 ..

Align seg 1/1 to: AAQ56926 from: 1 to: 2157

1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
278 GCTTGGACACCAATTACTGCTTCGCAACTTGGAGGAGAACTGCTGT 327

```
17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
328 GGGCCCCCTCTACATTGACTTCGACAGGATCGGGCTGGAAGTGGGTCC 377
34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
378 ATGAACCTAAGGCTACTATGCCAACTTCTGTCAGGCCCTTGCCCATAC 427
51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
428 CTCGCGAGTGCAGACACAACCCACAGCACGGTCTGGGACTGTACAACAC 477
67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
478 TCTGAACCCCTGAAGCATCTGCCTCGCTTGTGCATGCCGCCAGGACCTGG 527
84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
528 AGCCCCCTGACCAATCTCTACTATGTTGGGAGGACCCCCCAAGTGGAGCAG 577
101 LeuSerAsnMetValValLysSerCysLysCysSer 112
578 CTCTCCAACATGGTGTGAAGTCTTGTAAATGTAGC 613
seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1998.DAT:AAV52935
seq_documentation_block:
ID AAV52935 standard; cDNA; 2157 BP.
XX AC AAV52935;
XX DT 21-DEC-1998 (first entry)
XX DE Human transforming growth factor-beta 3 cDNA.
XX KW Transforming growth factor-beta 3; TGF-beta 3; human; ss.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX CDS 2..616
FT /*tag= a
FT /transl_except= (pos:50..52, aa:Thr)
XX US5801231-A.
XX PD 01-SEP-1998.
XX PF 22-MAR-1985; 85US-0715142.
XX PR 13-MAR-1987; 87US-0025423.
XX PR 22-MAR-1985; 85US-0715142.
XX PR 04-AUG-1989; 89US-0389929.
XX PR 04-MAR-1992; 92US-0845893.
XX PR 05-NOV-1993; 93US-0147364.
XX PR 30-MAY-1995; 95US-0454468.
XX PA (GETH ) GENENTECH INC.
XX PI Derynck RMA, Goeddel DV;
XX DR WPI: 1998-494840/42.
XX DR P-PSDB; AAW78787.
XX PT DNA encoding transforming growth factor-beta precursor sequence -
XX useful for analysis to perform manipulations to increase yield of
XX recombinant production of the protein
XX PS Example 6; Fig 4a-c; 26pp; English.
XX CC This nucleotide sequence, hu4, codes for a human partial
XX transforming growth factor-beta 3 (TGF-beta 3) sequence including
```

```
CC all of the mature sequence. Clone hu4 was isolated from a human
CC ovarian cDNA library using porcine TGF-beta 3 cDNA (see AAV52934)
CC as probe. The inventory relates to the recombinant production of
CC TGF-beta. Biologically active TGF-beta is defined as being capable
CC of inducing EGF-potentiated anchorage independent growth of target
CC cell lines and/or growth inhibition of neoplastic cell lines.
CC Nucleic acids encoding TGF-beta have been isolated and cloned into
CC vectors which are replicated in bacteria and expressed in
CC eukaryotic cells. TGF-beta recovered from transfected cells is
CC used in known therapeutic applications. TGF-beta nucleic acids are
CC also useful in diagnosis and identification of TGF-beta clones.
XX SQ Sequence 2157 BP; 621 A; 462 C; 492 G; 582 T; 0 other;
```

```
alignment_scores:
Quality: 630.00 Length: 112
Ratio: 5.625 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 99.107
alignment_block:
TGFb3P x AAV52935
Align seg 1/1 to: AAV52935 from: 1 to: 2157
1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGlnAsnCysCysVa 17
278 GCTTTGGACACCAATTACTGCTTCGCAACTTGGAGGAGAACTGCTGTGT 327
17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
328 GCGCCCCCTCTACATTGACTTCGACAGGATCTGGGCTGGAAGTGGGTCC 377
34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
378 ATGAACCTAAGGCTACTATGCCAACTTCTGCTCAGGCCCTTGCCCATAC 427
51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
428 CTCGCGAGTGCAGACACACACCCACAGCACGGTCTGGGACTGTACAACAC 477
67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
478 TCTGAACCCCTGAAGCATCTGCCTCGCTTGTGCATGCCGCCAGGACCTGG 527
84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
528 AGCCCCCTGACCAATCTCTACTATGTTGGGAGGACCCCCCAAGTGGAGCAG 577
101 LeuSerAsnMetValValLysSerCysLysCysSer 112
578 CTCTCCAACATGGTGTGAAGTCTTGTAAATGTAGC 613
```

```
seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1990.DAT:AAQ02820
seq_documentation_block:
ID AAQ02820 standard; DNA; 2158 BP.
XX AC AAQ02820;
XX DT 31-MAY-1989 (first entry)
XX DE cDNA sequence encoding human TGF-beta 3.
XX KW Transforming growth factor beta-3 (TGF beta 3); tumour cells; growth
XX inhibition.
XX PN W08912101-A.
XX PD 14-DEC-1989.
XX PF 08-JUN-1988; 88WO-US01945.
XX
```

PR 08-JUN-1988; 88WO-U001945.

XX (GETH) GENENTECH INC.

XX Dernityck RM, Goeddel DV;

XX WPI; 1990-007474/01.

XX Nucleotide sequence encoding transforming growth factor beta-3 -used as a probe; or to produce TGF beta 3, for inhibition of growth of normal and neoplastic cells, eg A549.

XX Disclosure; Fig. 4; 6lpp; English.

XX This sequence encodes human transforming growth factor-beta 3 (TGF-beta 3) polypeptide. The nucleic acid sequence encoding this subtype is useful as a probe or to produce TGF-beta 3 for both normal and neoplastic cell growth inhibition.

XX Sequence 2158 BP; 621 A; 462 C; 493 G; 582 T; 0 other;

alignment_scores:

Quality: 530.00 Length: 112
Ratio: 5.625 Gaps: 0

Percent Similarity: 100.000 Percent Identity: 99.107

alignment_block:

TGFB3P x AAQ02820 ..

Align seg 1/1 to: AAQ02820 from: 1 to: 2158

1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
|||||

278 GCTTGGACACCAATTAAGTCTCCGCAACTTGGAGGAGAACTGCTGTGT 327

17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
|||||

328 GCGCCCTCTACATTGACTTCCGACAGGATCTGGGCTGGAGTGGGTCC 377

34 iGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
|||||

378 ATGAACCTAAGGCTACTATGCCAATCTCTGCTCAGGCCCTTGCCCATAC 427

51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
|||||

428 CTCGCGAGTCAGACACCAACCCAGCAGCGTGTGGACTGTACACAC 477

67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
|||||

478 TCTGAACCTGAAGCATCTGCTGCGCTTCTGCTGATGCCCGCCAGACCTGG 527

84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
|||||

528 AGCCCTTGACCATCTCTACTATGTTGGAGGAGCCCGCCAAAGTGGAGCAG 577

101 LeuSerAsnMetValValLysSerCysLysCysSer 112
|||||

578 CTCTCCAACTGGTGGTGAAGTCTTGTAATGTAGC 613

seq_name: /SIDS1/gcgdata/geneseq/geneseq/NA1992.DAT:AAQ22229

seq_documentation_block:

ID AAQ22229 standard; cDNA; 1239 BP.

XX AC

XX AAQ22229;

DT 05-MAY-1992 (first entry)

XX Mutant transforming growth Factor beta 3 coding sequence.

XX TGF-beta 3; homodimer; ss.

XX

Synthetic.

XX

Key Location/Qualifiers

FT misc_feature 1..888

FT /tag= a

FT /note= "nucleotides 263-1150 of TGF-beta3"

FT misc_feature 889..903

FT /tag= b

FT /note= "encodes Factor Xa cleavage site followed by a methionine residue"

FT misc_feature 904..1212

FT /tag= c

FT /note= "nucleotides 1163-1471 of TGF-beta3"

FT misc_difference 1213..1215

FT /tag= d

FT /note= "wild-type codon = ATG. May be replaced by any other codon to give mutant sequence"

FT misc_feature 1216..1239

FT /tag= e

FT /note= "nucleotides 1475-1498 of TGF-beta3"

XX

PN WO9200318-A.

XX

PD 09-JAN-1992.

XX

PF 25-JUN-1991; 91WO-US04541.

XX

PR 25-JUN-1990; 90US-0543348.

XX

PA (ONCO-) ONCOGENE SCI INC.

XX

PI Iwata KK, Foulkes JG, Tendijke P, Haley JD;

XX

DR WPI; 1992-041510/05.

XX

DR P-PSDB; AAR22038.

XX

PT Transforming growth factor beta 3 proteins, precursors and mutants - obt'd. from polypeptide and antibodies, with optimal therapeutic use due to genetic manipulation of coding sequence

XX

PS Claim 12; Page 66; 107pp; English.

XX

CC This sequence has been compiled from the description of a mutant TGF-beta3 contained in the claims. The sequence coding for the Factor Xa cleavage site may be replaced by one encoding a similar protease recognition site, e.g. for collagenase. The coding sequence may also include a region encoding a hydrophobic transmembrane amino acid sequence, e.g. from c-erbB2 cDNA and a "stop transfer"

CC sequence. The protease recognition site is located between the C-terminal of the transmembrane region and the N-terminal of the TGF-beta 3 precursor. Mature TGF-beta 3 can then be efficiently cleaved from the membrane. See also AAQ20576 and AAR20622.

XX

SQ Sequence 1239 BP; 308 A; 348 C; 328 G; 248 T; 7 other;

alignment_scores:

Quality: 627.00 Length: 112
Ratio: 5.649 Gaps: 0

Percent Similarity: 99.107 Percent Identity: 99.107

alignment_block:

TGFB3P x AAQ22229 ..

Align seg 1/1 to: AAQ22229 from: 1 to: 1239

1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
|||||

904 GCTTTGGACCAATTAAGTCTCCGCAACTTGGAGGAGAACTGCTGTGT 953

17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
|||||

954 GCGCCCTCTACATTGACTTCCGACAGGATCTGGGCTGGAGTGGGTCC 1003

```
34  isGluProLysGlyTyrThrValAlaAsnPheCysSerGlyProCysProTyr 50
|||||
1004 ATGACCTAAGGCTACTATGCCAATCTTGCTCAGGCCCTTGCCCATAC 1053
|||||
51  LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
|||||
1054 CTCGCGAGTGCAGACACACACACAGCAGCGGTGCTGGGACTGTACAAAC 1103
|||||
67  rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
|||||
1104 TCTGAACCTGAAGCATCTGCTCGCTTGCTGCGTGCCCGCCAGGACCTG 1153
|||||
84  luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
|||||
1154 AGCCCTGTACCATCTGTACTATGTTGGGAGGACCCCAAGTGGAGCAG 1203
|||||
101  LeuSerAsnMetValValLysSerCysLysCysSer 112
|||||
1204 CTCCTCAACNNGTGGTGAAGTCTTGTAAATGTAGC 1239
|||||
```

seq_name: /SIDSL/gcgdata/geneseq/geneseqn/NA1998.DAT:AAV52934

seq_documentation_block:

ID AAV52934 standard; cDNA; 2639 BP.

XX AC AAV52934;

XX 21-DEC-1998 (first entry)

XX Pig transforming growth factor-beta 3 cDNA.

XX Transforming growth factor-beta 3; TGF-beta 3; pig; ss.

XX Sus scrofa.

XX Key Location/Qualifiers

XX CDS 127..1497

XX /*Tag= a

XX /transl_except= (pos:481..483, aa:Met)

XX US5801231-A.

XX 01-SEP-1998.

XX 22-MAR-1985; 85US-0715142.

XX 13-MAR-1987; 87US-0025423.

XX 22-MAR-1985; 85US-0715142.

XX 04-AUG-1989; 89US-0389929.

XX 04-MAR-1992; 92US-0845893.

XX 05-NOV-1993; 93US-0147364.

XX 30-MAY-1995; 95US-0454468.

XX (GETH) GENENTECH INC.

XX Derynck RNA, Goeddel DV;

XX WPI; 1998-494840/42.

XX P-PSDB; AAW78786.

XX DNA encoding transforming growth factor-beta precursor sequence -
PT useful for analysis to perform manipulations to increase yield of
PT recombinant production of the protein

XX Example 6; Fig 4a-c; 26pp; English.

XX This nucleotide sequence, termed 10+11.3, codes for the porcine
CC transforming growth factor-beta 3 precursor (prefGF-beta 3, see
CC AAW78786). A porcine ovarian cDNA library was screened using human
CC TGF-beta 1 cDNA (see AAV52933) as probe. A hybridising clone,
CC designated lambda 11.3, was used to rescreen the library to
CC identify clone lambda 10. The was combined with clone lambda 11.3

CC to provide the 10+11.3 sequence. The invention relates to the
CC recombinant production of TGF-beta. Biologically active TGF-beta
CC is defined as being capable of inducing EGF-potentiated anchorage
CC independent growth of target cell lines and/or growth inhibition of
CC neoplastic cell lines. Nucleic acids encoding TGF-beta have been
CC isolated and cloned into vectors which are replicated in bacteria
CC and expressed in eukaryotic cells. TGF-beta recovered from
CC transformed cells is used in known therapeutic applications.
CC TGF-beta nucleic acids are also useful in diagnosis and
CC identification of TGF-beta clones.

XX
SQ Sequence 2639 BP; 677 A; 702 C; 697 G; 563 T; 0 other;

alignment_scores:

Quality: 621.00 Length: 112

Ratio: 5.595 Gaps: 0

Percent Similarity: 99.107 Percent Identity: 98.214

alignment_block:

TGFB3P x AAV52934 ..

Align seg 1/1 to: AAV52934 from: 1 to: 2639

```
1  AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGlnAsnCysCysVa 17
|||||
1159 GCCCTGGACACCAACTACTGCTTCGCCAATTGGAGGAGAACTGCTGTGT 1208
|||||
17  lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
|||||
1209 GCGCCCTCTCTACATTGACTTCGCACAGGATCTGGGCTGGAAAGTGGGTCC 1258
|||||
34  isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
|||||
1259 ATGAACCTAAGGGCTACTATGCCAATCTTGCTCAGGGCCCTTGCCCGTAC 1308
|||||
51  LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
|||||
1309 CTCGCGAGTGCAGACACACACACAGCTCGGTGCTGGGGCTGTACACAC 1358
|||||
67  rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
|||||
1359 CCTGAACCCCGAAGCCTCGGCCCTCTCGTGTGCTGCCCGCCAGGACCTGG 1408
|||||
84  luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
|||||
1409 AGCCCTGTACCATCTGTACTACGTCGGGAGGACCCCAAGTGGAGCAG 1458
|||||
101  LeuSerAsnMetValValLysSerCysLysCysSer 112
|||||
1459 CTCCTCAACATGTTGGTGAAGTCTTGTAAATGTAGC 1494
|||||
```

seq_name: /SIDSL/gcgdata/geneseq/geneseqn/NA1994.DAT:AAQ56925

seq_documentation_block:

ID AAQ56925 standard; cDNA; 2669 BP.

XX AC AAQ56925;

XX 09-JUL-1994 (first entry)

XX Pig TGF-beta-3.

XX TGF-beta-1; TGF-beta-2; transforming growth factor beta-1;

XX transforming growth factor beta-3; recombinant; wound healing;

XX vulnerable; ss.

XX Sus scrofa.

XX US284763-A.

XX 08-FEB-1994.

XX

XX

XX

```

PF 22-MAR-1985; 85US-0715142.
XX
XX 22-MAR-1985; 85US-0715142.
PR 13-MAR-1987; 87US-0025423.
PR 04-AUG-1989; 89US-0389929.
XX 04-MAR-1992; 92US-0845893.
XX
PA (GETH ) GENENTECH INC.
XX
XX Derynk RMA, Goeddel DV;
PI
XX WPI; 1994-056343/07.
DR P-PSDB; AAR46228.
XX
XX Nucleic acid sequences encoding transforming growth factor-beta -
PT diagnostic probes, and for use in therapeutics
PT
XX
XX Disclosure; Fig 4a-c; 25pp; English.
XX
XX cDNA sequences were determined for human pre-TGF-beta-1 (AAQ56923),
CC pig TGF-beta-3 (AAQ56925) and human TGF-beta-3 (AAQ56926), and the
CC corresponding amino acid sequences were determined (AAR46227-29,
CC respectively). A genomic fragment corresponding to a human TGF-
CC beta-1 exon (AAQ56924) was also isolated and its amino acid sequence
CC determined (AAR46230). The sequences have been used in the
CC construction of vectors for the expression of recombinant TGF-
CC beta.
XX
XX Sequence 2669 BP; 706 A; 702 C; 697 G; 564 T; 0 other;
SQ

alignment_scores:
Quality: 621.00 Length: 112
Ratio: 5.595 Gaps: 0
Percent Similarity: 99.107 Percent Identity: 98.214

alignment_block:
TGFB3P x AAQ56925 ..
Align seg 1/1 to: AAQ56925 from: 1 to: 2669

1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluAsnCysCysVa 17
|||||
1159 GCGCTGGACACCACTACTGCTCCGCAATTTGGAGGAGAACTGCTGTGT 1208
|||||
17 lArqProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
|||||
1209 GCGCCCTCTCTACATTGACTTCCGACAGGATCTGGGCTGGAAGTGGGTCC 1258
|||||
34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
|||||
1259 ATGAACCTAAGGGCTACTATGCCAATTTCTGCTAGGCCCTTGCCCGTAC 1308
|||||
51 LeuArgSerAlaAspThrHisSerThrValLeuGlyLeuTyrAsnTh 67
|||||
1309 CTCGCGAGTGCAGACACACCCAGCTCGGTGCTGGGGCTGTACAACAC 1358
|||||
67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
|||||
1359 CCTGAACCCGGAAGCCCTCGGCTCTCCGTCGCTGCGTCCCGAGGACCTGG 1408
|||||
84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
|||||
1409 AGCCCTTGACCATCTCTACTAGCTCGGGAGGACCCCAAGGTGGAGCAG 1458
|||||
101 LeuSerAsnMetValValLysSerCysLysCysSer 112
|||||
1459 CTCTTAACATGGTGGTGAAGTCTCTGCAAGTGCAGC 1494
|||||
seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1990.DAT:AAQ03303
seq_documentation_block:
ID AAQ03303 standard; DNA; 2671 BP.

```

```

XX AAQ03303;
XX
XX 05-AUG-1990 (first entry)
XX
XX Entire porcine transforming growth factor (TGF) beta-3 cDNA sequence.
XX
XX Porcine transforming growth factor (TGF) beta-3; human ovarian cDNA;
XX human transforming growth factor (TGF) beta-3.
XX
XX Porcine.
XX
XX US4886747-A.
XX
XX 12-DEC-1989.
XX
XX 13-MAR-1987; 87US-0025423.
XX
XX 13-MAR-1987; 87US-0025423, US-715142.
XX
XX (GETH ) GENENTECH INC.
XX
XX Derynck RMA, Goeddel DV;
XX
XX WPI; 1990-051338/07.
XX
XX Nucleic acid encoding transforming growth factor-beta -
XX cloned into expression vectors for expression in eukaryotic host
XX cells for therapeutic use
XX
XX Disclosure; Fig 4a-c; 28pp; English.
XX
XX It was used to screen plaques from a human ovarian cDNA library to find
XX human TGF-beta-3.
XX
XX Sequence 2671 BP; 706 A; 705 C; 699 G; 561 T; 0 other;
SQ

alignment_scores:
Quality: 621.00 Length: 112
Ratio: 5.595 Gaps: 0
Percent Similarity: 99.107 Percent Identity: 98.214

alignment_block:
TGFB3P x AAQ03303 ..
Align seg 1/1 to: AAQ03303 from: 1 to: 2671

1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluAsnCysCysVa 17
|||||
1159 GCGCTGGACACCACTACTGCTCCGCAATTTGGAGGAGAACTGCTGTGT 1208
|||||
17 lArqProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
|||||
1209 GCGCCCTCTCTACATTGACTTCCGACAGGATCTGGGCTGGAAGTGGGTCC 1258
|||||
34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
|||||
1259 ATGAACCTAAGGGCTACTATGCCAATTTCTGCTAGGCCCTTGCCCGTAC 1308
|||||
51 LeuArgSerAlaAspThrHisSerThrValLeuGlyLeuTyrAsnTh 67
|||||
1309 CTCGCGAGTGCAGACACACCCAGCTCGGTGCTGGGGCTGTACAACAC 1358
|||||
67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
|||||
1359 CCTGAACCCGGAAGCCCTCGGCTCTCCGTCGCTGCGTCCCGAGGACCTGG 1408
|||||
84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
|||||
1409 AGCCCTTGACCATCTCTACTAGCTCGGGAGGACCCCAAGGTGGAGCAG 1458
|||||
101 LeuSerAsnMetValValLysSerCysLysCysSer 112

```

1459 CTCTCAACATGGTGTGAAGTCTGCAAGTGCAGC 1494

seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1996.DAT: AAT06496

seq_documentation_block:

ID AAT06496 standard; cDNA; 498 BP.

XX AC AAT06496;

XX DT 12-JUN-1996 (first entry)

XX DE Tissue-derived tumour growth inhibitor-1 coding sequence.

XX KW Tumour growth inhibitor; carcinoma; melanoma; leukaemia;
arteriosclerosis; inflammation; psoriasis; therapy; vulnery;

XX KW immunomodulator; ss.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers
FT CDS 1..498

FT FT /*tag= a

FT FT /product= tumour_growth_inhibitor_precursor

FT FT /note= "see AAR86771"

FT FT misc_feature 159..160

FT FT /*tag= b

FT FT /note= "the codons at positions -40 to -1 (i.e. 117
nucleotides) are not given in the
specification"

FT FT mat_peptide 160..495

FT FT /*tag= c

FT FT /product= mature_tumour_growth_inhibitor

FT FT /note= "see AAR86770"

FT FT EP684260-A2.

XX PD 29-NOV-1995.

XX XX 20-OCT-1987; 87EP-0109866.

XX PF 20-OCT-1986; 86US-0922121.

XX PR (ONCO-) ONCOGENE SCI INC.

XX PA Gold LI, Iwata KK, Stephenson JR;

XX PI WPI; 1996-000991/01.

XX DR P-PSDB; AAR86770, AAR86771.

XX XX Tissue-derived growth inhibitor and corresponding genes - useful for
PT detection of tumours, inhibition of tumour growth, treatment of
PT proliferative disorders and healing of burns and wounds.

XX XX Claim 6; Fig 29; 83pp; English.

XX XX The sequence encodes a 112 amino acid tumor growth inhibitor (TGI)
CC (AAR86770) or a 205 precursor TGI (AAR86771) comprising TGI with an
CC additional 93 amino acid residues at the N-terminus. However, the
CC nucleotides representing codons -40 to -1 of the precursor TGI are
CC not specified in Figure 29, i.e. the cDNA is 498 nucleotides in
CC length, but should be 615 nucleotides long. The DNA is used to
CC produce the inhibitors by recombinant methods i.e. vector
CC expression in bacterium or eukaryotic host cells. The proteins can
CC be used to inhibit the growth of human tumour cells, e.g.
CC carcinoma, melanoma or leukaemia cells, in the treatment of
CC proliferative disorders e.g. arteriosclerosis, inflammation and
CC psoriasis, or for the treatment of burns to facilitate wound
CC healing. They can also be used as immunomodulators. Although the
CC proteins have tumour growth inhibitory activity, they are not
CC transforming growth factor-beta-1 or -beta-2.

XX XX Sequence 498 BP; 122 A; 136 C; 129 G; 111 T; 0 other;

alignment_scores:
Quality: 620.00 Length: 112
Ratio: 5.586 Gaps: 0
Percent Similarity: 99.107 Percent Identity: 98.214
alignment_block:
TGFB3P x AAT06496 ..
Align seg 1/1 to: AAT06496 from: 1 to: 498
1 AlAlaLeuAspThrAsnTyrCysPheArgAsnLeuGluAsnCysCysVa 17
160 GCTTTGGACCACTTACTGCTTCCGCAACTTGGAGGAGAACTGTTGT 209
17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
210 GCGCCCCCTCTACATTGACTTCCGACAGGATCTGGGCTGGAAGTGGTCC 259
34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
260 ATCAACCTAAGGGCTACTATGCCAACTTCTGCTCAGCCCTTGCCCATAC 309
51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
310 CTCGGCAGTGCAGACACACACCCAGCACGCGTCTGGGACTGTACAACAC 359
67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
360 TCTGAACCCCTGAAGCATCTGCCTGGCCTTCTGCGTCCCGCCAGACCTGG 409
84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
410 AGCCCTGACCATCTCTACTATGTTGGGAGGACCCCAAGTGGAGCAG 459
101 LeuSerAsnMetValValLysSerCysLysCysSer 112
460 CTCTCCAACATGGTGTGAAGTCTTGTAAATGTAGC 495
seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1990.DAT: AAO06845
seq_documentation_block:
ID AAO06845 standard; cDNA; 2530 BP.
XX AC AAO06845;
XX DT 05-MAR-1991 (first entry)
XX DE Sequence encoding tumour growth inhibitor.
XX KW TGI; carcinoma; melanoma; leukaemia; arteriosclerosis; inflammation;
XX KW psoriasis; ss.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
FT CDS 263..1501
FT FT /*tag= a
FT FT polyA_signal 2506..2511
FT FT /*tag= b
FT FT polyA_site 2529
FT FT /*tag= c
XX XX WO9014360-A.
XX PN 29-NOV-1990.
XX PD 17-MAY-1990; 90WO-US02753.
XX PF 17-MAY-1989; 89US-0353410.
XX PR 19-APR-1985; 85US-0725003.
XX PR 07-APR-1986; 86US-0847931.

PR 20-OCT-1986; 86US-0992121.
PR 20-OCT-1987; 87US-0111022.
PR 20-APR-1988; 88US-0183224.
XX (ONCO-) ONCOGENE SCI INC.
XX Iwata KK, Stephenson JR, Tendijke P, Franco R, Gold LI, Foulkes JG;
XX PI
XX
XX WPI; 1990-375949/50.
DR P-PSDB; AAR08264.
XX
XX Tissue-derived tumour growth inhibitors - comprise specified
PT protein sequences used to detect, and treat tumours, burns and
PT wounds.
XX
XX Claim 10; Fig 41; 190pp; English.
XX
XX The plasmid was isolated from a human cDNA library prepd. from the
CC DNA of a chronic myelocytic leukaemia cell line (K562). The
CC sequence can be used to produce the tumour growth inhibitor (TGI)
CC by recombinant techniques. The protein may also be isolated from
CC human umbilical cord and placental tissues. It can be used to
CC inhibit tumour cell growth, to treat burns, to facilitate the
CC healing of wounds or to treat proliferative disorders. The
CC protein and Abs raised to it can be used for detection and typing
CC of tumours. The Abs can also be used to inhibit the activity of
CC the TGI.
XX
XX Sequence 2530 BP; 619 A; 671 C; 659 G; 581 T; 0 other;

alignment_scores:
Quality: 617.00 Length: 112
Ratio: 5.559 Gaps: 0
Percent Similarity: 99.107 Percent Identity: 97.321

alignment_block:
TGFB3P x AAQ06845 ..

Align seg 1/1 to: AAQ06845 from: 1 to: 2530

1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluAsnCysCysVa 17
1163 GCTTTGGACACCAATTTACTGCTTCGCCAACTTGGAGGAGAACTGCTGTGT 1212
17 largProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValh 34
1213 GCGCCCCCTCTACATTGACTTCGACAGGATCTGGCTGGAAGTGGGTCC 1262
34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
1263 ATGAACCTAAGGGCTACTATGCGCAACTTCTGCTCAGGCCCTTGCCCCATAC 1312
51 LeuArgSerAlaAspThrHisSerThrValLeuGlyLeuTyrAsnTh 67
1313 CTCGCGAGTGCAGACACACACCCACAGCAGCGTCTGGGACTGTACACAC 1362
67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
1363 TCTGAACCTGAAGCATCTGCTTCGCTTGTCTGCTGCGTCCCGCCAGACCTGG 1412
84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
1413 AGCCCCGTGACCATCTCTGTAATGTTGGGAGGACCCCAAGAGTGGAGCAAG 1462
101 LeuSerAsnMetValValLysSerCysLysCysSer 112
1463 CTCCTCAACATGGTGTGAAGTCTTGTAAATGTAGC 1498

seq_name: /SIDS1/gcgdata/geneseq/geneseq/NA1990.DAT:AAQ02819

seq_documentation_block:

ID AAQ02819 standard; DNA; 2676 BP.

XX AAQ02819;
AC
XX
XX 31-MAY-1989 (first entry)
XX
XX cDNA sequence encoding porcine TGF-beta 3.
XX
XX Transforming growth factor beta-3 (TGF beta 3); tumour cells; growth
KW inhibition.
KW
XX
XX WO8912101-A.
XX
XX 14-DEC-1989.
XX
XX 08-JUN-1988; 88WO-US01945.
XX
XX 08-JUN-1988; 88WO-UO01945.
XX
XX (GETH) GENENTECH INC.
XX
XX Dernyck RM, Goeddel DV;
XX
XX WPI; 1990-007474/01.
XX
XX P-PSDB; AAR04080.
XX
XX Nucleotide sequence encoding transforming growth factor beta-3 -used as a
PT probe, or to produce TGF beta 3, for inhibition of growth of normal
PT and neoplastic cells, eg A549.
XX
XX PS Disclosure; Fig. 4; 61pp; English.
XX
XX This sequence encodes porcine transforming growth factor-beta 3 (TGF-
CC beta 3) polypeptide. The nucleic acid sequence encoding this subtype is
CC useful as a probe or to produce TGF-beta 3 for both normal and neoplastic
CC cell growth inhibition.
XX
XX Sequence 2676 BP; 704 A; 705 C; 699 G; 568 T; 0 other;

alignment_scores:
Quality: 612.00 Length: 112
Ratio: 5.564 Gaps: 0
Percent Similarity: 98.214 Percent Identity: 97.321
alignment_block:
TGFB3P x AAQ02819 ..
Align seg 1/1 to: AAQ02819 from: 1 to: 2676

1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluAsnCysCysVa 17
1175 GCCCTGGACACCACTACTCTCCGCAATTTGGAGGAGAACTGCTGTGT 1224
17 largProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValh 34
1225 GCGCCCCCTCTACATTGACTTCGACAGGATCTGGCTGGAAGTGGGTCC 1274
34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
1275 ATGAACCTAAGGGCTACTATGCGCAACTTCTGCTCAGGCCCTTGCCCCATAC 1324
51 LeuArgSerAlaAspThrHisSerThrValLeuGlyLeuTyrAsnTh 67
1325 CTCGCGAGTGCAGACACACACCCACAGCAGCGTCTGGGACTGTACAAAC 1374
67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
1375 TCTGAACCTGAAGCATCTGCTTCGCTTGTCTGATGCCCGCCAGGACCTGG 1424
84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
1425 AGCCCCGTGACCATCTCTGTAATGTTGGGAGGACCCCAAGTGGAGCAG 1474

101 LeuSerAsnMetValValLysSerCysLysCysSer 112
 |||||
 1475 CTTCTAATGCTGGTGAAGTCTCGCAAGTGCAGC 1510

seq_name: /SIDSL/gcgdata/geneseq/geneseq/NA1993.DAT:AAQ41603

seq_documentation_block:

ID AAQ41603 standard; cDNA; 336 BP.

XX
 AC
 XX
 XX
 XX

26-AUG-1993 (first entry)

DE Transforming Growth Factor-beta1(44/45)beta3 hybrid.

XX hTGF-beta1; hTGF-beta3; hybrid protein; wound healing;
 KW cancer treatment; bone repair; growth regulation; ss.
 XX
 OS Homo sapiens.

XX Key Location/Qualifiers

FT mat_peptide 1..336

FT /*tag= a

FT /note= "TGF-beta1=1-132, TGF-beta3=133-336"

XX EP542679-A.

XX 19-MAY-1993.

XX 03-NOV-1992; 92EP-0810845.

XX 11-NOV-1991; 91EP-0810870.

XX (CIBA) CIBA GEIGY AG.

XX McMaster GK, Cox D, Cerletti N, Kuhla J;

XX WPI; 1993-161126/20.

DR P-PSDB; AAR39642.

XX New hybrid transforming growth factor-beta molecules - comprise

PT portions of mature TGF-beta isoforms; useful as wound healants,
 PT cardioprotective, antiinflammatory and immunosuppressive agents etc.

XX Claim 8; Page 26-27; 48pp; English.

XX The invention covers hybrid TGF-beta molecules consisting of parts
 CC of the human isoforms TGF-beta1, TGF-beta2 and TGF-beta3 (see AAQ41599,
 CC AAQ41600 and AAQ41601, respectively). The hinge points between parts
 CC derived from different parent isoforms are pref. between amino acids
 CC 44 and 45, 56 and 57, 79 and 80, 90 and 91, or 22 and 23. Of the 30
 CC possible hybrids using these hinge points and one part each
 CC from two of the isoforms, 6 are preferred including the hybrid
 CC TGF-beta1(44/45)beta3. The hybrid molecules promote cell migration,
 CC inhibit the growth of A375 melanoma cells, accelerate the healing of
 CC partial-thickness burn wounds and full-thickness incisional wounds and
 CC increase formation of fibrous granular tissue.
 CC See AAQ41602-Q41607 for the most pref. hybrids.

XX Sequence 336 BP; 75 A; 109 C; 86 G; 66 T; 0 other;

alignment_scores:

Quality: 595.00 Length: 112
 Ratio: 5.459 Gaps: 0
 Percent Similarity: 97.321 Percent Identity: 92.857

alignment_block:

TGFB3P x AAQ41603 ..

Align seg 1/1 to: AAQ41603 from: 1 to: 336

1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluAsnCysCysVa 17

|||||
 1 GCCTGGACACCAACTATTGCTTTCAGCTCCACGAGAAAGTCTGCGT 50
 |||||
 17 lAtGProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
 |||||
 51 CGGCGAGCTGTACATTGCTCCGCAAGGACCTCGGCTGGAAGTGGATCC 100
 |||||
 34 iSGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
 |||||
 101 ACGAGCCCAAGGCTACCATGCCCAACTTCTGCTCAGGCCCTTGCCCATAC 150
 |||||
 51 LeuArgSerAlaAspThrHisSerThrValLeuGlyLeuTyrAsnTh 67
 |||||
 151 CTCGCGAGTGCAGACACACCCACAGCACGCTGCTGGGACTGTACAACAC 200
 |||||
 67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
 |||||
 201 TCTGAACCTTGAAGCATCTGCTCGCCTTGTGCTGCCCGCCAGGACCTGG 250
 |||||
 84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
 |||||
 251 AGCCCTGACCATCTCTACTATGTTGGGAGGACCCCAAGTGGAGCAG 300
 |||||
 101 LeuSerAsnMetValValLysSerCysLysCysSer 112
 |||||
 301 CTCTCCAACATGCTGGTGAAGTCTTGTAAATGTAGC 336

seq_name: /SIDSL/gcgdata/geneseq/geneseq/NA1996.DAT:AAAT17237

seq_documentation_block:

ID AAAT17237 standard; DNA; 336 BP.

XX
 AC
 XX
 XX

DT 17-JUL-1996 (first entry)

DE Hybrid TGF-beta 1-3 DNA.

KW Transforming growth factor type beta; TGF-beta 1; TGF-beta 3;
 KW protein renaturation; protein folding; ds.
 XX Synthetic.

XX WO9603433-A1.

XX 08-FEB-1996.

XX 12-JUL-1995; 95WO-EP02719.

XX 25-JUL-1994; 94EP-0810439.

XX (CIBA) CIBA GEIGY AG.

XX Cerletti N;

XX WPI; 1996-117000/12.

XX P-PSDB; AAR92775.

PT Prodn. of dimeric biologically active transforming growth factor
 PT by refolding denatured monomer in detergent-free folding buffer
 PT contg. specific organic solvent to improve yield

XX Example 10; Page 36-37; 54pp; English.

XX A DNA sequence (AAAT17237) codes for a recombinant hybrid of human
 CC transforming growth factor-beta, TGF-beta 1-3 (AAR92775), in which
 CC the N-terminal 44 amino acids are from TGF-beta 1 (see also AAR92773)
 CC and the C-terminal 68 amino acids from TGF-beta 3 (see also AAR92772).
 CC The DNA was subcloned in pPLMu, yielding plasmid pPLMu.hTGF-beta
 CC 1(44/45)beta3. Non-soluble, monomeric hybrid TGF-beta 1-3 was
 CC recovered from E. coli transformants. A biologically active,
 CC dimeric form of the hybrid was obtd. by refolding the monomer in
 CC detergent-free buffer contg. DMSO and/or DMF. Hybrid dimers

CC TGF-beta 2-3 (AAR92776) and TGF-beta 3-2 (AAR92777) were similarly
CC produced.
XX
SQ Sequence 336 BP; 75 A; 109 C; 86 G; 66 T; 0 other;

alignment_scores:
Quality: 595.00 Length: 112
Ratio: 5.459 Gaps: 0
Percent Similarity: 97.321 Percent Identity: 92.857

alignment_block:
TGFB3P x AAT17237 ..

Align seg 1/1 to: AAT17237 from: 1 to: 336

1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
|||||
1 GCCCTGGACACCACTATTGCTTCAGCTCCACGGAGAGAACTGCTGCGT 50
17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
|||||
51 GCGGCAGCTGTACATTGACTTCGCAAGGACCTCGGCTGGAGTGGATCC 100
34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
|||||
101 ACGAGCCCAAGGCTACCACTTCTGCTCAGGCCCTTCCGCCATAC 150
51 LeuArgSerAlaAspThrHisSerThrValLeuGlyLeuTyrAsnTh 67
|||||
151 CTCGCGAGTGCAGACACACACACGACGCTGGGACTGTACAAAC 200
67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
|||||
201 TCTGAACCTTGAGCATCTGCGCTTGTGCGTGGCCCGGACCTGG 250
84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
|||||
251 AGCCCTGACCATCCTGTACTATGTTGGGAGGACCCCAAAAGTGGAGCAG 300
101 LeuSerAsnMetValLysSerCysLysCysSer 112
|||||
301 CTCCTCAACATGGTGGTGAAGTCTTGAATGTAGC 336

seq_name: /SIDS1/gcgdata/geneseq/geneseq/NA1996.DAT:AAT15465

seq_documentation_block:

ID AAT15465 standard; cDNA to mRNA; 336 BP.

AC AAT15465;

DT 10-JUN-1996 (first entry)

XX cDNA encoding human TGF-beta-like protein, TGF-beta-1-3.

XX Transforming growth factor beta; TGF; regulator; method;
XX proliferation; differentiation; wound healing; solvent; ds.

XX Homo sapiens.

XX Key Location/Qualifiers
XX CDS 1..336

FT /*tag= a
FT /product= hybrid_TGF-beta-1-3
FT 1..132

FT /*tag= b
FT /note= "encodes N-terminal 44 amino acids of
FT TGF-beta-1"

FT mat_peptide 133..336

FT /*tag= c
FT /note= "encodes C-terminal 68 amino acids of
FT TGF-beta-3"

XX

PN WO9603432-A1.
XX
PD 08-FEB-1996.
XX
PF 12-JUL-1995; 95WO-EP02718.
XX
PR 25-JUL-1994; 94EP-0810438.
XX
PA (CIBA) CIBA GEIGY AG.
XX
PI Cerletti N;
XX
DR WPI; 1996-116999/12.
XX P-PSDB; AAR91959.
XX
PT Prodn. of dimeric, biologically active transforming growth factor
PT beta - by refolding denatured monomer in buffer contg. mild
PT detergent and specific organic solvents to improve yields
XX
PS Claim 17; Page 39-40; 59pp; English.
XX
CC AAT15465 encodes transforming growth factor (TGF) beta-like protein,
CC TGF-beta-1-3. TGF beta-1-3 is a hybrid of TGF-1 and TGF-3. TGF beta
CC hybrids were made using a new process of producing dimeric,
CC biologically active TGF beta-like proteins. The new process involves
CC treating denatured TGF beta monomers with folding buffer contg. a
CC mild detergent (CHAPS, CHAPSO or digitonin) and at least one of the
CC solvents DMSO (dimethyl sulphoxide), DMSO2 (dimethylsulphone) and
CC DMF (dimethyl formamide). The detergent allows folding of the monomer
CC such that, after dimerisation, the TGF beta-like protein retains
CC biological activity and remains in soluble form. The method allows
CC relatively high yields of biologically active TGF beta-like proteins
CC in their native dimeric form. TGF-beta like proteins are multifunctional
CC regulators of cellular activity and a typical use is to stimulate wound
XX healing.
SQ Sequence 336 BP; 75 A; 109 C; 86 G; 66 T; 0 other;

alignment_scores:

Quality: 595.00 Length: 112
Ratio: 5.459 Gaps: 0
Percent Similarity: 97.321 Percent Identity: 92.857

alignment_block:

TGFB3P x AAT15465 ..

Align seg 1/1 to: AAT15465 from: 1 to: 336

1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
|||||
1 GCCCTGGACACCACTATTGCTTCAGCTCCACGGAGAGAACTGCTGCGT 50
17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
|||||
51 GCGGCAGCTGTACATTGACTTCGCAAGGACCTCGGCTGGAGTGGATCC 100
34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
|||||
101 ACGAGCCCAAGGCTACCACTTCTGCTCAGGCCCTTCCGCCATAC 150
51 LeuArgSerAlaAspThrHisSerThrValLeuGlyLeuTyrAsnTh 67
|||||
151 CTCGCGAGTGCAGACACACACGACGCTGGGACTGTACAAAC 200
67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
|||||
201 TCTGAACCTTGAGCATCTGCGCTTGTGCGTGGCCCGGACCTGG 250
84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
|||||
251 AGCCCTGACCATCCTGTACTATGTTGGGAGGACCCCAAAAGTGGAGCAG 300

101 LeuSerAsnMetValValLysSerCysLysCysSer 112
|||||
301 CTCCTCAACATGGTGGTGAAGCTTGTAAATGTAGC 336

seq_name: /SIDS1/gcgdata/geneseq/geneseq/NA1993.DAT:AAQ41605

seq_documentation_block:
ID AAQ41605 standard; cDNA; 336 BP.
AC AAQ41605;
XX
XX
XX 26-AUG-1993 (first entry)
XX
XX Transforming Growth Factor-beta2(44/45)beta3 hybrid.
DE
XX
XX hTGF-beta2; hTGF-beta3; hybrid protein; wound healing;
KW cancer treatment; bone repair; growth regulation; ss.
XX
XX Homo sapiens.
XX
XX
FH Key Location/Qualifiers
FT mat_peptide 1..336
FT /*tag= a
FT /note= "TGF-beta2=1-132, TGF-beta3=133-336"
XX
XX EP542679-A.
XX
XX 19-MAY-1993.
XX
XX 03-NOV-1992; 92EP-0810845.
XX
XX 11-NOV-1991; 91EP-0810870.
XX
XX (CIBA) CIBA GEIGY AG.
XX
XX McMaster GK, Cox D, Cerletti N, Kuhla J;
XX
XX WPI; 1993-161126/20.
DR P-PSDB; AAR39644.
XX
XX New hybrid transforming growth factor-beta molecules - comprise
PT portions of mature TGF-beta isoforms; useful as wound healants,
PT cardioprotective, antiinflammatory and immunosuppressive agents etc.
XX
XX Claim 8; Page 29-30; 48pp; English.
XX
XX The invention covers hybrid TGF-beta molecules consisting of parts
CC of the human isoforms TGF-beta1, TGF-beta2 and TGF-beta3 (see AAQ41599,
CC AAQ41600 and AAQ41601, respectively). The hinge points between parts
CC derived from different parent isoforms are pref. between amino acids
CC 44 and 45, 56 and 57, 79 and 80, 90 and 91, or 22 and 23. Of the 30
CC possible hybrids using these hinge points and one part each
CC from two of the isoforms, 6 are preferred including the hybrid
CC TGF-beta2(44/45)beta3. The hybrid molecules promote cell migration,
CC inhibit the growth of A375 melanoma cells, accelerate the healing of
CC partial-thickness burn wounds and full-thickness incisional wounds and
CC increase formation of fibrous granular tissue.
CC See AAQ41602-Q41607 for the most pref. hybrids.
XX
XX Sequence 336 BP; 81 A; 94 C; 84 G; 77 T; 0 other;

alignment_scores:
Quality: 591.00 Length: 112
Ratio: 5.373 Gaps: 0
Percent Similarity: 98.214 Percent Identity: 91.071

alignment_block:
TGFB3P x AAQ41605 ..

Align seg 1/1 to: AAQ41605 from: 1 to: 336

1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17

|||||
1 GCCTTGGATCGGCCTATTGCTTTAGAAATGTGCAGGATAATTGCTGCCT 50
17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
51 ACCTCCACTTTACATTGATTTCAAGAGGATCTAGGTTGGAATGGATAC 100
34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
101 ACGAACCCAAAGGGTACAAATGCCAACTTCTGCTCAGGCCCTTGCCCATAC 150
51 LeuArgSerAlaAspThrHisSerThrValLeuGlyLeuTyrAsnTh 67
151 CTCGGCAGTGCAGACACACACCCACAGCAGCGTCTGGGACTGTACAACAC 200
67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
201 TCTGAACCTTGAAGCATCTGCCTCGCTTGTGCTGCGTCCCGAGGACCTGG 250
84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
251 AGCCCTCGACCATCTGTACTATGTTGGGAGGACCCCAAGTGGAGCAG 300
101 LeuSerAsnMetValLysSerCysLysCysSer 112
301 CTCCTCAACATGGTGGTGAAGCTTGTAAATGTAGC 336

seq_name: /SIDS1/gcgdata/geneseq/geneseq/NA1996.DAT:AA17238

seq_documentation_block:
ID AA17238 standard; DNA; 336 BP.
XX
XX AA17238;
XX
XX 17-JUL-1996 (first entry)
XX
XX Hybrid TGF-beta 2-3 DNA.
DE
XX
XX Transforming growth factor type beta; TGF-beta 2; TGF-beta 3;
KW protein renaturation; protein folding; ds.
XX
XX Synthetic.
OS
XX WO9603433-A1.
XX
XX 08-FEB-1996.
XX
XX 12-JUL-1995; 95WO-EP02719.
XX
XX 25-JUL-1994; 94EP-0810439.
XX
XX (CIBA) CIBA GEIGY AG.
XX
XX Cerletti N;
XX
XX WPI; 1996-117000/12.
DR P-PSDB; AAR92776.
XX
XX Prodn. of dimeric biologically active transforming growth factor -
PT by refolding denatured monomer in detergent-free folding buffer
PT contg. specific organic solvent to improve yield
XX
XX Example 10; Page 39-40; 54pp; English.
XX
XX A DNA sequence (AA17238) codes for a recombinant hybrid of human
CC transforming growth factor-beta, TGF-beta 2-3 (AAR92776), in which
CC the N-terminal 44 amino acids are from TGF-beta 2 (see also AAR92774)
CC and the C-terminal 68 amino acids from TGF-beta 3 (see also AAR92772).
CC The DNA was subcloned in pPLMu, yielding plasmid pPLMu.hTGF-beta
CC 2(44/45)beta3. Non-soluble, monomeric hybrid TGF-beta 1-3 was
CC recovered from E. coli LC137 transformants. A biologically active,
CC dimeric form of the hybrid was obtd. by refolding the monomer in
CC detergent-free buffer contg. DMSO and/or DMF. Hybrid dimers


```
101 LeuSerAsnMetValValLysSerCysLysCysSer 112
|||||
301 CTTCCAAACATGGTGAAGTCTTGAATAGC 336

seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1993.DAT:AAQ41607
seq_documentation_block:
ID AAQ41607 standard; cDNA; 336 BP.
AC AAQ41607;
XX
XX 26-AUG-1993 (first entry)
XX
XX Transforming Growth Factor-beta3(44/45)beta2 hybrid.
XX
XX hTGF-beta2; hTGF-beta3; hybrid protein; wound healing;
KW cancer treatment; bone repair; growth regulation; ss.
XX
XX Homo sapiens.
XX
FH Key Location/Qualifiers
FT mat_peptide 1..336
FT /*tag= a
FT /note= "TGF-beta3=1-132, TGF-beta2=133-336"
XX
XX EF542679-A.
XX
XX 19-MAY-1993.
XX
XX 03-NOV-1992; 92EP-0810845.
XX
XX 11-NOV-1991; 91EP-0810870.
XX
XX (CIBA ) CIBA GEIGY AG.
XX
XX McMaster GK, Cox D, Cerletti N, Kuhla J;
XX
XX WPI; 1993-161126/20.
DR P-PSDB; AAR39646.
XX
XX New hybrid transforming growth factor-beta molecules - comprise
PT portions of mature TGF-beta isoforms; useful as wound healants,
PT cardioprotective, antiinflammatory and immunosuppressive agents etc.
XX
XX Claim 9; Page 32; 48pp; English.
XX
XX The invention covers hybrid TGF-beta molecules consisting of parts
CC of the human isoforms TGF-beta1, TGF-beta2 and TGF-beta3 (see AAQ41599,
CC AAQ41600 and AAQ41601, respectively). The hinge points between parts
CC derived from different parent isoforms are pref. between amino acids
CC 44 and 45, 56 and 57, 79 and 80, 90 and 91, or 22 and 23. Of the 30
CC possible hybrids using these hinge points and one part each
CC from two of the isoforms, 6 are preferred, esp. the hybrid
CC TGF-beta3(44/45)beta2. The hybrid molecules promote cell migration,
CC inhibit the growth of A375 melanoma cells, accelerate the healing of
CC partial-thickness burn wounds and full-thickness incisional wounds and
CC increase formation of fibrous granular tissue.
CC See AAQ41602-Q41606 for the other pref. hybrids.
XX
XX Sequence 336 BP; 88 A; 87 C; 71 G; 90 T; 0 other;
SQ
```

```
alignment_scores:
Quality: 577.00 Length: 112
Ratio: 5.393 Gaps: 0
Percent Similarity: 95.536 Percent Identity: 88.393

alignment_block:
TGFB3P x AAQ41607 ..
Align seg 1/1 to: AAQ41607 from: 1 to: 336

1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
```

```
|||||
1 GCATTGGACACCAATTACTGCTTCGCAACTTGGAGGAGAACTGCTGTGT 50
|||||
17 lArGProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValh 34
|||||
51 GCGCCCTCTCTACATTGACCTCCGACAGGATCTGGGCTGGAAGTGGGTCC 100
|||||
34 lSGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
|||||
101 ATGAAGCTAAGGGCTACTATGCCAACTTCTGTCTGGAGCATGCCGTAT 150
|||||
51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
|||||
151 TTATGGAGITTCAGACACTCAGCACAGCGGTCTCTGAGCTTATATAATAC 200
|||||
67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
|||||
201 CATAAATCCAGAGCATCTGCTTCTCTCTGCTGGTGTCCCAAGATTAG 250
|||||
84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
|||||
251 AACCTCTAACCATCTCTACTACATTGGCAAAACACCAAGATTGAACAG 300
|||||
101 LeuSerAsnMetValValLysSerCysLysCysSer 112
|||||
301 CTTTCTAATATGATTGTAAGTCTTGCAATGCAGC 336

seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1996.DAT:AA17239
seq_documentation_block:
ID AA17239 standard; DNA; 336 BP.
XX
XX AC AA17239;
XX
XX DT 17-JUL-1996 (first entry)
XX
XX DE Hybrid TGF-beta 3-2 DNA.
XX
XX KW Transforming growth factor type beta; TGF-beta 2; TGF-beta 3;
XX protein renaturation; protein folding; ds.
XX
XX OS Synthetic.
XX
XX PN WO9603433-A1.
XX
XX PD 08-FEB-1996.
XX
XX PF 12-JUL-1995; 95WO-EP02719.
XX
XX PR 25-JUL-1994; 94EP-0810439.
XX
XX PA (CIBA ) CIBA GEIGY AG.
XX
XX PI Cerletti N;
XX
XX DR WPI; 1996-117000/12.
XX
XX DR P-PSDB; AAR92777.
XX
XX PT Prodn. of dimeric biologically active transforming growth factor -
XX by refolding denatured monomer in detergent-free folding buffer
XX contg. specific organic solvent to improve yield
XX
XX PS Example 10; Page 41-42; 54pp; English.
XX
XX CC A DNA sequence (AA17239) codes for a recombinant hybrid of human
XX transforming growth factor-beta, TGF-beta 3-2 (AAR92777), in which
XX the N-terminal 44 amino acids are from TGF-beta 3 (see also AAR92772)
XX and the C-terminal 68 amino acids from TGF-beta 2 (see also AAR92774).
XX The DNA was subcloned in pPLMu, yielding plasmid pPLMu.hTGF-beta
XX 3(44/45)beta2. Non-soluble, monomeric hybrid TGF-beta 3-2 was
XX recovered from E. coli LC137 transformants. A biologically active,
XX dimeric form of the hybrid was obtd. by refolding the monomer in
XX detergent-free buffer contg. DMSO and/or DMF. Hybrid dimers
```


101 LeuSerAsnMetValValLysSerCysLysCysSer 112
|||||
301 CTTTCTAATATGATTGTAAGTCTTGCAATGCAGC 336

seq_name: /SIDS1/gcgdata/geneseq/geneseq/NA1993.DAT:AAQ41602

seq_documentation_block:

ID_AAQ41602 standard; cDNA; 336 BP.

XX_AAQ41602;

XX_26-AUG-1993 (first entry)

XX_Transforming Growth Factor-betal(44/45)beta2 hybrid.

XX_hTGF-beta1; hTGF-beta2; hybrid protein; wound healing;
KW_cancer treatment; bone repair; growth regulation; ss.

XX_Homo sapiens.

XX_Key Location/Qualifiers

FT_mat_peptide 1..336

FT/*tag= a

FT/note= "TGF-beta1-1-132, TGF-beta2-133-336"

XX_EP542679-A.

XX_19-MAY-1993.

XX_03-NOV-1992; 92EP-0810845.

XX_11-NOV-1991; 91EP-0810870.

XX_(CIBA) CIBA GEIGY AG.

XX_McMaster GK, Cox D, Cerletti N, Kuhla J;

XX_WPI; 1993-161126/20.

XX_P-PSDB; AAR39641.

XX_New hybrid transforming growth factor-beta molecules - comprise
PT_portions of mature TGF-beta isoforms; useful as wound healants,
PT_cardioprotective, antinflammatory and immunosuppressive agents etc.

XX_Claim 8; Page 25-26; 48pp; English.

XX_The invention covers hybrid TGF-beta molecules consisting of parts
CC_of the human isoforms TGF-beta1, TGF-beta2 and TGF-beta3 (see AAQ41599,
CC_AAQ41600 and AAQ41601, respectively). The hinge points between parts
CC_derived from different parent isoforms are pref. between amino acids
CC_44 and 45, 56 and 57, 79 and 80, 90 and 91, or 22 and 23. Of the 30
CC_possible hybrids using these hinge points and one part each
CC_from two of the isoforms, 6 are preferred including the hybrid
CC_TGF-beta1(44/45)beta2. The hybrid molecules promote cell migration,
CC_inhibit the growth of A375 melanoma cells, accelerate the healing of
CC_partial-thickness burn wounds and full-thickness incisional wounds and
CC_increase formation of fibrous granular tissue.
CC_See also AAQ41603-041607 for the other pref. hybrids.

XX_Sequence 336 BP; 90 A; 92 C; 72 G; 82 T; 0 other;

alignment_scores:

Quality: 539.00 Length: 112
Ratio: 5.183 Gaps: 0
Percent Similarity: 92.857 Percent Identity: 81.250

alignment_block:

TGFB3P x AAQ41602 ..

Align seg 1/1 to: AAQ41602 from: 1 to: 336

1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluAsnCysCysVa 17

|||||
1 GCCTTGACACCAACTATTGCTTCACTCCACGGAGAAAGTCTGCGT 50
|||||
17 lArGProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
|||||
51 GCGGACAGCTGTACATTGACTTCGCAAGGACCTCGGCTGGAAGTGGATCC 100
|||||
34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
|||||
101 ACGAGCCCAAGGGCTACCATGCCAACTTCTGTGTGGAGCATGCCCGTAT 150
|||||
51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
|||||
151 TTATGGAGTTTCAGACACTCAGCAGCAGGGTCTCTGAGCTTATATAATAC 200
|||||
67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
|||||
201 CATAAATCCAGAAGCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 250
|||||
84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
|||||
251 AACCTCTAACCATCTCTACTACTATGGCAAAACACCCCAAGATTGAACAG 300
|||||
101 LeuSerAsnMetValValLysSerCysLysCysSer 112
|||||
301 CTTTCTAATATGATTGTAAGTCTTGCAATGCAGC 336

seq_name: /SIDS1/gcgdata/geneseq/geneseq/NA1993.DAT:AAQ41606

seq_documentation_block:

ID_AAQ41606 standard; cDNA; 336 BP.

XX_AAQ41606;

XX_26-AUG-1993 (first entry)

XX_Transforming Growth Factor-beta3(44/45)beta1 hybrid.

XX_hTGF-beta1; hTGF-beta3; hybrid protein; wound healing;
KW_cancer treatment; bone repair; growth regulation; ss.

XX_Homo sapiens.

XX_Key Location/Qualifiers

FT_mat_peptide 1..336

FT/*tag= a

FT/note= "TGF-beta3-1-132, TGF-beta1-133-336"

XX_EP542679-A.

XX_19-MAY-1993.

XX_03-NOV-1992; 92EP-0810845.

XX_11-NOV-1991; 91EP-0810870.

XX_(CIBA) CIBA GEIGY AG.

XX_McMaster GK, Cox D, Cerletti N, Kuhla J;

XX_WPI; 1993-161126/20.

XX_P-PSDB; AAR39645.

XX_New hybrid transforming growth factor-beta molecules - comprise
PT_portions of mature TGF-beta isoforms; useful as wound healants,
PT_cardioprotective, antinflammatory and immunosuppressive agents etc.

XX_Claim 8; Page 30-31; 48pp; English.

XX_The invention covers hybrid TGF-beta molecules consisting of parts
CC_of the human isoforms TGF-beta1, TGF-beta2 and TGF-beta3 (see AAQ41599,
CC_AAQ41600 and AAQ41601, respectively). The hinge points between parts
CC_derived from different parent isoforms are pref. between amino acids

CC 44 and 45, 56 and 57, 79 and 80, 90 and 91, or 22 and 23. Of the 30
 CC possible hybrids using these hinge points and one part each
 CC from two of the isoforms, 6 are preferred including the hybrid
 CC TGF-beta3(44/45)beta1. The hybrid molecules promote cell migration,
 CC inhibit the growth of A375 melanoma cells, accelerate the healing of
 CC partial-thickness burn wounds and full-thickness incisional wounds and
 CC increase formation of fibrous granular tissue.
 CC See AAQ41602-041607 for the most pref. hybrids.
 XX
 SQ Sequence 336 BP; 63 A; 109 C; 98 G; 66 T; 0 other;

alignment_scores:
 Quality: 538.00 Length: 112
 Ratio: 5.327 Gaps: 0
 Percent Similarity: 90.179 Percent Identity: 83.929

alignment_block:

TGFB3P x AAQ41606 ..

Align seg 1/1 to: AAQ41606 from: 1 to: 336

```

1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
|||||
1 GCFTTGACACCAATTTACTGCTTCCGCAACTTGGAGGAGAACTGCTGTGT 50

17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTyrLysTyrValH 34
|||||
51 GCGCCCCCTCTAGATTGACTTCGACAGGATCTGGGCTGGAAGTGGTCC 100

34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
|||||
101 ATGAACCTAAGGCTACTATGCCAACTTCTGCTCGGCCCTGCCCTAC 150

51 LeuArgSerAlaAspThrHrHisSerThrValLeuGlyLeuTyrAsnTh 67
::: ||| ||||| ::||| ||||| ::|||
151 ATTGTGAGCTGTCGACACGACGATACAGCAAGTCTCTGCGCTGTACACCA 200

67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
|||||
201 GCNTAACCGCGGCGCTCGCGCGCGCTGCTGCTGCGCGCGCGCTG 250

84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
|||||
251 AGCGCGTGGCCATCGTACTAGTGGCGCGCAAGCCCAAGTGGAGCAG 300

101 LeuSerAsnMetValValLysSerCysLysCysSer 112
|||||
301 CTGTCCACATGATCGTGGCTCTGCAAGTGCAGC 336

```

seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1991.DAT:AAQ11994

seq_documentation_block:

ID AAQ11994 standard; DNA; 339 BP.

XX AC AAQ11994;

XX DT 29-AUG-1991 (first entry)

XX DE Encodes Transforming Growth Factor beta 2.

XX KW TGF-beta2; biologically active protein production; ss.

XX OS Homo sapiens.

XX PN EP43225-A.

XX PD 19-JUN-1991.

XX PF 27-NOV-1990; 90EP-0810922.

XX PR 06-DEC-1989; 89GB-0027546.

XX

(CIBA) CIBA GEIGY AG.

XX Cerletti N, McMaster GK, Cox D, Schmitz A, Meyhack B;

XX WPI; 1991-180005/25.

XX P-PSDB; AARI2403.

XX Prodn. of Transforming Growth Factor type-beta-like proteins - by

XX subjecting denatured monomeric form to refolding conditions

XX Example; Page 27; 35pp; English.

XX This coding sequence was isolated from the CI-215 human glioma cell
 CC line. It was incorporated into an appropriate vector to transform
 CC Saccharomyces cerevisiae or E.coli. Monomeric TGF-beta1 was purified,
 CC denatured and dissolved in 140ml 50mM Tris/HCl pH8. 1M NaCl, 5mM EDTA,
 CC 2mM reduced glutathione, 1mM oxidised glutathione and 33mM Chaps.
 CC After 72 hrs at 4 deg C, pH was adjusted to 2.5 and the mixture was
 CC conc. 10 times. The conc. soln was diluted to the original vol. with
 CC 10mM HCl and conc to a final vol of 10 ml. The supernatant from
 CC centrifugation at 5000g for 30 min contained disulphide-linked dimeric
 CC TGF-beta2.

XX Sequence 339 BP; 98 A; 77 C; 70 G; 94 T; 0 other;

alignment_scores:

Quality: 535.00 Length: 112

Ratio: 5.095 Gaps: 0

Percent Similarity: 93.750 Percent Identity: 79.464

alignment_block:

TGFB3P x AAQ11994 ..

Align seg 1/1 to: AAQ11994 from: 1 to: 339

```

1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
|||||
1 GCFTTGATGCGGCTATTGCTTTAGAAATGTCAGGATAATTGCTGCT 50

17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTyrLysTyrValH 34
|||||
51 ACGTCCACTTTACATTGATTTCAAGAGGATCTAGGTTGGAATGGATAC 100

34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
|||||
101 ACGAACCCAAAGGTACAAATGCCAACTTCTGCTGCGAGCATGCCCGTAT 150

51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
151 TTATGGAGTTCAGACATCAGCAGCAGAGGGTCTGAGCTTATATAATAC 200

67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
|||||
201 CATAAATCCAGAAGCATCTGCTTCTCTTGTGCGCTGCCAAGATTAG 250

84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
|||||
251 AACCTCTAACCATTTCTCTACTACATTGGCAAAACACCAAGATTGAACAG 300

101 LeuSerAsnMetValValLysSerCysLysCysSer 112
|||||
301 CTTTCTAATATGATTGTAAAGTCTTGCAAAATGCAGC 336

```

seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1993.DAT:AAQ41600

seq_documentation_block:

ID AAQ41600 standard; cDNA; 339 BP.

XX AC AAQ41600;

XX DT 26-AUG-1993 (first entry)

XX


```

1  GCTTTGGATCGCGCTATTGCTTTAGAAATGTCAGGATAAATTCCTGCCT 50
17  lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
51  ACCTCCACTTTACATTGATTTCAAGAGGGATCTAGGGTGGAAATGGATAC 100
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
34  lSGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
101  ACGAACCCAAAGGGTACAATGCCAACTTCGTGCTGGAGCATGCCCGTAT 150
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
51  lLeuArgSerAlaAspThrHisSerThrValLeuGlyLeuTyrAsnTh 67
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
151  TTATGGAGTTCAGACACTCAGCACACAGCGTCTGAGCTTATATAATAC 200
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
67  rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
201  CATAAATCCAGAGCATCTGCTTCTCTGCTGCGTGTCCCAAGATTAG 250
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
84  luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
251  AACCTCTAACCATTTCTACTACTGATTGGCAAAACACCCCAAGATTGAAC 300
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
101  LeuSerAsnMetValValLysSerCysLysCysSer 112
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
301  CTTTCTAATATGATTGTAAGTCTTGCAATGCAGC 336

```

seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1996.DAT:AA15463

seq_documentation_block:

ID AA15463 standard; cDNA to mRNA; 339 BP.

XX AC
XX AA15463;

XX DT 10-JUN-1996 (first entry)

XX DE Human transforming growth factor beta 2 encoding cDNA.

XX KW Transforming growth factor beta; TGF; regulator; method;
XX KW proliferation; differentiation; wound healing; solvent; ds.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers
XX FT 1..339

XX FT /*tag= a
XX FT /product= human_TGF-beta-2

XX FN W09603432-A1.

XX PD 08-FEB-1996.

XX PF 12-JUL-1995; 95WO-EP02718.

XX PR 25-JUL-1994; 94EP-0810438.

XX PA (CIBA) CIBA GEIGY AG.

XX PI Cerletti N;

XX DR WPI; 1996-116999/12.

XX DR P-PSDB; AAR91957.

XX PT Prodn. of dimeric, biologically active transforming growth factor
XX PT beta - by refolding denatured monomer in buffer contg. mild
XX PT detergent and specific organic solvents to improve yields

XX PS Example 1; Page 34-35; 59pp; English.

XX CC AA15462-T15464 encode transforming growth factor (TGF) beta-1,

XX CC TGF beta-2 and TGF beta-3 which are produced using recombinant

XX CC DNA technology and used to produce TGF beta-like proteins in

XX CC dimeric form. The TGF beta-like proteins produced are hybrids of

XX CC 2 different types of TGF beta e.g. TGF beta-1-3, TGF beta-2-3, etc.

CC or bone morphogenic proteins e.g. BMP-2. The TGF beta hybrids were
CC made using a new process of producing dimeric, biologically active
CC TGF beta-like proteins. The new process involves treating denatured
CC TGF beta monomers with folding buffer contg. a mild detergent (CHAPS,
CC CHAPS or digitonin) and at least one of the solvents DMSO (dimethyl
CC sulphoxide), DMSO2 (dimethylsulphone) and DMF (dimethyl formamide).
CC The detergent allows folding of the monomer such that, after
CC dimerisation, the TGF beta-like protein retains biological activity
CC and remains in soluble form. The method allows relatively high yields
CC of biologically active TGF beta-like proteins in their native dimeric
CC form. TGF-beta like proteins are multifunctional regulators of
CC cellular activity and a typical use is to stimulate wound healing.

XX S0 Sequence 339 BP; 98 A; 77 C; 70 G; 94 T; 0 other;

alignment_scores:

Quality: 535.00 Length: 112
Ratio: 5.095 Gaps: 0
Percent Similarity: 93.750 Percent Identity: 79.464

alignment_block:

TGFB3P x AA15463 ..

Align seg 1/1 to: AA15463 from: 1 to: 339

```

1  AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnProCysVa 17
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1  GCTTTGGATCGCGCTATTGCTTTAGAAATGTCAGGATAAATTCCTGCCT 50
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
17  lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
51  ACGTCCACTTTACATTGATTTCAAGAGGGATCTAGGGTGGAAATGGATAC 100
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
34  lSGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
101  ACGAACCCAAAGGGTACAATGCCAACTTCTGCTGCTGGAGCATGCCCGTAT 150
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
51  LeuArgSerAlaAspThrHisSerThrValLeuGlyLeuTyrAsnTh 67
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
151  TTATGGAGTTCAGACACTCAGCACACAGCGGTCTGAGCTTATATAATAC 200
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
67  rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
201  CATAAATCCAGAGCATCTGCTTCTCTGCTGCTGCTGCCAAGATTAG 250
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
84  luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
251  AACCTCTAACCATTTCTACTACTACATTGGCAAAACACCCCAAGATTGAAC 300
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
101  LeuSerAsnMetValValLysSerCysLysCysSer 112
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
301  CTTTCTAATATGATTGTAAGTCTTGCAATGCAGC 336

```

seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1997.DAT:AA15463

seq_documentation_block:

ID AA15463 standard; cDNA; 339 BP.

XX AC
XX AA15463;

XX DT 26-AUG-1997 (first entry)

XX DE TGF active fragment of a TGF-beta fusion protein encoding cDNA.

XX KW Transforming growth factor-beta fusion protein; wound healing;
XX KW artificial skin; surgery recovery time; ss.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT 1..339

XX FT /*tag= a

```

ET /function= TGF active fragment
XX
PN W09639430-A1.
XX
PD 12-DEC-1996.
XX
PF 05-JUN-1996; 96WO-US08973.
XX
PR 06-JUN-1995; 95US-0470837.
XX
PA (CHEU/) CHEUNG D T.
PA (HALL/) HALL F L.
PA (NIMN/) NIMNI M E.
PA (TUAN/) TUAN T.
PA (WULL/) WU L.
XX
PI Cheung DT, Hall FL, Nimni ME, Tuan T, Wu L;
XX
DR WPI; 1997-043065/04.
DR P-PSDB; AAW08174.
XX
PT Prepn. of transforming growth factor-beta fusion protein - useful to
XX reduce surgery recovery time and to prepare artificial skin
XX
PS Disclosure; Page 46-47; 59pp; English.
XX
CC A novel transforming growth factor-beta (TGF-beta) fusion protein
CC comprises a purification tag and a TGF active fragment. The present
CC sequence encodes a specifically claimed TGF active fragment.
CC Additionally, the fusion protein may comprise proteinase-sensitive
CC linker sites and binding domain so the protein sequence may contain
CC some or all of the following elements: purification tag;proteinase
CC site;ECM binding site;proteinase site:TGF-beta. TGF-beta promotes
CC wound healing, and the fusion protein can be used to reduce surgery
CC recovery time and in the preparation of artificial skin. The inclusion
CC of a purification tag facilitates purification of the fusion protein.
CC The proteinase site is included to permit cleavage and release of the
CC purification tag after purification if desired. The extracellular
CC matrix binding site facilitates delivery of the fusion protein to the
CC desired site of action. Delivery of the TGF-beta to the site to be
CC treated reduces the amount of TGF-beta required to be administered to
CC be effective and reduces the concentration of circulating TGF-beta
CC which may result in undesirable effects.
XX
SQ Sequence 339 BP; 98 A; 77 C; 70 G; 94 T; 0 other;

```

```

alignment_scores:
  Quality: 535.00      Length: 112
  Ratio: 5.095        Gaps: 0
Percent Similarity: 93.750 Percent Identity: 79.464

alignment_block:
TGFB3P x AAT42772 ..
Align seg 1/1 to: AAT42772 from: 1 to: 339

1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluAsnCysCysVa 17
|||||:  |||||||:|||||:|||||:|||||:|||||:|||||:
1 GCTTTGGATGGCGCCCTATTGCTTTAGAAATGTGCAGGATAATGCTGCT 50

17 largProLeuThrIleAspPheArgGlnAspLeuGlyTrpValH 34
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
51 ACGTCCACTTTACATVTGATTTCAAGAGGAGTCTAGGGTGGAAATGGATAC 100

34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
101 AGRACCCAAAGGGTACAATGCCACTTCTGTGCTGGAGCATGCCCGTAT 150

51 LeuArgSerAlaAspThrHisSerThrValLeuGlyLeuTyrAsnTh 67
|||:|||||:|||||:|||||:|||||:|||||:|||||:
151 TTATGGAGTTACAGACTCAGCACAGCAGGCTCTGAGCTTATATAATAC 200

```

```

67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
|:::|||||:|||||:|||||:|||||:|||||:|||||:
201 CATAAATCCAGAAGCATCTGCTTCTCTTGTGCTGTCCTCCCAAGATTAG 250

84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
251 AACCTCTAACCATTTCTACTACATTGGCAAAACACCCCAAGATTGAACAG 300

101 LeuSerAsnMetValValLysSerCysLysCysSer 112
|:::|||||:|||||:|||||:|||||:|||||:
301 CTTTCTAATATGATTGTAAGTCTTGCATAATGCAGC 336

seq_name: /SIDS1/gcgdata/geneseq/geneseq/NA1999.DAT:AA15246
seq_documentation_block:
ID AAX15246 standard; cDNA; 339 BP.
XX
AC AAX15246;
XX
DT 28-APR-1999 (first entry)
XX
DE cDNA encoding the mature form of transforming growth factor-beta-2.
XX
KW Transforming growth factor-beta-2; TGF-beta-like protein;
KW S-sulphonated TGF-beta-like protein; wound treatment; cancer;
KW bone repair; tissue repair; bone marrow protective agent;
KW cardioprotection; anti-inflammatory; immunosuppressive;
KW ulcer; bed sore; ds.
XX
OS Homo sapiens.
XX
PN EP891985-A1.
XX
PD 20-JAN-1999.
XX
PF 27-NOV-1990; 90EP-0810922.
XX
PR 06-DEC-1989; 89GB-0027546.
XX
PA (NOVS ) NOVARTIS AG.
XX
PI Cerletti N, Cox D, McMaster GK, Meyhack B, Schmitz A;
XX
DR WPI; 1999-083520/08.
DR P-PSDB; AAW97092.
XX
PT Producing biologically active dimeric Transforming Growth
PT Factor-beta - by refolding new monomeric Transforming Growth
XX Factor-beta, useful for treatment of wounds and cancer
XX
PS Example 1; Page 29; 32pp; English.
XX
CC The present sequence encodes the mature form of transforming growth
CC factor-beta-2. Dimeric, biologically active TGF-beta-like protein
CC can be produced by subjecting the denatured monomeric form to refolding
CC conditions. The new monomeric S-sulphonated TGF-beta-like protein is
CC useful for the production of the dimeric, biologically active
CC TGF-beta-like protein, which is useful for the treatment of wounds
CC (surface or internal) and cancer in a mammal, in bone and tissue
CC repair, as a bone marrow protective agent, a mediator of
CC cardioprotection, for the production of an anti-inflammatory or
CC immunosuppressive preparation. Treatment is useful for animals,
CC especially humans, and wound treatment (e.g. ulcers, bed sores etc.) is
CC particularly useful for the elderly.
XX
SQ Sequence 339 BP; 98 A; 77 C; 70 G; 94 T; 0 other;

```

```

alignment_scores:
  Quality: 535.00      Length: 112
  Ratio: 5.095        Gaps: 0
Percent Similarity: 93.750 Percent Identity: 79.464

```



```
FT CDS 182..1426
FT /*tag= a
FT /product= transforming growth factor-beta 2
XX
PN W09526745-A1.
XX
XX 12-OCT-1995.
XX
XX 05-APR-1994; 94WO-US03705.
XX
XX 05-APR-1994; 94WO-US03705.
XX (HARD ) HARVARD COLLEGE.
XX
XX Lee M, Perrella MA;
XX
XX WPI; 1995-358443/46.
XX P-PSDB; AAR83055.
XX
XX Treatment of hypotension, esp. in septic shock - by administering
PT transforming growth factor-beta e.g. to inhibit inducible nitric
PT oxide synthase gene transcription
XX
XX Disclosure; Fig 16; 52pp; English.
XX
XX The CDNA encodes transforming growth factor-beta 2 (TGF-beta 2) which
CC has been found to inhibit inducible nitric oxide synthase (iNOS) gene
CC transcription, esp. in interleukin-1-beta (IL1-beta) stimulated rat
CC smooth muscle cells, and at a dose which does not inhibit constitutive
CC NOS. TGF-beta 1 or 2 (AAR83055) or their active fragments, can be used
CC in the treatment of hypotension, such as that associated with severe
CC inflammation or septic shock.
XX
XX Sequence 1695 BP; 523 A; 386 C; 354 G; 432 T; 0 other;
SQ
alignment_scores:
Quality: 535.00 Length: 112
Ratio: 5.095 Gaps: 0
Percent Similarity: 93.750 Percent Identity: 79.464
alignment_block:
TGFB3P x AAT05877 ..
Align seg 1/1 to: AAT05877 from: 1 to: 1695
1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
1088 GCTTGGATCGGCCCTATGCTTTAGAATGTGCAGATAATGTGCGCT 1137
17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
1138 ACGTCCACTTTACATTGATTTCAAGAGGATCTAGGGTGGAAATGGATAC 1187
34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
1188 ACGAACCCAAAGGGTACAATGCCAACTTCTGCTGGAGATGCCCGTAT 1237
51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 57
1238 TTATGGAGTTCCAGACACTCAGCAGCAGAGGTCCTGAGCTTATATAATAC 1287
67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
1288 CATAATCCAGAGCATCTGCTTCTCCTGCTGCTGCCAAGATTAG 1337
84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
1338 AACCTCTAACCATTTCTCTACTACATTGGCAAAACACCCCAAGATTGAACAG 1387
101 LeuSerAsnMetValValLysSerCysLysCysSer 112
1388 CTTTCTAATATGATGTAAAGTCTTGGCAATGCAGC 1423
```

```
seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1992.DAT-AAQ20291
seq_documentation_block:
ID AAQ20291 standard; cDNA; 2208 BP.
XX
XX AC AAQ20291;
XX
XX 16-APR-1992 (first entry)
XX
XX Sequence encoding hybrid transforming growth factor (TGF)-
DE beta-1/beta-2.
XX
XX Hypertension therapy; hypotensive agent; blood pressure modulator;
KW ss.
XX
XX Homo sapiens and monkey.
XX
XX Key Location/Qualifiers
FT CDS 262..282
FT /*tag= a
FT sig_peptide 283..324
FT /*tag= b
FT CDS 325..1095
FT /*tag= c
FT mat_peptide 1096..1434
FT /*tag= d
FT polyA_site 2208
FT /*tag= e
XX
XX W09119513-A.
XX
XX 26-DEC-1991.
XX
XX 20-JUN-1991; 91WO-US04449.
XX
XX 20-JUN-1990; 90US-0541221.
XX (BRIM ) BRISTOL-MYERS SQUIB.
XX
XX Oleson FB, Comerreski CR;
XX
XX WPI; 1992-024199/03.
XX P-PSDB; AAR20126.
XX
XX Use of transforming growth factor (TGF)-beta and their
PT antagonists - for modulating blood pressure, for treating
PT hypertension and hypotension
XX
XX Disclosure; Fig 3; 42pp; English.
XX
XX A new method for treating hypertension comprises administering a
CC transforming growth factor (TGF)-beta to an individual at a dose
CC effective for lowering blood pressure; the TGF-beta may be e.g.
CC mature TGF-beta, TGF-beta2, a mature TGF-beta1/beta2 hybrid, TGF-
CC beta1 precursor, a latent TGF-beta2 precursor, hybrid TGF-beta1/TGF-
CC beta2 precursor, a latent TGF-beta1 complex or a latent TGF-beta2
CC complex.
XX
XX Sequence 2208 BP; 599 A; 576 C; 534 G; 499 T; 0 other;
SQ
alignment_scores:
Quality: 535.00 Length: 112
Ratio: 5.095 Gaps: 0
Percent Similarity: 93.750 Percent Identity: 79.464
alignment_block:
TGFB3P x AAQ20291 ..
Align seg 1/1 to: AAQ20291 from: 1 to: 2208
1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
```



```

1506 ACGTCCACTTTACATTGATTTCAAGAGGATCTAGGGTGGAAATGGATAC 1555
34  IsGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
1556 ACGAACCCAAAGGGTACAATGCCAACTTCTGTCTGGAGCATGCCCGTAT 1605
51  LeuArgSerAlaAspThrHisSerThrValLeuGlyLeuTyrAsnTh 67
1606 TTATGGAGTTCAGACACTCAGCAGCAGGAGGCTCTGAGCTTATATAATAC 1655
67  rLeuAsnProGluAlaSerProCysCysValProGlnAspLeuG 84
1656 CATAAATCCAGAGCATCTGCTTCTCTGCTGCTGCCAAGATTAG 1705
84  luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
1706 AACCTCTAACCATCTCTACTACTATGGCAAAACACCCCAAGATTGAACAG 1755
101 LeuSerAsnMetValLysSerCysLysCysSer 112
1756 CTTTCTAATATGATTGTAAGTCTTGCAAAATGCAGC 1791
```

seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1990.DAT:AAQ05126

seq_documentation_block:

ID AAQ05126 standard; DNA; 2569 BP.
AC AAQ05126;
DT 02-NOV-1990 (first entry)
DE Human TGF-Beta2-442 precursor cDNA.
KW Human TGF-Beta2 precursor; cancer; tumorcide; ss.
XX Synthetic.

Key Location/Qualifiers

CDS 467..1792

FT mat_peptide 1457..1792

FT /*tag= b

PN EP376785-A.

PD 04-JUL-1990.

PF 14-DEC-1989; 89EP-0403480.

PR 16-DEC-1988; 88US-0285140.

PR 05-DEC-1989; 89US-0446020.

XX (ONCO-) ONCOGEN LTD PARTNER.

PI Purchio AF, Madisen L, Webb N;

DR WPI; 1990-203127/27.

DR P-PSDB; AAR05748.

XX Cloning and expression of transforming growth factor beta 2 -
XX used for treatment of tumors or for augmenting wound healing.
PS Claim 1; Fig 1a; 58pp; English.

CC TGF-Beta2 may be used in treatment of tumors at effective doses,
CC and may also be useful in augmenting wound healing by stimulating
CC cell proliferation. The growth factor can be produced at high
CC levels from a CHO expression system.
XX Sequence 2569 BP; 772 A; 598 C; 512 G; 687 T; 0 other;

alignment_scores:
Quality: 535.00 Length: 112
Ratio: 5.095 Gaps: 0
Percent Similarity: 93.750 Percent Identity: 79.464
alignment_block:
TGFB3P x AAQ05126 ..
Align seg 1/1 to: AAQ05126 from: 1 to: 2569
1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGlnAsnCysCysVa 17
1457 GCTTTGGATGCGGCCCTATTGCTTTAGAAATGTGCAAGTAATGTCGCT 1506
17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTyrValH 34
1507 AGCTCCACTTTACATTGATTTCAAGAGGATCTAGGGTGGAAATGGATAC 1556
34 IsGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
1557 ACGAACCCAAAGGGTACAATGCCAACTTCTGTCTGGAGCATGCCCGTAT 1606
51 LeuArgSerAlaAspThrHisSerThrValLeuGlyLeuTyrAsnTh 67
1607 TTATGGAGTTCAGACACTCAGCAGCAGGAGGCTCTGAGCTTATATAATAC 1656
67 rLeuAsnProGluAlaSerProCysCysValProGlnAspLeuG 84
1657 CATAAATCCAGAGCATCTGCTTCTCTGCTGCTGCCAAGATTAG 1706
84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
1707 AACCTCTAACCATCTCTACTATATGGCAAAACACCCCAAGATTGAACAG 1756
101 LeuSerAsnMetValLysSerCysLysCysSer 112
1757 CTTTCTAATATGATTGTAAGTCTTGCAAAATGCAGC 1792

seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1992.DAT:AAQ20290

seq_documentation_block:

ID AAQ20290 standard; cDNA; 2569 BP.

XX AAQ20290;

XX 16-APR-1992 (first entry)

DE Sequence encoding human transforming growth factor (TGF) -

DE beta-2-442.

XX Hypertension therapy; hypotensive agent; blood pressure modulator;
KW ss.

XX Homo sapiens.

XX Key Location/Qualifiers

FT CDS 467..475

FT /*tag= a

FT sig_peptide 478..525

FT /*tag= b

FT CDS 526..1456

FT /*tag= c

FT mat_peptide 1457..1792

FT /*tag= d

FT polyA_site 2569

FT /*tag= e

PN WO9119513-A.

XX 26-DEC-1991.

XX 20-JUN-1991;

XX 91WO-US04449.

67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
 |:::|||||
 1684 CATAAATCCAGAAGCATCTGCTTCTCTGCTGCTGCCAAGATTAG 1733
 |:::|||||
 84 luProLeuThrIleLeuTyrrValGlyArgThrProLysValGluGln 100
 |:::|||||
 1734 AACCTCTAACCATTTCTTACATTTGGCAAAACACCAAGATTGAACAG 1783
 |:::|||||
 101 LeuSerAsnMetValLysSerCysLysCysSer 112
 |:::|||||
 1784 CTTTCTAATATGATGTAAGTCTTGCAATGCAGC 1819
 |:::|||||

seq_name: /SDSL/gcgdata/geneseq/geneseqn/NA1990.DAT:AAQ03510

seq_documentation_block:
 ID AAQ03510 standard; DNA; 2206 BP.

AC AAQ03510;
 DT 14-AUG-1990 (first entry)
 DE Human Transforming growth factor from TGF-Beta2-442 cDNA.
 KW HIV; AIDS; SIV; vaccine; AZT; CD4; cytokines; growth
 KW factors; ds.

XX Key Location/Qualifiers
 FH CDS 260..1429
 FT /*tag= a
 FT mat_peptide 1091..1429
 FT /*tag= b
 FT label= mature TGF-Beta2

XX EP356935-A.
 PN 07-MAR-1990.
 PD 25-AUG-1989; 89EP-0115719.
 PF 25-AUG-1988; 88US-0236698.
 PR (ONCO-) ONCOGEN LTD PARTNER.
 PA Brankovan V, Lioubin M, Purchio A;
 PI WPI; 1990-068723/10.
 DR P-PSDB; AAR05665.
 XX Compns. contg. transforming growth factor beta -
 PT used for inhibitions of HIV infection and replication in vivo.
 XX TGF-beta may be used in vivo to prevent formation of syncytia and
 CC inhibit HIV infection. TGF may also be used with other HIV treatments
 CC (AZT, soluble CD4 etc.).
 XX Disclosure; Fig 2; 20pp; English.
 PS Sequence 2206 BP; 600 A; 577 C; 530 G; 499 T; 0 other;
 SQ

alignment_scores:
 Quality: 532.00 Length: 112
 Ratio: 5.115 Gaps: 0
 Percent Similarity: 92.857 Percent Identity: 79.464

alignment_block:

TGFB3P x AAQ03510 ..

Align seg 1/1 to: AAQ03510 from: 1 to: 2206

1 AlaLeuAspThrAsnTyrrCysPheArgAsnLeuGluGlnAsnCysCysVa 17
 |:::|||||
 |:::|||||

1094 GCTTTGGATCCGGCCTATTGCTTTAGAAAATGTCAGCATAATTGCTGCCT 1143
 17 lArgProLeuTyrrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
 |:::|||||
 1144 AGCTCCACTTTACATTGATTTCAAGAGGGATCTAGGTTGAATGGATAC 1193
 |:::|||||
 34 lsgLProLysGlyTyrrAlaAsnPheCysSerGlyProCysProTyr 50
 |:::|||||
 1194 AGCAACCCAAAGGTACAATGCCAACTTCTGTCTGGAGCATGCCGTAT 1243
 |:::|||||
 51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrrAsnTh 67
 |:::|||||
 1244 TTATGGAGTTACACACTCAGCACAGCGGTCCTGAGCTTATATAATAC 1293
 |:::|||||
 67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
 |:::|||||
 1294 CATAAATCCAGAAGCATCTGCTTCTCTGCTGCTGCCAAGATTAG 1343
 |:::|||||
 84 luProLeuThrIleLeuTyrrValGlyArgThrProLysValGluGln 100
 |:::|||||
 1344 AACCTCTAACCATTTCTTACTACTATTGGCAAAACACCAAGATTGAACAG 1393
 |:::|||||
 101 LeuSerAsnMetValLysSerCysLysCysSer 112
 |:::|||||
 1394 CTTTCTAATATGATGTAAGTCTTGCAATGCAGC 1429
 |:::|||||

seq_name: /SDSL/gcgdata/geneseq/geneseqn/NA1990.DAT:AAQ03511

seq_documentation_block:
 ID AAQ03511 standard; DNA; 2207 BP.

XX AC AAQ03511;
 XX DT 14-AUG-1990 (first entry)
 XX DE Hybrid transforming growth factor TGF-beta1/beta2.
 KW HIV; AIDS; SIV; vaccine; AZT; CD4; cytokines; growth
 KW factors; ds.

XX Key Location/Qualifiers
 FH CDS 267..1437
 FT /*tag= a
 FT mat_peptide 1103..1437
 FT /*tag= b

XX EP356935-A.
 PN 07-MAR-1990.
 PD 25-AUG-1989; 89EP-0115719.
 PF 25-AUG-1988; 88US-0236698.
 PR (ONCO-) ONCOGEN LTD PARTNER.
 PA Brankovan V, Lioubin M, Purchio A;
 PI WPI; 1990-068723/10.
 DR P-PSDB; AAR05666.
 XX Compns. contg. transforming growth factor beta -
 PT used for inhibitions of HIV infection and replication in vivo.
 XX TGF-beta may be used in vivo to prevent formation of syncytia and
 CC inhibit HIV infection. TGF may also be used with other HIV treatments
 CC (AZT, soluble CD4 etc.).
 XX Disclosure; Fig 3; 20pp; English.
 PS Sequence 2207 BP; 600 A; 576 C; 532 G; 499 T; 0 other;
 SQ


```

FT CDS /note="Claimed"
FT 268..1443
FT /tag= b
FT sig_peptide 289..330
FT /tag= c
FT mat_peptide 1102..1440
FT /tag= d
FT misc_difference 1161
FT /tag= e
FT /label=G
FT misc_difference 1218 /tag= f
FT /label=A
FT polyA_site 2217 /note="As above"
FT /tag= g
FT 1114..1116
FT /tag= h
FT /codon=(seq:ccg,aa:Ala)
FT
FT DE3833897-A.
FT
FT 03-MAY-1989.
FT
FT 05-OCT-1988; 88DE-3833897.
FT
FT 18-AUG-1988; 88US-0234065.
FT
FT (ONCO-) ONCOGEN.
FT
FT Purchio AF, Madisen L, Webb N;
FT
FT WPI; 1989-138796/19.
FT P-PSDB; AAP91900.
FT
FT New DNA sequence encoding transforming growth factor beta 2 -
FT used for large scale expression in eucaryotic cells
FT
FT Disclosure; Fig 1b; 27pp; German.
FT
FT PolyA-RNA was isolated from the tamoxifen-treated, human prostatic
FT adenocarcinoma cell line PC-3 and converted to cDNA. TGF DNA is pref.
FT used for control of the SV40 promoter. and expressed in CHO cells.
FT
FT Sequence 2217 BP; 600 A; 577 C; 531 G; 499 T; 10 other;
FT
FT
FT alignment_scores:
FT Quality: 532.00 Length: 112
FT Ratio: 5.115 Gaps: 0
FT Percent Similarity: 92.857 Percent Identity: 79.464
FT
FT alignment_block:
FT TGFb3P x AAN90768 ..
FT
FT Align seg 1/1 to: AAN90768 from: 1 to: 2217
FT
FT 1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
FT ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
FT 1105 GCTTTGGATCCGCCCTATTGCTTTAGAAATGTCAGCATAAATGTCGCT 1154
FT
FT 17 largProLeuTyrIleAspPheArgGlnAspLeuGlyTrpTyrValH 34
FT :|||: ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
FT 1155 ACGTCCACTTACATTGATTTCAAGAGGGATCTAGGGTGAATGGATAC 1204
FT
FT 34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
FT ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
FT 1205 ACGAACCCAAAGGGTACATGCGCAACTTCTGTGCTGGAGCATGCCGAT 1254
FT
FT 51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
FT ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
FT 1255 TTATGGAGTTCAGCACTCAGCACAGCAGGGTCTTGAGCTTATATATAC 1304

```

```

67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
FT |:::||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1305 CATAAATCCAGAAGCATCTGCTTCTCTGCGTGTCCCAAGATTAG 1354
FT
84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
FT ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1355 AACCTCTAACCATCTCTACTACATTGGCAAAACACCCAGATTGAACAG 1404
FT
101 LeuSerAsnMetValValLysSerCysLysCysSer 112
FT ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1405 CTTTCTAATATGATTGAAGTCTTGCAATGCAGC 1440
FT
seq_name: /SIDS1/gcgdata/geneseq/geneseq/NA1995.DAT:AA04115
seq_documentation_block:
ID_ AA04115 standard; DNA; 2200 BP.
XX
AC AA04115;
XX
DT 26-MAR-1996 (first entry)
XX
DE Simian-human hybrid TGF-beta1/TGF-beta2 precursor DNA.
XX
KW TGF-beta1; TGF-beta2; transforming growth factor; protein;
KW cell differentiation; cell proliferation; CHO; Chinese hamster;
KW ovary; COS; monkey kidney; animal; mammal; ss.
XX
OS Homo sapiens.
XX
XX
FH Key Location/Qualifiers
FT mat_peptide 257..1423
FT /tag= a
FT /note= "hybrid TGF-beta1/TGF-beta2 precursor"
FT mat_peptide 257..1084
FT /tag= b
FT /note= "simian TGF-beta1 precursor"
FT mat_peptide 1085..1423
FT /tag= c
FT /note= "human TGF-beta2 precursor"
FT sig_peptide 278..319
FT /tag= d
XX
PN EP676474-Al.
XX
PD 11-OCT-1995.
XX
XX
PF 14-DEC-1989; 89EP-0104223.
XX
XX
PR 05-DEC-1989; 89US-0446020.
PR 16-DEC-1988; 88US-0285140.
XX
XX
PA (ONCO ) ONCOGEN LP.
XX
XX
PI Madisen L, Purchio AF, Webb N;
XX
DR WPI; 1995-346094/45.
DR P-PSDB; AAR79921.
XX
XX
PT Hybrid transforming growth factor beta-1/TGF-beta-2 precursor - used
PT to produce biologically active, mature TGF-beta-2
XX
XX
PS Claim 1, 2 and 3; Fig.1b; 52pp; English.
XX
XX
CC This hybrid DNA sequence is expressed in a host cell, preferably a
CC COS or CHO cell, containing a recombinant vector encoding this
CC sequence under the control of a 2nd nucleotide sequence that
CC regulates gene expression, preferably the SV40 promoter, so the host
CC cell produces active TGF-beta2. The produced TGF-beta2 protein can
CC be used to regulate cellular differentiation and proliferation.
XX
XX
SQ Sequence 2200 BP; 597 A; 588 C; 517 G; 498 T; 0 other;

```

```

DR WPT: 1990-187401/25.
DR P-PSDB: AAR05492.
XX
XX
PT New chimeric transforming growth factor -
PT with TGF-beta biological activity and increased secretion
PT efficiency.
XX
PS Claim 2; Fig 1; 18pp; English.
XX
XX Chimeric gene has TGF activity and may be more desirable than its
CC parents TGF-beta1 and TGF-beta2. CHO cells expressing the product
CC from a plasmid vector (p5beta/dhfr) are 2.5 times more bioactive
CC than normal. The product is useful in treatment of cancer and wound
CC healing.
CC See also EP-373994.
XX
XX Sequence 1561 BP; 304 A; 543 C; 443 G; 271 T; 0 Other;

alignment_scores:
    Quality: 503.00      Length: 112
    Ratio: 5.030         Gaps: 0
Percent Similarity: 89.286      Percent Identity: 75.893

alignment_block:
TGFbeta3P x AAQ04908  ..

Align seg 1/1 to: AAQ04908 from: 1 to: 1561

1  AlALeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
   |||||
1096 GCCTCGGACCAACACTACTGCTTCAGAAATGTGCAGATAAATTGCTGCCT 1145
   |||||

17  lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTyrLysTyrValh 34
   |||||
1146 AGCTCGCTTTACATTGACTTCAAGAGGACCTCGGCTGGAAGTGGATCC 1195
   |||||

34  iSGLuProLysGlyTyrTyrAlaAsnPheCysSergGlyProCysProTyr 50
   |||||
1196 ACGAGCCCAAGGGCTACCATGCGCAACTTCTGCTGGGGCCCTGTCCCTAC 1245
   |||||

51  LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnth 67
   |||||
1246 ATTTGGAGCTGGACGCGAGTACACAAAGGTCTGCGCCCTGTACACCA 1295
   |||||

67  rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeug 84
   |||||
1296 GCATACCCGGCGGCGCTCGGGGGCGCGTCTGCTGGGCCGCGAGCGCTGG 1345
   |||||

84  luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
   |||||
1346 AGCCACTGCCATCGTGACTACGTGGCGCGCAAGCCCAAGGTGGAGCAG 1395
   |||||

101 LeuSerAsnMetValVallySerCysLysCysSer 112
   |||||
1396 CTGTCCAAATGATCGTGGCTCCGTCAAATGCAGC 1431
   |||||

seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1992.DAT:AAQ29177
seq_documentation_block:
ID AAQ29177 standard; DNA; 1561 BP.
XX
XX
AC AAQ29177;
XX
XX
DT 10-MAR-1993 (first entry)
XX
XX TGF-beta 1/beta 2 chimeric gene.
XX
XX Transforming growth factor; TGF; TGF-beta; TGF-5 beta; simian:
KW Simian virus 40; SV40; expression vector; Chinese Hamster ovary; CHO
KW vascular endothelial cell; ss.
XX
XX Synthetic.
XX

```

XX Key Location/Qualifiers
 FT CDS 262..1434
 FT /*tag= a
 FT mat_peptide 1096..1431
 FT /*tag= b
 FT /*note= "Mature TGF-5 beta"
 FT sig_peptide 262..348
 FT /*tag= c
 FT precursor_RNA /*note= "TGF-5 beta pre-pro-protein"
 FT 349..1095
 FT /*tag= d
 FT mutation /*note= "TGF-5 beta pro-protein"
 FT 1120..1122
 FT /*tag= e
 FT mutation /label= S9R
 FT 1123..1125
 FT /*tag= f
 FT mutation /label= S10N
 FT 1126..1128
 FT /*tag= g
 FT mutation /label= T11V
 FT 1129..1131
 FT /*tag= h
 FT mutation /label= E12Q
 FT 1132..1134
 FT /*tag= i
 FT mutation /label= K13D
 FT 1144..1146
 FT /*tag= j
 FT mutation /label= V17L
 FT 1150..1152
 FT /*tag= k
 FT mutation /label= Q19P
 FT 1188..1170
 FT /*tag= l
 FT mutation /label= R25K
 FT 1171..1173
 FT /*tag= m
 FT old_sequence /label= K26R
 FT 1120..1155
 FT /*tag= n
 FT /*note= "Mutagenic linker"
 FT 179..200
 FT /*tag= o
 FT /*note= "Feature not labelled in the specification"

XX WO9216228-A.

XX 01-OCT-1992.

XX 13-MAR-1992; 92WO-US01993.

XX 14-MAR-1991; 91US-0669171.

XX (BRIM) BRISTOL-MYERS SQUIBB CO.

XX Madisen L, Merwin J, Purchio AF;

XX WPI; 1992-348938/42.

XX P-PSDB; AAR27522.

XX Compn. comprising new chimeric TGF-B (TGF-beta 1-beta 2) -
 XX inhibits proliferation of vascular endothelial cells, useful for
 XX treating cancer and to promote wound healing

XX Disclosure; Fig 1; 45pp; English.

XX The sequence given encodes a hybrid transforming growth factor
 CC (TGF)-beta termed TGF-beta 1/beta 2 (or TGF-5 beta). The mutations
 CC indicated in the features table represent replacements of TGF-beta 1
 CC bases with those from the corresponding positions of TGF-beta 2.
 CC Simian codon usage was maintained. This DNA sequence could be placed

CC under the control of Simian virus 40 (SV40) expression regulatory
 CC region within an expression vector and used to transfect Chinese
 CC Hamster ovary (CHO) cells. CHO transfectants can be seen to synthesize
 CC and secrete high levels of mature TGF-5 beta. TGF-5 beta induces
 CC effects on the proliferation of vascular endothelial cells equivalent
 CC to those produced by TGF-beta 1.

XX SQ Sequence 1561 BP; 306 A; 541 C; 443 G; 271 T; 0 other;

alignment_scores:
 Quality: 503.00 Length: 112
 Ratio: 5.030 Gaps: 0
 Percent Similarity: 89.286 Percent Identity: 75.893

alignment_block:
 TGFβ3p x AAQ29177 ..

Align seg 1/1 to: AAQ29177 from: 1 to: 1561

1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
 |||||
 1096 GCCTCGACACCAACTACTGCTTCAGAAATGTCAGGATATTTGCTGCT 1145
 17 lArGProLeuTyrIleAspPheArgGlnAspLeuGlyTyrLysTrpValH 34
 :|||
 1146 ACGTCGCTTTACATTGACTTCAAGAGGGACCTCGGCTGGAAGTGGATCC 1195
 34 iSGLuProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
 |||||
 1196 ACGAGCCCAAGGGCTACCATGCCAACTTCTGCTGGGGCCCTGTCCCTAC 1245
 51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
 :|||
 1246 ATTTGGAGCTGGACACGACGAGTACAGCAAGTCTCTGCCCTGTACACCA 1295
 67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
 |||||
 1296 GCATAACCCGGCGCTCGCGCGCGCTGCTGGTCCGCGAGCGCTGG 1345
 84 lUProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
 |||||
 1346 AGCCACTGCCCATCGTGTACTAGTGGCGCGCAAGCCCAAGGTGGAGCAG 1395
 101 LeuSerAsnMetValValLysSerCysLysCysSer 112
 |||||
 1396 CTGTCCAACATGATCGTGGCTCCGTCAATGTCAGC 1431

seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1996.DAT:AA17235

seq_documentation_block:

ID AA17235 standard; cDNA to mRNA; 339 BP.

XX AC AA17235;

XX DT 17-JUL-1996 (first entry)

XX DE Human TGF-beta 1 cDNA.

XX KW Transforming growth factor type beta; TGF-beta 1;
 XX protein renaturation; protein folding; ds.

XX OS Homo sapiens.

XX PN WO9603433-Al.

XX PD 08-FEB-1996.

XX PF 12-JUL-1995; 95WO-EP02719.

XX PR 25-JUL-1994; 94EP-0810439.

XX PA (CIBA) CIBA GEIGY AG.

|||||
101 ACGAGCCCAAGGCTACCATGCTGCTGGGCGCTGCCCTAC 150
XX
51 LeuArgSerAlaAspThrHisSerThrValLeuGlyLeuTyrAsnTh 67
::: ||| ||||| :||| |||||
151 ATTTGGAGCTGGACACGACGATACAGCAAGGCTGGCCCTGTACACCA 200
XX
67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
||||| ||||| :||| |||||
201 GCATAACCGCGCGCTGGGCGCGCTGCTGGCGCAGGCGCTGG 250
XX
84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
||||| ||||| :||| |||||
251 AGCCCTGCCCATGCTGCTACTACGTGGGCGCGCAAGCTGGAGCAG 300
XX
101 LeuSerAsnMetValValLysSerCysLysCysSer 112
||||| ||||| :||| |||||
301 CTGTCCACATGATGCTGGCTGCTGCAAGTGCACT 336
XX

seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1997.DAT: AAT42771

seq_documentation_block:

ID AAT42771 standard; cDNA; 339 BP.

AC AAT42771;

XX 26-AUG-1997 (first entry)

XX TGF-beta1 active fragment of a TGF-beta fusion protein encoding cDNA.

DE Transforming growth factor-beta fusion protein; wound healing;

XX artificial skin; surgery recovery time; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

FT CDS 1..339

FT /*tag= a

FT /function= TGF active fragment

XX W09639430-A1.

XX 12-DEC-1996.

XX 05-JUN-1996; 96WO-US08973.

XX 06-JUN-1995; 95US-0470837.

XX (CHEU/) CHEUNG D T.

XX (HALL/) HALL F L.

XX (NIMN/) NIMNI M E.

XX (TUAN/) TUAN T.

XX (WULL/) WU L.

XX Cheung DT, Hall FL, Nimni ME, Tuan T, Wu L;

XX WPI: 1997-043065/04.

XX P-PSDB; AAW08173.

XX Prepn. of transforming growth factor-beta fusion protein - useful to

XX reduce surgery recovery time and to prepare artificial skin

XX Disclosure; Page 44-45; 59pp; English.

XX A novel transforming growth factor-beta (TGF-beta) fusion protein

XX comprises a purification tag and a TGF active fragment. The present

CC of a purification tag facilitates purification of the fusion protein.
CC The proteinase site is included to permit cleavage and release of the
CC purification tag after purification if desired. The extracellular
CC matrix binding site facilitates delivery of the fusion protein to the
CC desired site of action. Delivery of the TGF-beta to the site to be
CC treated reduces the amount of TGF-beta required to be administered to
CC be effective and reduces the concentration of circulating TGF-beta
CC which may result in undesirable effects.
XX
SQ Sequence 339 BP; 66 A; 113 C; 100 G; 60 T; 0 other;

alignment_scores:

Quality: 500.00 Length: 112

Ratio: 5.102 Gaps: 0

Percent Similarity: 87.500 Percent Identity: 76.786

alignment_block:

TGFB3P x AAT42771 ..

Align seg 1/1 to: AAT42771 from: 1 to: 339

1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17

||||| ||||| :||| |||||

1 GCCCTGGACACCAACTATTGCTTCAGCTCCACGGAGAACTGCTGCGT 50

17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTyrLysTyrValH 34

||||| ||||| :||| |||||

51 GCGGACGCTGTACTATTGACTTCGCAAGGACCTCGGCTGGAAGTGGATCC 100

34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50

||||| ||||| :||| |||||

101 ATGAGCCCAAGGCTACCATGCCAATCTGCTCGGGCCCTGCCCTAC 150

51 LeuArgSerAlaAspThrHisSerThrValLeuGlyLeuTyrAsnTh 67

||||| ||||| :||| |||||

151 ATTTGGAGCTGGACACGAGTACAGCAAGTCTGCTGCGCGCAGGCGTGG 250

67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84

||||| ||||| :||| |||||

201 GCATAACCGCGCGCTGGGCGCGCTGCTGCTGCGCGCAGGCGCTGG 250

84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100

||||| ||||| :||| |||||

251 AGCGCGCTGCCCATCGTGTACTACGTGGCGCGCAAGCCCAAGTGGAGCAG 300

101 LeuSerAsnMetValValLysSerCysLysCysSer 112

||||| ||||| :||| |||||

301 CTGTCCACATGATGCTGGCTGCTGCAAGTGCACT 336

seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1999.DAT: AAX15245

seq_documentation_block:

ID AAX15245 standard; cDNA; 339 BP.

XX AC AAX15245;

XX XX 28-APR-1999 (first entry)

XX DE cDNA encoding the mature form of transforming growth factor-beta-1.

XX KW Transforming growth factor-beta-1; TGF-beta-like protein;

XX KW S-sulphonated TGF-beta-like protein; wound treatment; cancer;

XX KW bone repair; tissue repair; bone marrow protective agent;

XX KW cardioprotection; anti-inflammatory; immunosuppressive;

XX KW ulcer; bed sore; ds.

XX OS Homo sapiens.

XX XX EP891985-A1.

XX XX 20-JAN-1999.

XX

```

PF 27-NOV-1990; 90EP-0810922.
XX
PR 06-DEC-1989; 89GB-0027546.
XX
PA (NOVS ) NOVARTIS AG.
XX
PI Cerletti N, Cox D, McMaster GK, Meyhack B, Schmitz A;
XX
DR WPI; 1999-083520/08.
DR P-PSDB; AAW97091.
XX
PT Producing biologically active dimeric Transforming Growth
PT Factor-beta - by refolding new monomeric Transforming Growth
PT Factor-beta, useful for treatment of wounds and cancer
XX
XX
PS Example 1; Page 28; 32pp; English.
XX
CC The present sequence encodes the mature form of transforming growth
CC factor-beta-1. Dimeric, biologically active TGF-beta-like protein
CC can be produced by subjecting the denatured monomeric form to refolding
CC conditions. The new monomeric S-sulphonated TGF-beta-like protein is
CC useful for the production of the dimeric, biologically active
CC TGF-beta-like protein, which is useful for the treatment of wounds
CC (surface or internal) and cancer in a mammal, in bone and tissue
CC repair, as a bone marrow protective agent, a mediator of
CC cardioprotection, for the production of an anti-inflammatory or
CC immunosuppressive preparation. Treatment is useful for animals,
CC especially humans, and wound treatment (e.g. ulcers, bed sores etc.) is
CC particularly useful for the elderly.
XX
SQ Sequence 339 BP; 66 A; 114 C; 100 G; 59 T; 0 other;

alignment_scores:
    Quality: 500.00      Length: 112
    Ratio: 5.102        Gaps: 0
    Percent Similarity: 87.500      Percent Identity: 76.786

alignment_block:
TGFB3P x AAX15245 ..
Align seg 1/1 to: AAX15245 from: 1 to: 339
1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluAsnCysCysVa 17
|||||
1 GCCCTGGACACCACTATTGCTTCAGCTCCACGGAGAAAGAACTGCTGCGT 50
17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
|||
51 GCGGCAGCTGTACATTGACTTCCGCAAGGACCTCGGCTGGAGTGGATCC 100
34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
|||||
101 ACGAGCCAAAGGGCTACCATGCCAACTCTCGCTCGGGCCCTGCCCTAC 150
51 LeuArgSerAlaAspThrHrHisSerThrValLeuGlyLeuTyrAsnTh 67
::: ||| ||||| ::||| ||||| ::||| ::||| ::||| ::|||
151 ATTTGAGCGCTGACAGCGATACAGCAAGGTCCTGGCCCTGTACAACCA 200
67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
|||||
201 GCATAACCCGGCGCTCGGGCGCGCGCTGCTGCTGCGCGAGCGCGCTGG 250
84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
|||||
251 AGCGGTGCCCATCGTCTACTACGTGGCGCGCAAGCCCAAGGTGGAGCAG 300
101 LeuSerAsnMetValValLysSerCysLysCysSer 112
|||||
301 CTGTCCAACATGATCGTGCCTCTCTGCAAGTGCAGC 336
seq_name: /SIDS1/gcgdata/geneseq/geneseq/nal1999.DAT-AAV99375

```

```

seq_documentation_block:
ID AAV99375 standard; cDNA; 339 BP.
XX
AC AAV99375;
XX
DT 25-MAR-1999 (first entry)
XX
DE cDNA encoding a transforming growth factor beta active fragment.
XX
KW Proteinase site; bone morphogenetic fusion protein; bone binding site;
KW bone morphogenetic protein; transforming growth factor beta;
KW active fragment; wound healing; bone growth; purification tag; ds.
XX
OS Homo sapiens.
XX
PN WO9855137-A1.
XX
PD 10-DEC-1998.
XX
PF 02-JUN-1998; 98WO-US11189.
XX
PR 03-JUN-1997; 97US-0868452.
XX
PA (HALL/) HALL F L.
PA (HANB/) HAN B.
PA (NIMN/) NIMNI M E.
PA (SHOR/) SHORS E C.
PA (WULL/) WU L.
XX
PI Hall FL, Han B, Nimni ME, Shors EC, Wu L;
XX
DR WPI; 1999-059875/05.
DR P-PSDB; AAW84207.
XX
PT New bone morphogenetic fusion proteins - comprising a purification
PT tag and a bone morphogenetic active fragment, used for enhancing
PT wound healing or bone growth
XX
PS Example 1; Page 41; 64pp; English.
XX
CC The present sequence encodes a transforming growth factor beta active
CC fragment. The protein can be used in place of a bone morphogenetic
CC active fragment to create the fusion proteins of the invention. When a
CC bone morphogenetic active fragment is used, the fusion proteins are
CC designated bone morphogenetic fusion proteins. The bone morphogenetic
CC fusion protein may contain some or all of the following elements: a
CC purification tag, a proteinase site, an ECM/bone binding site, a second
CC proteinase site, and a bone morphogenetic protein active fragment.
CC The bone morphogenetic fusion proteins can be used for enhancing wound
CC healing or bone growth.
XX
SQ Sequence 339 BP; 66 A; 113 C; 100 G; 60 T; 0 other;

alignment_scores:
    Quality: 500.00      Length: 112
    Ratio: 5.102        Gaps: 0
    Percent Similarity: 87.500      Percent Identity: 76.786

alignment_block:
TGFB3P x AAV99375 ..
Align seg 1/1 to: AAV99375 from: 1 to: 339
1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
|||||
1 GCCCTGGACACCACTATTGCTTCAGCTCCACGGAGAAAGAACTGCTGCGT 50
17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
|||
51 GCGGCAGCTGTACATTGACTTCCGCAAGGACCTCGGCTGGAGTGGATCC 100
34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50

```

```

|||||
101 ATGAGCCCAAGGCTACCACTTCTGCTCGGCGCTGCCCTAC 150
|||||
51 LeuArgSerAlaAspThrThrHisThrValLeuGlyLeuTyrAsnTh 67
::: ||| ||||| ::||| |||||::|||
151 ATTTGGAGCCTGGACACGAGTACAGCAAGTCTGCGCTGTACAACCA 200
|||||
67 rLeuAsnProGluAlaSerAlaSerProCysValProGlnAspLeuG 84
|||||
201 GCATAACCGCGGCTCGCGCGCGCTGCTGCGTGCAGCGCTGG 250
|||||
84 luProLeuThrIleLeuTyrValGlyArgThrProLysValGluGln 100
|||||
251 AGCCGCTGCCATCGTGTACTAGTGGCGCGCAAGCCCAAGTGGAGCAG 300
|||||
101 LeuSerAsnMetValValLysSerCysLysCysSer 112
|||||
301 CTGTCCAACATGATGCTGCGCTCCTGCAAGTGCAGC 336

```

seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1990.DAT:AAQ09317

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seq_documentation_block:
ID   AAQ09317 standard; cDNA; 1303 BP.
XX
AC   AAQ09317;
XX
DT   12-AUG-1990 (first entry)
XX
DE   Monkey transforming growth factor-beta cDNA.
XX
KW   Transforming growth factor-beta; simian; psoriasis;
KW   TGF-beta.
XX
OS   Monkey.
XX
FH   Key
FT   sig_peptide      22..63
FT                     /*tag= a
FT   mat_peptide      836..1170
FT                     /*tag= b
FT                     /product=monkey transforming growth factor-beta
FT
FT
XX
XX   EP353772-A.
XX
XX   07-FEB-1990.
XX
XX   04-AUG-1989; 89EP-0114458.
XX
XX   05-AUG-1988; 88US-0229133.
XX
XX   (ONCO-) ONCOGEN LTD PARTNER.
XX
XX   Twardzik DR, Purchio AF, Ranchalis JE, Stevens V;
XX
XX   WPI; 1990-038499/06.
XX   P-PSDB; AAR03743.
XX
XX   Inhibition of proliferation of epidermal cells -
XX   used to treat psoriasis by contacting cells with compositions
XX   containing transforming growth factor-beta.
XX
XX   'disclosure; fig 1; 20pp; English.
XX
XX   TGF-beta may be used in the treatment of hyperplasia
XX   associated with acanthosis-categorised skin diseases, and
XX   in alleviating psoriatic symptoms associated with cytokine-
XX   induced phenomena. See also AAQ03268 and AAR03750.
XX
XX   Sequence 1303 BP; 263 A; 442 C; 378 G; 217 T; 3 other;

```

alignment_scores:
Quality: 500.00 Length: 112

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Ratio: 5.102 Gaps: 0
Percent Similarity: 87.500 Percent Identity: 76.786

alignment_block:
TGF3P x AAQ09317 ..

Align seg 1/1 to: AAQ09317 from: 1 to: 1303

1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGlnAsnCysCysVa 17
|||||
838 GCCTCGACACCAACTACTGCTTACGCTCCACGGAAGAAGTCTGCTCGT 887
|||||
17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
|||||
888 CGCGCAGCTGTATATTACTTCCGCAAGGACCTCGGCTGGAAGTGGATCC 937
|||||
34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
|||||
938 ACAGCCCAAGGCTACCATGCCAATCTTGCCTGGGGCCCTGTCCCTAC 987
|||||
51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
::: ||| ||||| ::||| |||||::|||
988 ATTTGGAGCCTGGACACGAGTACAGCAAGTCTGCGCTGTACAACCA 1037
|||||
67 rLeuAsnProGluAlaSerAlaSerProCysValProGlnAspLeuG 84
|||||
1038 GCATAACCGCGGCGCTCGCGCGCGCTGCTGCGTGCAGCGCTGG 1087
|||||
84 luProLeuThrIleLeuTyrValGlyArgThrProLysValGluGln 100
|||||
1088 AGCCACTGCCATCGTGTACTAGTGGCGCGCAAGCCCAAGTGGAGCAG 1137
|||||
101 LeuSerAsnMetValValLysSerCysLysCysSer 112
|||||
1138 CTGTCCAACATGATGCTGCGCTCCTGCAATGCAGC 1173

seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1992.DAT:AAQ20289
seq_documentation_block:
ID   AAQ20289 standard; cDNA; 1559 BP.
XX
AC   AAQ20289;
XX
DT   16-APR-1992 (first entry)
XX
DE   Sequence encoding simian transforming growth factor (TGF) beta-1.
XX
KW   Hypertension therapy; hypotensive agent; blood pressure modulator;
KW   ss.
XX
OS   Monkey.
XX
FH   Key
FT   CDS
FT                     Location/Qualifiers
FT                     -262..282
FT                     /*tag= a
FT                     283..324
FT                     /*tag= b
FT                     325..1098
FT                     /*tag= c
FT                     1099..1436
FT                     /*tag= d
FT
XX
XX   WO9119513-A.
XX
XX   26-DEC-1991.
XX
XX   20-JUN-1991; 91WO-US04449.
XX
XX   20-JUN-1990; 90US-0541221.
XX
XX   (BRIM ) BRISTOL-MYERS SQUIB.
XX
XX   Oleson FB, Comereski CR;

```

XX WPI; 1992-024199/03.
DR P-PSDB; AAR20124.
XX
XX Use of transforming growth factor (TGF)-beta and their
PT antagonists - for modulating blood pressure, for treating
PT hypertension and hypotension
XX
XX Disclosure; Fig 1; 42pp; English.
XX
XX A new method for treating hypertension comprises administering a
CC transforming growth factor (TGF)-beta to an individual at a dose
CC effective for lowering blood pressure; the TGF-beta may be e.g.
CC mature TGF-beta, TGF-beta2, a mature TGF-beta1/beta2 hybrid, TGF-
CC beta1 precursor, a latent TGF-beta2 precursor, hybrid TGF-beta1/TGF-
CC beta2 precursor, a latent TGF-beta1 complex or a latent TGF-beta2
CC complex.
XX
XX Sequence 1559 BP; 300 A; 546 C; 446 G; '267 T; 0 other;

alignment_scores:
Quality: 500.00 Length: 112
Ratio: 5.102 Gaps: 0
Percent Similarity: 87.500 Percent Identity: 76.786

alignment_block:
TGFB3P x AAQ02089 ..

Align seg 1/1 to: AAQ02089 from: 1 to: 1559

1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
|||||
1095 GCCTGGACACCACTACTGCTTCACCTCCACGGAGAAGACTGCTGCGT 1144

17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
|||||
1145 GGGCAGCTGTATATTGACTTCGCAAGGACCTCGGCTGGAAGTGGATCC 1194

34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
|||||
1195 ACGAGCCCAAGGGCTACCATGCAACTTTCGCTGGGGCCCTGCTCCCTAC 1244

51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
::: ||| ||||| ::::: |||||
1245 ATTTGGAGCTTGACACGACGATACACAGGTCCTGGCCCTGTACACCA 1294

67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
|||||
1295 GCATAACCCGGCGCTCGCGCGCGCTGCTGCTGCGCGAGCGCTGG 1344

84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
|||||
1345 AGCCACTGCCCATCGTGTACTAGTGGCGCGCAAGCCCAAGGTGGAGCAG 1394

101 LeuSerAsnMetValValLysSerCysLysCysSer 112
|||||
1395 CTGTCCAACTATGCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1430

seq_name: /SIDS1/cgdata/geneseq/geneseq/NA1990.DAT:AAQ03268

seq_documentation_block:
ID AAQ03268 standard; DNA; 1561 BP.

XX
XX AC AAQ03268;
XX
XX DT 12-AUG-1990 (first entry)
XX
XX DE Simian transforming growth factor-beta cDNA.
XX
XX KW Transforming growth factor-beta; psoriasis; TGF-beta; ss.
XX
XX OS Monkey.

XX Key Location/Qualifiers
FH sig_peptide 283..324
FT /*tag= a
FT mat_peptide 1096..1431
FT /*tag= b
FT /product=human transforming growth factor-beta
XX
XX EP353772-A.
XX
XX 07-FEB-1990.
XX
XX 04-AUG-1989; 89EP-0114458.
XX
XX 05-AUG-1988; 88US-0229133.
XX
XX (ONCO-) ONCOGEN LTD PARTNER.
XX
XX Twardzik DR, Purchio AF, Ranchalis JE, Stevens V;
PI
XX
XX WPI; 1990-038499/06.
DR P-PSDB; AAR03743.
XX
XX Inhibition of proliferation of epidermal cells -
PT used to treat psoriasis by contacting cells with compositions
PT containing transforming growth factor-beta.
XX
XX Disclosure; fig 1; 20pp; English.
XX
XX TGF-beta may be used in the treatment of hyperplasia
CC associated with acanthosis-categorised skin diseases, and
CC in alleviating psoriatic symptoms associated with cytokine-
CC induced phenomena. See also AAQ03269 and AAR03750.
XX
XX Sequence 1561 BP; 301 A; 547 C; 446 G; 267 T; 0 other;

alignment_scores:
Quality: 500.00 Length: 112
Ratio: 5.102 Gaps: 0
Percent Similarity: 87.500 Percent Identity: 76.786

alignment_block:
TGFB3P x AAQ03268 ..

Align seg 1/1 to: AAQ03268 from: 1 to: 1561

1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
|||||
1096 GCCTGGACACCACTACTGCTTCAGCTCCACGGAGAAGACTGCTGCGT 1145

17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
|||||
1146 GCGCAGCTGTATATTGACTTCGCAAGGACCTCGGCTGGAAGTGGATCC 1195

34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
|||||
1196 ACGAGCCCAAGGGCTACCATGCAACTTTCGCTGGGGCCCTGCTCCCTAC 1245

51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
::: ||| ||||| ::::: |||||
1246 ATTTGGAGCTTGACACGACGATACAGAGGTCCTGGCCCTGTACACCA 1295

67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
|||||
1296 GCATAACCCGGCGCTCGCGCGCGCTGCTGCTGCGCGAGCGCTGG 1345

84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
|||||
1346 AGCCACTGCCCATCGTGTACTAGTGGCGCGCAAGCCCAAGGTGGAGCAG 1395

101 LeuSerAsnMetValValLysSerCysLysCysSer 112
|||||

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1396 CTGTCCACATGATCGTGGCTCTCTGCAAAATGCAGC 1431
seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1990.DAT:AAQ03269
seq_documentation_block:
ID   AAQ03269 standard; DNA; 1571 BP.
XX
AC   AAQ03269;
XX
DT   12-AUG-1990 (first entry)
XX
DE   Human transforming growth factor-beta cDNA.
XX
KW   Transforming growth factor-beta; psoriasis;
KW   TGF-beta.
XX
OS   Homo sapiens.
XX
FH   Key
FT   sig_peptide 22..63
FT               /*tag= a
FT   mat_peptide 836..1170
FT               /*tag= b
FT               /product=human transforming growth factor-beta
XX
XX   EP353772-A.
PN
XX   07-FEB-1990.
PD
XX
XX   04-AUG-1989; 89EP-0114458.
XX
XX   05-AUG-1988; 88US-0229133.
XX
XX   (ONCO-) ONCOGEN LTD PARTNER.
XX
XX   Twardzik DR, Purchio AF, Ranchalis JE, Stevens V;
XX
XX   WPI; 1990-038499/06.
DR   P-PSDB; AAR03750.
XX
XX   Inhibition of proliferation of epidermal cells -
XX   used to treat psoriasis by contacting cells with compositions
XX   containing transforming growth factor-beta.
XX
XX   Disclosure; fig 1; 20pp; English.
XX
XX   TGF-beta may be used in the treatment of hyperplasia
XX   associated with acanthosis-categorised skin diseases, and
XX   in alleviating psoriatic symptoms associated with cytokine-
XX   induced phenomena. See also AAQ03268 and AAR03743.
XX
XX   Sequence 1571 BP; 299 A; 563 C; 443 G; 266 T; 0 other;
SQ

alignment_scores:
Quality: 500.00 Length: 112
Ratio: 5.102 Gaps: 0
Percent Similarity: 87.500 Percent Identity: 76.786

alignment_block:
TGFB3P x AAQ03269 ..
Align seg 1/1 to: AAQ03269 from: 1 to: 1571

1 AlalaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
|||||
1106 GCCCTGGACACCACTACTGCTTACGCTCCACGAGAGAAAGTCTGCGT 1155

17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
|||||
1156 GCGGACGCTGATATTGACTTCCGCAAGGACCTCGGCTGGAAGTGATGCC 1205

34 lSGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
|||
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|||||
1206 ACAGGCCCAAGGCTACCATGCCCAACTTCTGCTGGGGCCCTGTCCTAC 1255
51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
::: ||| ||||| ::||| |||||:::|||||
1256 ATTTGGAGCTGGACAGCAGTACAGCAAGTCTGCTGCGCTGTACAACCA 1305
67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
||||| |||||:::||||| ||||| ||||| |||||
1306 GCATAACCCGGCGCTCGGCGCGCGTCTGCTGCTGCCGCGAGCGCTGG 1355
84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
||||| ||||| ||||| ||||| ||||| ||||| |||||
1356 AGCCACTGCCATCGTGTACTAGTGGCGCGCAAGCCCAAGGTGGAGCAG 1405
101 LeuSerAsnMetValValLysSerCysLysCysSer 112
||||| |||||:::||||| ||||| ||||| |||||
1406 CTGTCCACATGATGCTGCGCTCTCTGCAAAATGCAGC 1441
seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1991.DAT:AAQ13392
seq_documentation_block:
ID   AAQ13392 standard; DNA; 1821 BP.
XX
AC   AAQ13392;
XX
DT   20-NOV-1991 (first entry)
XX
DE   Human pro-TGF-beta 1 gene.
XX
KW   Osteogenetic; tumoricidal; ss.
XX
XX   Homo sapiens.
XX
FH   Key
FT   CDS 512..1684
FT               /*tag= a
FT   sig_peptide 512..598
FT               /*tag= b
FT   misc_RNA 599..1684
FT               /*tag= c
FT               /*note= "pro-TGF-beta 1"
FT   mat_peptide 1346..1684
FT               /*tag= e
FT               /*note= "TGF-beta 1"
XX
XX   JP03180192-A.
PN
XX   06-AUG-1991.
PD
XX   07-DEC-1989; 89JP-0318243.
XX
XX   07-DEC-1989; 89JP-0318243.
XX
XX   (KIRI ) KIRIN BREWERY KK.
XX
XX   WPI; 1991-271579/37.
DR   P-PSDB; AAR13813.
XX
XX   Human pro-TGF-beta 1 prodn., for osteo-genetic activity - by
XX   preparing DNA chain contg. base sequence coding for human
XX   pre-pro-TGF-beta 1, forming expression vector etc.
XX
XX   Claim 1; Fig 1; 16pp; Japanese.
XX
XX   The DNA sequence encodes human prepro-TGF-beta 1 which can be
XX   produced by recombinant methods, it has osteogenetic and
XX   tumoricidal activity.
XX
XX   Sequence 1821 BP; 326 A; 679 C; 508 G; 308 T; 0 other;
SQ

alignment_scores:
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Quality: 500.00          Length: 112
Ratio: 5.102            Gaps: 0
Percent Similarity: 87.500 Percent Identity: 76.786

alignment_block:
TGFB3P x AAQ13392 ..
Align seg 1/1 to: AAQ13392 from: 1 to: 1821

1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluAsnCysCysVa 17
|||||
1346 GCCCTGGACACCAACTATTGCTTCAGCTCCACGGAGAAGAACTGCTGCGT 1395

17 largProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
|||||
1396 GCGGCAGCTGTACATTGACTTCGCAAGGACCTCGGCTGGAGTGGATCC 1445

34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
|||||
1446 ACGAGCCCAAGGGCTACCATGCACTTCGCTCGGGCCCTGCCCTAC 1495

51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
::: ||| ||||| ::||| ||||| ::|||
1496 ATTTGGAGCTTGACACGCGAGTACAGCAAGGTCCTGGCCCTGTACAACCA 1545

67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
|||||
1546 GCATAACCCGGCGCTCGCGCGCGCTGCTGCTGCGCGAGCGCTGG 1595

84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGln 100
|||||
1596 AGCCGCTGCCCATCGTACTACGTGGCGCGCAAGCCCAAGGTGGAGCAG 1645

101 LeuSerAsnMetValValLysSerCysLysCysSer 112
|||||
1646 CTGTCCAAATGATGCTGCGCTCCTGCAAGTGCAGC 1681

seq_name: /SIDS1/gcgdata/geneseq/geneseq/NA1986.DAT:AA60972

seq_documentation_block:
ID AA60972 standard; cDNA; 2537 BP.
XX
AC AA60972;
XX
DT 28-Oct-1991 (first entry)
XX
DE Sequence encoding preTGF-beta.
XX
KW Transforming growth factor beta; cancer; wound healing.
XX
FH Key Location/Qualifiers
FT misc_structure 37..113
FT /*tag= a
FT /note= "Sequence can form stable hairpin loops"
FT CDS 842..2014
FT /*tag= b
FT mat_peptide 1676..2011
FT /*tag= c
XX
XX EP200341-A.
XX
XX 10-DEC-1986.
XX
XX 21-MAR-1986; 86EP-0302112.
XX
XX 22-MAR-1985; 85US-0715142.
XX
XX 13-MAR-1987; 87US-0025423.
XX
XX (GETH ) GENENTECH INC.
XX
XX Derynck RMA;
XX
XX WPI; 1986-326875/50.

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DR P-PSDB; AAP61468.
XX
PT TGF-beta prodn. from transformed hosts - useful esp. for treating
PT wounds (J6 2/9/86).
XX
PS Disclosure; Fig 1b; 26pp; English.
XX
CC The gene product is known to stimulate cell proliferation and
CC inhibit anchorage-dependent growth of a variety of human cancer cell
CC lines, it is esp. useful in treatment of burns and the promotion of
CC surface and internal wound healing. TGF-beta may be expressed from a
CC transformed CHO cell line.
XX
SQ Sequence 2537 BP; 473 A; 893 C; 739 G; 432 T; 0 other;

alignment_scores:
Quality: 500.00          Length: 112
Ratio: 5.102            Gaps: 0
Percent Similarity: 87.500 Percent Identity: 76.786

alignment_block:
TGFB3P x AA60972 ..
Align seg 1/1 to: AA60972 from: 1 to: 2537

1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluAsnCysCysVa 17
|||||
1676 GCCCTGGACACCAACTATTGCTTCAGCTCCACGGAGAAGAACTGCTGCGT 1725

17 largProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
|||||
1726 GCGGCAGCTGTACATTGACTTCGCAAGGACCTCGGCTGGAGTGGATCC 1775

34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
|||||
1776 ACGAGCCCAAGGGCTACCATGCACTTCGCTCGGGCCCTGCCCTAC 1825

51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
::: ||| ||||| ::||| ||||| ::|||
1826 ATTTGGAGCTTGGACACGACGACGACCAAGGTCCTGGCCCTGTACAACCA 1875

67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
|||||
1876 GCATAACCCGGCGCTCGCGCGCGCTGCTGCTGCGCGAGCGCTGG 1925

84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGln 100
|||||
1926 AGCCGCTGCCCATCGTACTACGTGGCGCGCAAGCCCAAGGTGGAGCAG 1975

101 LeuSerAsnMetValValLysSerCysLysCysSer 112
|||||
1976 CTGTCCAAATGATGCTGCGCTCCTGCAAGTGCAGC 2011

seq_name: /SIDS1/gcgdata/geneseq/geneseq/NA1990.DAT:AAQ03301

seq_documentation_block:
ID AAQ03301 standard; DNA; 2537 BP.
XX
XX AAQ03301;
XX
XX AC
XX
DT 05-AUG-1990 (first entry)
XX
DE cDNA encoding human pre-transforming growth factor-beta-1 (pre-TGF-beta-1).
XX
XX DE
XX
XX KW Transforming growth factor-beta-1 (TGF-beta-1);
XX KW neoplastic cell line inhibition;
XX KW EGF-potential anchorage-independent growth;
XX
XX OS Homo sapiens.
XX
XX FH Key Location/Qualifiers

```

```
FT CDS      842..2014
FT          /*tag= a
FT mat_peptide 1676..2011
FT          /*tag= b
FT misc_difference 37..113
FT          /*tag= c
FT          /note="stable hairpin loops"
FT misc_feature 2015..2100
FT          /*tag= d
FT          /note="G-C rich sequence
FT          and a downstream TATA-like sequence"
FT
FT XX
FT PN US4886747-A.
FT PD 12-DEC-1989.
FT
FT XX
FT PF 13-MAR-1987; 87US-0025423.
FT XX
FT PR 13-MAR-1987; 87US-0025423.
FT XX
FT PA (GETH ) GENENTECH INC.
FT XX
FT PI Derynck RMA, Goeddel DV;
FT XX
FT DR WPI; 1990-051338/07.
FT DR P-PSDB; AAR05258.
FT XX
FT PT Nucleic acid encoding transforming growth factor-beta -
FT cloned into expression vectors for expression in eukaryotic host
FT cells for therapeutic use
FT
FT XX
FT PS Disclosure; Flg 1b; 28pp; English.
FT XX
FT CC It was obtained by an analysis of several overlapping cDNAs and gene
FT fragments, leading to the detn. of a continuous sequence corres. to the
FT TGF-beta-1 precursor mRNA. It is useful in constructing vectors that
FT encode biologically active transforming growth factor (TGF-beta),
FT operably linked to DNA that encodes a secretory leader (SL). It, or a
FT nucleic acid capable of hybridising with it, can also be labelled and
FT used in diagnostic assays for DNA or mRNA encoding TGF-beta or related
FT proteins.
FT XX
FT SQ Sequence 2537 BP; 473 A; 893 C; 739 G; 432 T; 0 other;

alignment_scores:
      Quality: 500.00      Length: 112
      Ratio: 5.102      Gaps: 0
Percent Similarity: 87.500 Percent Identity: 76.786

alignment_block:
TGFB3P x AAQ03301 ..
Align seg 1/1 to: AAQ03301 from: 1 to: 2537
1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
1676 GCCCTGGACACCACTATGCTTCAGTCCACGAGAGAACTGCTGCT 1725
17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
1726 GCGGAGCTGTACATTGACTTCGCAAGGACCTCGGCTGGAAGTGGATCC 1775
34 lSGLuProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
1776 ACGAGCCCAAGGGCTACCATCTGCTCCACTTCTGCTCGGGCCCTGCCCTAC 1825
51 LeuArgSerAlaAspThrHisSerThrValLeuGlyLeuTyrAsnTh 67
1826 ATTTGGAGCCTGACACCGCAGTACAGCAAGGTCCTGGCCCTGTACAACA 1875
67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
```

```
1876 GCATAACCGGGCGCTCGGGCGCGCTGCTGCTGCGCGCAGCGCTGG 1925
84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
1926 AGCCGCTGCCCATCTGCTACTAGTGGCGCAAGCCCAAGGTGGAGCAG 1975
101 LeuSerAsnMetValValLysSerCysLysCysSer 112
1976 CTGTCCAACATGATCGTGGCTCTCTGCAAGTGCAGC 2011
seq_name: /SIDS1/gcgdata/geneseq/geneseq/NA1990.DAT:AAQ02814
seq_documentation_block:
ID AAQ02814 standard; cDNA; 2537 BP.
XX
AC AAQ02814;
XX
DT 31-MAY-1989 (first entry)
XX
DE Sequence of pre-TGF-beta1 cDNA.
XX
KW Transforming growth factor beta-3 (TGF beta 3); tumour cells; growth
inhibition.
XX
FH Key
FT CDS      842..2011
FT          /*tag= a
FT          /label=pre-TGF beta 1
FT CDS      1677..2011
FT          /*tag= b
FT          /label=mature TGF-beta 1
FT GC_signal 2015..2092
FT          /*tag= c
FT misc_feature 2093..2099
FT          /*tag= d
FT          /label=TATA-like sequence
FT stem_loop 37..113
FT          /*tag= e
FT misc_feature 863..911
FT          /*tag= f
FT          /label=hydrophobic domain
FT
FT XX
FT PN WO8912101-A.
FT XX
FT PD 14-DEC-1989.
FT XX
FT PF 08-JUN-1988; 88WO-US01945.
FT XX
FT PR 08-JUN-1988; 88WO-UO01945.
FT XX
FT PA (GETH ) GENENTECH INC.
FT XX
FT PI Derynck RM, Goeddel DV;
FT XX
FT DR WPI; 1990-007474/01.
FT DR P-PSDB; AAR04034.
FT XX
FT PT Nucleotide sequence encoding transforming growth factor beta-3 -used as a
FT probe, or to produce TGF beta 3, for growth inhibition of certain normal
FT and neoplastic cells, eg A549.
FT XX
FT PS Disclosure; Fig. 1b; 61pp; English.
FT XX
FT CC Sequence encodes the 390 amino acid (AA) precursor transforming growth
FT factor-beta 1 (pre-TGF-beta 1) polypeptide. The 5' untranslated region of
FT the TGF-beta 1 mRNA is 841 bases long, is purine rich and has a region of
FT potential secondary structure. The TATA-like sequence in the 3' untrans-
FT lated region of the gene is presumably a polyadenylation signal. Mature
FT TGF-beta 1 comprises the C-terminal 112 AA's of pre-TGF-beta 1 and is
FT cleaved at the Arg-Arg dipeptide preceding its NH2 terminus. The nucleic
FT acid encoding the second subtype of TGF-beta (TGF-beta 3) is useful as a
FT probe or to produce TGF-beta 3 for inhibition of growth of normal and
FT neoplastic cells.
FT CC
```

```
XX
SQ Sequence 2537 BP; 473 A; 893 C; 739 G; 432 T; 0 other;

alignment_scores:
  Quality: 500.00 Length: 112
  Ratio: 5.102 Gaps: 0
Percent Similarity: 87.500 Percent Identity: 76.786

alignment_block:
  TGF3P x AAQ02814 ..
  Align seg 1/1 to: AAQ02814 from: 1 to: 2537
  1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGlnAsnCysCysVa 17
  1676 GCCCTGGACACCAACTATTCTTCAGCTCCACGAGAGAACTGCTGGT 1725
  17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
  1726 GCGGCAGCTGTACATTGACTTCGCGCAAGGACCTCGGCTGGAAGTGGATCC 1775
  34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
  1776 ACGAGCCCAAGGGCTACCATGCGCAACTTCTGCGCGGCCCTGCCCTAC 1825
  51 LeuArgSerAlaAspThrHisSerThrValLeuGlyLeuTyrAsnTh 67
  1826 ATTTGGAGCTGGACACGAGTACAGCAAGGTCTGCGCTGTACAACCA 1875
  67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
  1876 GCATAACCGCGCGCCCTCGCGCGCGCGTCTGCTGCCGCGAGCGCTGG 1925
  84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
  1926 AGCCGCTGCCCATCGTGTACTACGTGGGGCGCAAGCCCAAGGTGGAGCAG 1975
  101 LeuSerAsnMetValValLysSerCysLysCysSer 112
  1976 CTGTCCAACATGATGTGCGCTCTGCAAGTGCAGC 2011

seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1994.DAT:AAQ56923
seq_documentation_block:
ID AAQ56923 standard; cDNA; 2537 BP.
XX
AC AAQ56923;
XX
DT 09-JUL-1994 (first entry)
XX
DE Human pre-TGF-beta-1.
XX
KW TGF-beta-1; TGF-beta-2; transforming growth factor beta-1;
KW transforming growth factor beta-3; recombinant; wound healing;
KW vulnerary; Ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT misc_structure 47..113 /*tag= a
FT /*note= "possible hairpin loop region"
FT CDS 842..2014 /*tag= b
FT FT 1676..2011 /*tag= c
FT mat_peptide 2515..2521 /*tag= d
FT polyA_signal
FT
XX
PN US5284763-A.
XX
PD 08-FEB-1994.
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```
XX
PF 22-MAR-1985; 85US-0715142.
XX
PR 22-MAR-1985; 85US-0715142.
PR 13-MAR-1987; 87US-0025423.
PR 04-AUG-1989; 89US-0389929.
PR 04-MAR-1992; 92US-0845893.
XX
PA (GETH ) GENENTECH INC.
XX
PI Derynk RMA, Goeddel DV;
XX
DR WPI; 1994-056343/07.
DR P-PSDB; AAR46227.
XX
PT Nucleic acid sequences encoding transforming growth factor-beta -
PT diagnostic probes, and for use in therapeutics
XX
PS Disclosure; Fig 1b; 25pp; English.
XX
CC cDNA sequences were determined for human pre-TGF-beta-1 (AAQ56923),
CC plg TGF-beta-3 (AAQ56925) and human TGF-beta-3 (AAQ56926), and the
CC corresponding amino acid sequences were determined (AAR46227-29,
CC respectively). A genomic fragment corresponding to a human TGF-
CC beta-1 exon (AAQ56924) was also isolated and its amino acid sequence
CC determined (AAR46230). The sequences have been used in the
CC construction of vectors for the expression of recombinant TGF-
CC beta.
XX
SQ Sequence 2537 BP; 473 A; 890 C; 742 G; 432 T; 0 other;

alignment_scores:
  Quality: 500.00 Length: 112
  Ratio: 5.102 Gaps: 0
Percent Similarity: 87.500 Percent Identity: 76.786

alignment_block:
  TGF3P x AAQ56923 ..
  Align seg 1/1 to: AAQ56923 from: 1 to: 2537
  1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGlnAsnCysCysVa 17
  1676 GCCCTGGACACCAACTATTCTTCAGCTCCACGAGAGAACTGCTGGT 1725
  17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
  1726 GCGGCAGCTGTACATTGACTTCGCGCAAGGACCTCGGCTGGAAGTGGATCC 1775
  34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
  1776 ACGAGCCCAAGGGCTACCATGCGCAACTTCTGCGCGGCCCTGCCCTAC 1825
  51 LeuArgSerAlaAspThrHisSerThrValLeuGlyLeuTyrAsnTh 67
  1826 ATTTGGAGCTGGACACGAGTACAGCAAGGTCTGCGCTGTACAACCA 1875
  67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
  1876 GCATAACCGCGCGCCCTCGCGCGCGCGTCTGCTGCCGCGAGCGCTGG 1925
  84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
  1926 AGCCGCTGCCCATCGTGTACTACGTGGGGCGCAAGCCCAAGGTGGAGCAG 1975
  101 LeuSerAsnMetValValLysSerCysLysCysSer 112
  1976 CTGTCCAACATGATGTGCGCTCTGCAAGTGCAGC 2011

seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1996.DAT:AA15720
seq_documentation_block:
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ID XX AAT15720 standard; cDNA; 2537 BP.
AC AAT15720;
XX 24-JUL-1997 (revised)
DT 25-JAN-1980 (first entry)
XX Pre-transforming growth factor beta 1 cDNA.
DE transforming growth factor beta 1; wound healing;
KW recombinant production; ss.
XX Homo sapiens.
XX Key Location/Qualifiers
FH 1..841
FT 5'UTR
FT /*tag= a
FT 37..113
FT misc_feature
FT /*tag= b
FT /note= "GC-rich region forms stable hairpin loops;
FT similar to structural organisation of c-myc RNA,
FT could play role in mRNA stability or in
FT regulation of transcription"
FT CDS
FT 842..2014
FT /*tag= c
FT /product= pre-TGF_beta_1
FT 1676..2011
FT /*tag= d
FT /product= mature_TGF_beta_1
FT repeat_region
FT 2015..2100
FT /*tag= e
FT /note= "GC-rich region; possibly responsible for the
FT fact 3'UTR of mRNA could not be cloned as cDNA;
FT may be important for transcription efficiency"
FT repeat_unit
FT 2019..2023
FT /*tag= f
FT TATA_signal
FT 2094..2100
FT /*tag= g
FT /note= "TATA-like sequence; no evidence that this
FT functions a promoter"
FT polyA_signal
FT 2514..2520
FT /*tag= h
FT misc_signal
FT 2529..2536
FT /*tag= i
FT /note= "consensus sequence immediately precedes
FT polyA-tail (Benoist et al)"
XX US5482851-A.
XX 09-JAN-1996.
XX 22-MAR-1985; 85US-0715142.
XX 13-MAR-1987; 87US-0025423.
XX 22-MAR-1985; 85US-0715142.
XX 04-AUG-1989; 89US-0389929.
XX 04-MAR-1992; 92US-0845893.
XX 05-NOV-1993; 93US-0147364.
XX (GETH) GENENTECH INC.
XX Derynck RMA, Goeddel DV;
XX WPI; 1996-076891/08.
XX P-PSDB; AAR90827.
XX New recombinant human transforming growth factor-beta prods. - produced
XX using Chinese hamster ovary cells, for use in diagnostic applications
XX or in therapy
XX Example 3; Fig 1; 26pp; English.
XX The cDNA encodes the pre-transforming growth factor (TGF) beta 1 protein.
CC

CC The nucleotide sequence was obtbd. by an analysis of several overlapping
CC cDNAs and gene fragments. The DNA is useful for the recombinant
CC production of TGF beta 1, which can be used in, e.g. wound healing.
CC (Revised entry submitted to correct sequence analysis breakdown.)
XX
XX Sequence 2537 BP; 473 A; 893 C; 739 G; 432 T; 0 other;
SQ
alignment_scores:
Quality: 500.00 Length: 112
Ratio: 5.102 Gaps: 0
Percent Similarity: 87.500 Percent Identity: 76.786
alignment_block:
TGFb3p x AAT15720 ..
Align seg 1/1 to: AAT15720 from: 1 to: 2537
1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
|||||
1676 GCCTGGACACCAACTATTCTTCAGCTCCACGGAGAGAAGAACTGCTGGT 1725
|||||
17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
|||||
1726 GCGGCAGCTGTACATTGACTTCGCAAGGACCTCGGCTGGAAGTGGATCC 1775
|||||
34 iGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
|||||
1776 ACGAGCCCAAGGGCTACCATGCCAATCTCGCTCGGGCCCTGCCCTAC 1825
|||||
51 LeuArgSerAlaAspThrHisSerThrValLeuGlyLeuTyrAsnTh 67
|||||
1826 ATTTGGAGCCTGCAGCAGCAGTACAGCAAGTCTCGCCCTGTACAACCA 1875
|||||
67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
|||||
1876 GCATAACCCGGCGCCTCGCGCGCGCTGCTGCGTCCGCGCAGCGCTGG 1925
|||||
84 lProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
|||||
1926 AGCGGCTGCCCATCGTGTACTAGTGGCGCGCAAGCCCAAGGTGGAGCAG 1975
|||||
101 LeuSerAsnMetValValLysSerCysLysCysSer 112
|||||
1976 CTGTCCAACATGATCGTGGCTCTCTCAAGTGGCAGC 2011
seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1998.DAT:AAV52933
seq_documentation_block:
ID AAV52933 standard; cDNA; 2537 BP.
XX
XX AC AAV52933;
XX 21-DEC-1998 (first entry)
XX Human pre-transforming growth factor-beta 1 cDNA.
XX Transforming growth factor-beta 1; TGF-beta 1; human; ss.
XX Homo sapiens.
XX Key Location/Qualifiers
FH 842..2014
FT CDS
FT /*tag= a
FT 1676..2011
FT mat_peptide
FT /*tag= b
FT 37..113
FT stem_loop
FT /*tag= b
FT /note= "putative stable hairpin loop"
FT 2015..2100
FT misc_feature
FT /*tag= c
FT /note= "GC-rich sequence"
FT polyA_signal
FT 2514..2520

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FT      /*tag= d
PN      US5801231-A.
XX
XX
PD      01-SEP-1998.
XX
XX      22-MAR-1985; 85US-0715142.
XX
PR      13-MAR-1987; 87US-0025423.
PR      22-MAR-1985; 85US-0715142.
PR      04-AUG-1989; 89US-0389929.
PR      04-MAR-1992; 92US-0845893.
PR      05-NOV-1993; 93US-0147364.
PR      30-MAY-1995; 95US-0454466.
XX
PA      (GETH ) GENENTECH INC.
XX
XX      Derynck RNA, Goeddel DV;
XX
DR      WPI; 1998-494840/42.
DR      P-PSDB; AAW78785.
XX
XX      DNA encoding transforming growth factor-beta precursor sequence -
PT      useful for analysis to perform manipulations to increase yield of
PT      recombinant production of the protein
XX
PS      Example 3; Fig 1B 1-3; 26pp; English.
XX
CC      This nucleotide sequence codes for the human transforming growth
CC      factor-beta 1 precursor (preTGF-beta 1, see AAW78785). It is a
CC      composite of overlapping cDNA clones isolated from different cDNA
CC      libraries (placenta, A172 glioblastoma, HT1080 fibroblastoma) using
CC      TGF-beta exon (see AAV52936) restriction fragments as probes.
CC      The 3' region of the sequence was determined using cloned genomic
CC      DNA. The invention relates to the recombinant production of
CC      TGF-beta. Biologically active TGF-beta is defined as being capable
CC      of inducing EGF-potentiated anchorage independent growth of target
CC      cell lines and/or growth inhibition of neoplastic cell lines.
CC      Nucleic acids encoding TGF-beta have been isolated and cloned into
CC      vectors which are replicated in bacteria and expressed in
CC      eukaryotic cells. TGF-beta recovered from transformed cells is
CC      used in known therapeutic applications. TGF-beta nucleic acids are
CC      also useful in diagnosis and identification of TGF-beta clones.
XX
SQ      Sequence 2537 BP; 475 A; 895 C; 736 G; 431 T; 0 other;

alignment_scores:
    Quality: 500.00      Length: 112
    Ratio: 5.102        Gaps: 0
Percent Similarity: 87.500      Percent Identity: 76.786

alignment_block:
TGFB3P x AAV52933      ..
Align seg 1/1 to: AAV52933      from: 1 to: 2537

1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
|||||
1676 GCCTGCACACCAACTATTGCTTCAGCTCCACGAGAGAAGTCTCGCT 1725

17 largProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
|||||
1726 GCGGCAGCTGTACATTGACTTCGCGAAGACCTCGGCTGGAGTGGATCC 1775

34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
|||||
1776 ACAGAGCCCAAGGCTACCAATGCGCAACTTCGCTCGGCGCTGCCCTAC 1825

51 LeuArgSerAlaAspThrHisSerThrValLeuGlyLeuTyrAsnTh 67
::: |||
1826 ATTTGGAGCTGGACACGACGATACAGCAAGGTCTTGGCTGTACACCA 1875

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67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
|||||
1876 GCATAACCCGGCGCTCGCGCGCGCTGCTGCTGCTGCGCGAGCGCTGG 1925

84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
|||||
1926 AGCCCTGCCATCGTACTGCTGCGCGCGCAAGCCCAAGGTGGAGCAG 1975

101 LeuSerAsnMetValValLysSerCysLysCysSer 112
|||||
1976 CTGTCCAACATGATGCTGCGCTCTGCAAGTGCAGC 2011

seq_name: /STD1/gcgdata/geneseq/geneseq/NA1995.DAT:AAAT05876

seq_documentation_block:
ID      AAT05876 standard; cDNA; 2745 BP.
XX
XX      AC      AAT05876;
XX
XX      DT      25-JUN-1996 (first entry)
XX
XX      DE      cDNA encoding transforming growth factor-beta 1.
XX
XX      KW      macrophage inducible nitric oxide synthase; iNOS; constitutive NOS;
KW      interleukin-1-beta; transforming growth factor-beta; TGF-beta; IL1-beta;
KW      nitric oxide production; hypotension; inflammation; septic shock;
KW      treatment; ds.
XX
XX      OS      Mammalian sp.
XX
XX      FH      Key      Location/Qualifiers
XX      CDS      842..2017
XX      FT      /*tag= a
XX      FT      /product= transforming growth factor-beta 1
XX
XX      PN      W09526745-A1.
XX
XX      PD      12-OCT-1995.
XX
XX      PF      05-APR-1994; 94WO-US03705.
XX
XX      PR      05-APR-1994; 94WO-US03705.
XX
XX      PA      (HARD ) HARVARD COLLEGE.
XX
XX      PI      Lee M, Perrella MA;
XX
XX      DR      WPI; 1995-358443/46.
XX      DR      P-PSDB; AAR83054.
XX
XX      PT      Treatment of hypotension, esp. in septic shock - by administering
XX      transforming growth factor-beta e.g. to inhibit inducible nitric
XX      oxide synthase gene transcription
XX
XX      PS      Disclosure; Fig 15; 52pp; English.
XX
XX      CC      The cDNA encodes transforming growth factor-beta 1 (TGF-beta 1) which
XX      has been found to inhibit inducible nitric oxide synthase (iNOS) gene
XX      transcription, esp. in interleukin-1-beta (IL1-beta) stimulated rat
XX      smooth muscle cells, and at a dose which does not inhibit constitutive
XX      NOS. TGF-beta 1 or 2 (AAR83055) or their active fragments, can be used
XX      in the treatment of hypotension, such as that associated with severe
XX      inflammation or septic shock.
XX
XX      SQ      Sequence 2745 BP; 527 A; 938 C; 801 G; 479 T; 0 other;

alignment_scores:
    Quality: 500.00      Length: 112
    Ratio: 5.102        Gaps: 0
Percent Similarity: 87.500      Percent Identity: 76.786

alignment_block:

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TGFB3P x AAT05876 ..
Align seg 1/1 to: AAT05876 from: 1 to: 2745

1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
|||||
1679 GCCCTGGACACCAACTATTGCTTACGCTCCAGCGAGAAAGAACTGCTGCGT 1728

17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTyrIleValh 34
|||||
1729 GCGGAGCTGTACATTGACTTCCGCAAGGACCTCGCTGGAAGTGGATCC 1778

34 lSgluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
|||||
1779 ACGAGCCCAAGGCTACCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1828

51 LeuArgSerAlaAspThrHisSerThrValLeuGlyLeuTyrAsnTh 67
::: ||| ||||| ::||| ||||| ::||| |||||
1829 ATTTGGAGCCTGGACACGACGATACAGCAAGGTCTCTGCGCCTGTACAACCA 1878

67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
|||||
1879 GCATTAACCGGCGCTCGGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1928

84 lProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
|||||
1929 AGCGCTGCCCATCGTGTACTACGTGGCGCGCAAGCCCAAGGTGGAGCAG 1978

101 LeuSerAsnMetValValLysSerCysLysCysSer 112
|||||
1979 CTGTCCAACATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2014

seq_name: /SIDS1/gcgdata/geneseq/geneseq/NA1996.DAT:AAT16516
seq_documentation_block:
ID AAT16516 standard; DNA; 3541 BP.
XX
AC AAT16516;
XX
DT 01-OCT-1996 (first entry)
XX
DE Collagen A1/TGF-beta-1 chimeric gene.
XX
KW Transforming growth factor; TGF-beta-1; collagen IA; osteogenesis;
KW bone formation; tissue repair; ds.
XX
OS Synthetic.
XX
FH Key
FT CDS
FT
FT
FT misc_difference 2679
FT /tag= a
FT /product= collagen IA/TGF-beta-1 fusion protein
FT
FT /tag= b
FT /note= "base 2679 is not identified in the
FT specification"
FT
FT misc_difference 2688
FT /tag= c
FT /note= "base 2688 is not identified in the
FT specification"
FT
FT
FT CA2151547-A.
XX
XX 11-DEC-1995.
XX
XX 12-JUN-1995; 95CA-2151547.
XX
XX 10-JUN-1994; 94US-0259263.
XX
XX (USSU ) US SURGICAL CORP.
XX
XX Espino P, Gruskin EA;
XX

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WPI; 1996-140144/15.
P-PSDB; AAR89470.

Chimaeric DNA encoding protein contg. extracellular matrix protein domain - and cellular regulatory factor domain, partic. useful as osteogenic agents, also related vectors, transformed cells and chimaeric proteins.

Disclosure; Fig 2; 59pp; English.

A chimeric gene (AAT16516) codes for a fusion protein (AAR89470) between the helical region of human collagen I(a) and human transforming growth factor beta-1 (TGF-beta-1). The collagen moiety was cloned from human fibroblast AG02261A cells by PCR amplification. The construct was inserted into a pMal vector for expression in E. coli. The fusion protein provides sustained release and delivery of TGF-beta-1 to a target tissue. The TGF increases efficacy of the body's normal soft tissue repair response and also induces osteogenesis.

Sequence 3541 BP; 504 A; 1143 C; 1188 G; 704 T; 2 other;

alignment_scores:
Quality: 500.00 Length: 112
Ratio: 5.102 Gaps: 0
Percent Similarity: 87.500 Percent Identity: 76.786

alignment_block:
TGFB3P x AAT16516 ..

Align seg 1/1 to: AAT16516 from: 1 to: 3541

1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
|||||
3197 GCCCTGGACACCAACTATTGCTTACGCTCCAGCGAGAAAGAACTGCTGCGT 3246

17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTyrIleValh 34
|||||
3247 GCGGAGCTGTACATTGACTTCCGCAAGGACCTCGCTGGAAGTGGATCC 3296

34 lSgluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
|||||
3297 ACGAGCCCAAGGCTACCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3346

51 LeuArgSerAlaAspThrHisSerThrValLeuGlyLeuTyrAsnTh 67
::: ||| ||||| ::||| ||||| ::||| |||||
3347 ATTTGGAGCCTGGACACGACGATACAGCAAGGTCTCTGCGCCTGTACAACCA 3396

67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
|||||
3397 GCATAACCGGCGCTCGGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3446

84 lProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
|||||
3447 AGCGCTGCCCATCGTGTACTACGTGGCGCGCAAGCCCAAGGTGGAGCAG 3496

101 LeuSerAsnMetValValLysSerCysLysCysSer 112
|||||
3497 CTGTCCAACATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3532

seq_name: /SIDS1/gcgdata/geneseq/geneseq/NA2000.DAT:AAAL2498

seq_documentation_block:
ID AAAL2498 standard; cDNA; 3541 BP.
XX
XX
AC AAAL2498;
XX
DT 25-JUL-2000 (first entry)
XX
DE cDNA encoding a chimeric collagen I (alpha1)/TGF-beta1 protein.
XX
KW Extracellular matrix protein; self aggregation; hydroxylated proline;

trans-4-hydroxyproline; 3-hydroxyproline; recombinant protein production; collagen; fibronectin; post translational hydroxylation; ss. transforming growth factor-beta1; TGF-beta1; chimera; ss.

Chimeric - Homo sapiens.
Chimeric - Unidentified.

Key Location/Qualifiers
CDS 20..3535
FT /*tag= a
FT /product= "chimeric collagen 1 (alpha1)/TGF-beta1
FT protein"
FT /transl_except= (pos: 2591..2593, aa: Gly)

PN Ep992586-A2.

PD 12-APR-2000.

XX 07-OCT-1999; 99EP-0119184.

XX 09-OCT-1998; 98US-0169768.

XX (USSU) US SURGICAL CORP.

XX Gruskin EA, Buechter DD, Zhang G, Connolly K;

XX WPI; 2000-259138/23.

XX P-PSDB; AAY84538.

XX Production of extracellular matrix proteins containing

PT 4-trans-hydroxyproline results in native self aggregating proteins,

PT useful on medical implants -

PS Disclosure; Fig 16A-C; 260pp; English.

XX The specification describes a method for producing an extracellular matrix protein or its fragment. The extracellular matrix protein is capable of self aggregating in a cell which does not ordinarily hydroxylated prolines. The method comprises optimising a nucleic acid sequence for expression in the cell by substitution of codons preferred by that cell for naturally occurring codons not preferred by the cell; incorporating the nucleic acid sequence into the cell; and contacting the cell with a hypertonic growth medium containing at least one amino acid, selected from the group consisting of trans-4-hydroxyproline and 3-hydroxyproline to allow at least one of the amino acids to be assimilated into the cell and incorporated into the extracellular matrix protein. The method may be used to make host cells assimilate and incorporate trans-4-hydroxyproline into proteins. This is especially useful in the recombinant production of proteins such as collagen, fibronectin and fibronectin whose ability to self aggregate and produce functional proteins depends on the post translational hydroxylation of proline. The method is also useful in studying the structure and function of polypeptides which do not normally contain trans-4-hydroxyproline. The present sequence encodes a chimeric collagen 1 (alpha1)/transforming growth factor-beta1 (TGF-beta1) protein, which may be produced using the method of the invention.

XX Sequence 3541 BP; 504 A; 1145 C; 1188 G; 704 T; 0 other;

alignment_scores:
Quality: 500.00 Length: 112
Ratio: 5.102 Gaps: 0
Percent Similarity: 87.500 Percent Identity: 76.786

alignment_block:

TGFB3P x AAAL2498 ..

Align seg 1/1 to: AAAL2498 from: 1 to: 3541

1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluAsnCysCysVa 17
|||||
3197 GCCTGGACCACTATTCTCAGCTCCAGGAGAACTCTCGCT 3246

17 lArgProLeuTyrIleAspPheArgGlnAsnLeuGlyTyrLysTrpValH 34
|||||
3247 GCGGAGCTGTACTTGGCTCCGCAAGACCTCGGCTGGAGTGATCC 3296
34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
|||||
3297 ACGAGCCCAAGGGCTACCATGCCAACTTCTGCTCGGGCCCTGCCCTAC 3346
51 LeuArgSerAlaAspThrHisSerThrValLeuGlyLeuTyrAsnTh 67
::: ||| ||||| ::||| ||||| ::|||
3347 ATTTGGAGCTGGACACGAGTACAGCAAGTCTGCGCTGTACACCA 3396
67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAsnLeuG 84
|||||
3397 GCATAACCGCGCGCTCGGGCGCGCTGCTGCGTCCGCGCAGCGCTGG 3446
84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
|||||
3447 AGCCGCTGCCATCGTACTACTGTTGGCGCAAGCCCAAGGTGGAGCAG 3496
101 LeuSerAsnMetValLysSerCysLysCysSer 112
|||||
3497 CTGTCCAACATGATGCTGCGCTCTCAAGTGCAGC 3532

seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1994.DAT:AAQ55624

seq_documentation_block:

ID AAQ55624 standard; DNA; 4105 BP.

XX AAQ55624;

XX 12-JUL-1994 (first entry)

XX TGFbeta1 5'-UTR-CDS-3'-UTR.

XX Transforming Growth Factor beta 1; TGF; non-coding region;
KW coding region; resonance; interaction; optimisation; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

FT mRNA 1..4105
FT /*tag= a
FT /note= "the inventor has used T instead of U in
FT the TGFbeta1 full-length mRNA"

FT 5'UTR 1..2202

FT enhancer /*tag= b

FT misc_RNA 1..230

FT misc_RNA 632..910

FT misc_RNA 911..1039

FT CDS 2203..3378

FT 3'UTR /product= TGFbeta1

FT /note= "p region"

FT /note= "N1 region"

FT /note= "N2 region"

FT /note= "the N residues at positions 3464 and

FT 3465 each appear as the letter F in

FT the specification"

XX FR26292594-A.

XX 24-DEC-1993.

XX 22-JUN-1992; 92FR-0007571.

```

KW 22-JUN-1992; 92FR-0007571.
XX (PERE/) PEREZ J.
XX Perez J;
XX WPI; 1994-028256/04.
XX Application of optimised gene expression - for scientific,
XX industrial and therapeutic purposes
XX Disclosure; Fig 1; 110pp; French.
XX The TGFbeta1 mRNA was divided into 3 regions (i.e. 5'-UTR, CDS and
XX 3'-UTR) for various "perturbation" experiments. The relative order
XX of the 3 regions was altered, e.g. the 3'-UTR was positioned
XX upstream of the CDS and the 5'-UTR was positioned downstream of the
XX CDS. The experiments showed that interactions between coding and non-
XX coding regions are destroyed by such perturbations.
XX Sequence 4105 BP; 744 A; 1407 C; 1201 G; 751 T; 2 other;

alignment_scores:
    Quality: 500.00      Length: 112
    Ratio: 5.102        Gaps: 0
    Percent Similarity: 87.500    Percent Identity: 76.786

alignment_block:
TGFB3P x AAQ55624 ..

Align seg 1/1 to: AAQ55624 from: 1 to: 4105
1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
3040 GCGCTGGACCAACATATTGCTTCAGCTCCACGGAGAAGAACTGCTGCGT 3089
17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTyrLysTrpValH 34
3090 GCGGAGCTGTACATTGACTTCGCGAAGCACTCGGCTGGAAGTGGATCC 3139
34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
3140 ACGAGGCCAAGGCTACCATGCCAATCTGCTCGGCGCCCTGCCCTAC 3189
51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
3190 ATTTGGAGCTGGACACGACGATGACAGCAAGGTCTGCGCTGTACAACCA 3239
67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
3240 GCATAACCGCGCGCTGCGCGCGCGTGTGCTGCGTGCAGCGCGCTGG 3289
84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
3290 AGCGCTGCCCATCGTGTACTAGTGGCGGCAAGCCCAAGGTGGAGCAG 3339
101 LeuSerAsnMetValValLysSerCysLysCysSer 112
3340 CTGTCCAACATGATGCTGGCGCTCCTCAAGTGCAGC 3375

seq_name: /SIDS1/cgdata/geneseq/geneseq/NA1993.DAT:AAQ41604
seq_documentation_block:
ID_AAQ41604 standard; cDNA; 336 BP.
XX AC
XX AAQ41604;
XX
XX 26-AUG-1993 (first entry)
XX
XX Transforming Growth Factor-beta2(44/45)beta1 hybrid.
XX

```

```

KW htGF-beta1; htGF-beta2; hybrid protein; wound healing;
XX cancer treatment; bone repair; growth regulation; ss.
XX Homo sapiens.
XX OS
XX FH Location/Qualifiers
XX mat_peptide 1..336
XX /*tag= a
XX /note= "TGF-beta2=1-132, TGF-beta1=133-336"
XX EP542679-A.
XX PN
XX 19-MAY-1993.
XX PD
XX 03-NOV-1992; 92EP-0810845.
XX PR 11-NOV-1991; 91EP-0810870.
XX XX (CIBA ) CIBA GEIGY AG.
XX PA
XX McMaster GK, Cox D, Cerletti N, Kuhla J;
XX WPI: 1993-161126/20.
XX P-PSDB; AAR39643.
XX New hybrid transforming growth factor-beta molecules - comprise
XX portions of mature TGF-beta isoforms; useful as wound healants,
XX cardioprotective, antiinflammatory and immunosuppressive agents etc.
XX PS Claim 8; Page 28; 48pp; English.
XX CC The invention covers hybrid TGF-beta molecules consisting of parts
XX of the human isoforms TGF-beta1, TGF-beta2 and TGF-beta3 (see AAQ41599,
XX AAQ41600 and AAQ41601, respectively). The hinge points between parts
XX derived from different parent isoforms are pref. between amino acids
XX 44 and 45, 56 and 57, 79 and 80, 90 and 91, or 22 and 23. Of the 30
XX possible hybrids using these hinge points and one part each
XX from two of the isoforms, 6 are preferred including the hybrid
XX TGF-beta2(44/45)beta1. The hybrid molecules promote cell migration,
XX inhibit the growth of A375 melanoma cells, accelerate the healing of
XX partial-thickness burn wounds and full-thickness incisional wounds and
XX increase formation of fibrous granular tissue.
XX See AAQ41602-Q41607 for the most pref. hybrids.
XX SQ Sequence 336 BP; 71 A; 99 C; 97 G; 69 T; 0 other;

alignment_scores:
    Quality: 496.00      Length: 112
    Ratio: 5.010        Gaps: 0
    Percent Similarity: 88.393    Percent Identity: 75.000

alignment_block:
TGFB3P x AAQ41604 ..

Align seg 1/1 to: AAQ41604 from: 1 to: 336
1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
1 GCTTTGGATCGGCGCTATTGCTTTAGAAATGTCAGGATAATTGCTGCT 50
17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTyrLysTrpValH 34
51 ACGTCCACTTTACATTGATTTCAAGAGGGATCTAGGGTGGAAATGGATAC 100
34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
101 ACGAACCCAAAGGGTACAATGCCAATCTGCGCTCGGCGCTGCCCTAC 150
51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
151 ATTTGGAGCTGGACACGACGATACAGCAAGGTCTGCGCTGTACAACCA 200

```

```

67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
||||| |||||||:||||| ||||| |||||
201 GCATAACCCGGCGCGCTCGCGCGCGTCTGCTGCTGCCGCGCGCTGG 250
||||| |||||||:||||| ||||| |||||
84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
||||| |||||||:||||| ||||| |||||
251 AGCCGCTGCCCATCGGTACTACGTGGCGCGCAAGCCCAAGGTGGAGCAG 300
||||| |||||||:||||| ||||| |||||
101 LeuSerAsnMetValValLysSerCysLysCysSer 112
||||| |||||||:||||| ||||| |||||
301 CTGTCCAACATGATCGTGGCTCTGCAAGTGCAGC 336
||||| |||||||:||||| ||||| |||||

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seq_name: /SIDSI/gcgdata/geneseq/geneseqn/NA1993.DAT:AAQ41599

seq_documentation_block:

ID_ AAQ41599 standard; cDNA; 345 BP.

XX AAQ41599;

XX 26-AUG-1993 (first entry)

XX Mature human Transforming Growth Factor-beta1.

XX hTGF-beta1; hybrid protein; wound healing; cancer treatment;
KW bone repair; growth regulation; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

FT mat_peptide 1..336

FT /*tag= a

XX EP542679-A.

XX PN 19-MAY-1993.

XX 03-NOV-1992; 92EP-0810845.

XX 11-NOV-1991; 91EP-0810870.

XX (CIBA) CIBA GEIGY AG.

XX McMaster GK, Cox D, Cerletti N, Kuhla J;

XX WPI; 1993-161126/20.

XX P-PSDB; AAR39638.

XX New hybrid transforming growth factor-beta molecules - comprise
PT portions of mature TGF-beta isoforms; useful as wound healants,
PT cardioprotective, antiinflammatory and immunosuppressive agents etc.

XX Claim 4; Page 21-22; 48pp; English.

XX The invention covers hybrid TGF-beta molecules consisting of parts
CC of the human isoforms TGF-beta1, TGF-beta2 and TGF-beta3 (see AAQ41599,
CC AAQ41600 and AAQ41601, respectively). The hinge points between parts
CC derived from different parent isoforms are pref. between amino acids
CC 44 and 45, 56 and 57, 79 and 80, 90 and 91, or 22 and 23. The hybrid
CC molecules promote cell migration, inhibit the growth of A375
CC melanoma cells, accelerate the healing of partial-thickness burn
CC wounds and full-thickness incisional wounds and increase formation
CC of fibrous granular tissue. See e.g. AAQ41602-Q41607 for pref. hybrids.

XX Sequence 345 BP; 68 A; 115 C; 102 G; 60 T; 0 other;

alignment_scores:

Quality: 496.00 Length: 111
Ratio: 5.113 Gaps: 0
Percent Similarity: 87.387 Percent Identity: 76.577

alignment_block:

TGFB3P x AAQ41599 ..

Align seg 1/1 to: AAQ41599 from: 1 to: 345

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1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGlnAsnCysCysVa 17
||||| |||||||:||||| ||||| |||||
1 GCCCTGGACACCACTATTGCTTCAGCTCCACGAGAGAACTGCTGCGT 50
||||| |||||||:||||| ||||| |||||
17 largProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
||||| |||||||:||||| ||||| |||||
51 CGGCAGCTGTACATTGACTTCCGCAAGACCTCGCTGGAAGTGGATCC 100
||||| |||||||:||||| ||||| |||||
34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
||||| |||||||:||||| ||||| |||||
101 ACGAGCCCAAGGGCTACCATGCCAACTTCTGCTCGGGCCCTGCCCTAC 150
||||| |||||||:||||| ||||| |||||
51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnH 67
::: ||||| |||||||:||||| ||||| |||||
151 ATTGGAGCCTGGACACGACAGTACAGCAAGGTCTGGGCCCTGTACAA 200
||||| |||||||:||||| ||||| |||||
67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
||||| |||||||:||||| ||||| |||||
201 GCATAACCCGGCGCGCTCGCGCGCGTCTGCTGCTGCCGCGCGCTGG 250
||||| |||||||:||||| ||||| |||||
84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
||||| |||||||:||||| ||||| |||||
251 AGCCGCTGCCCATCGGTACTACGTGGCGCGCAAGCCCAAGGTGGAGCAG 300
||||| |||||||:||||| ||||| |||||
101 LeuSerAsnMetValValLysSerCysLysCysCys 111
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301 CTGTCCAACATGATCGTGGCTCTGCAAGTGC 333
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seq_name: /SIDSI/gcgdata/geneseq/geneseqn/NA1991.DAT:AAQ11993

seq_documentation_block:

ID_ AAQ11993 standard; cDNA; 339 BP.

XX AAQ11993;

XX 29-AUG-1991 (first entry)

XX Transforming Growth Factor beta 1.

XX TGF-beta1; biologically active protein production; ss.

XX Homo sapiens.

XX EP433225-A.

XX 19-JUN-1991.

XX 27-NOV-1990; 90EP-0810922.

XX 06-DEC-1989; 89GB-0027546.

XX (CIBA) CIBA GEIGY AG.

XX Cerletti N, McMaster GK, Cox D, Schmitz A, Meyhack B;

XX WPI; 1991-180005/25.

XX P-PSDB; AAR12402.

XX Prodn. of Transforming Growth Factor type-beta-like proteins - by
PT subjecting denatured monomeric form to refolding conditions

XX Disclosure; Page 27; 35pp; English.

XX TGF-beta1 is one example of a novel TGF-beta produced as a dimeric,
CC biologically active protein using the method of the invention.
CC This coding sequence was isolated from the CI-215 human glioma cell
CC line. It was incorporated into an appropriate vector to transform
CC Saccharomyces cerevisiae or E.coli. Monomeric TGF-beta1 was purified,
CC denatured and dissolved in 140ml 50mM Tris/HCl pH8. 1M NaCl, 5mM EDTA,
CC 2mM reduced glutathione, 1mM oxidised glutathione and 33mM Chaps.

CC After 72 hrs at 4 deg C, pH was adjusted to 2.5 and the mixture was
CC conc. 10 times. The conc. soln was diluted to the original vol. with
CC 10mM HCl and conc to a final vol of 10 ml. The supernatant from
CC centrifugation at 5000g for 30 min contained disulphide-linked dimeric
CC TGF-beta1.

SQ Sequence 339 BP; 66 A; 113 C; 101 G; 59 T; 0 other;

alignment_scores:		
Quality:	494.00	Length: 112
Ratio:	5.041	Gaps: 0
Percent Similarity:	87.500	Percent Identity: 75.893

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alignment_block:
  TGF3P x AAQ11993  ..
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Align seg 1/1 to: AAQ11993 from: 1 to: 339

1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluAsnCysCysVa 17
 1 GCGCTGGACACCAACTATTGCTTCAGCTCCAGGAGAAGAACTGTCGT 50
 17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
 51 GCGGCGAGCTGTACATTGACTTCGCAAGGAGCCTCGCTGGAAGTGGATCC 100
 34 iSGluProLysGlyTyrTyrAlaAsnPhcCysSerGlyProCysProTyr 50
 101 ACGAGCCCAAGGGCTACCATGCCAACCTCTGCCTCGGGCCCTGCCCCAC 150
 51 LeuArgSerAlaAspThrHisSerThrValLeuGlyLeuTyrAsnTh 67
 151 ATTGGAGCCTGGACACGCAGTACAGCAAGTCTCTGGCCCTGTACAACCA 200
 67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
 201 GCATAAGCCGGCGCCCTCGCGGGCGCGTGTGGTGCAGGCGCGCTGG 250
 84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
 251 AGCGCGTGGCCATCGTGTACTACTGTGGGCGCCAGCCCAAGGTGGAGCAG 300
 101 LeuSerAsnMetValValLysSerCysLysCysSer 112
 301 CTGTCCAACATGATCGTCGCTCTCTGCAAGTGCAGC 336

seq_name: /SIDS1/gcgdata/geneseq/geneseq/NA1992.DAT:AAQ29178

seq_documentation_block:

ID	AAQ29178 standard; DNA; 1565 BP.
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8	8
9	9
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11	11
12	12
13	13
14	14
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93	93
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97	97
98	98
99	99
100	100

AC AAQ29178; .

DT 10-MAR-1993 (first entry)

DE TGF-beta 1.

Transforming growth factor; TGF; TGF-beta; TGF-5 beta; simian; Simian virus 40; SV40; expression vector; Chinese Hamster ovary; CHO; vascular endothelial cell; TGF-beta 1; TGF-beta 2; ss.

OS Homo sapiens.

FH	Key	Location/Qualifiers
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FT	sig_peptide	269..355
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3	1	1
4	1	1
5	1	1
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100	1	1

FT /note= "Signal peptide, pre-pro-protein"

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FT precursor_RNA 356..1105
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FT      /*tag= b
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FUT mat peptide /note= "Pro-protein"
FUT mat peptide 1106 1438

```

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FT mat_peptide
1106..1438
/*tag= c
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FI
/day= C

20

XX	WO9216228-A.		
PN			
XX	01-OCT-1992.		
XX			
XX	13-MAR-1992;	92WO-US01993.	
XX			
XX	14-MAR-1991;	91US-0669171.	
XX			
XX	(BRIM) BRISTOL-MYERS SQUIBB CO.		
XX			
XX	Madisen L, Merwin J, Purchio AF;		
PI			
XX	WPI; 1992-348938/42.		
DR			
DR	P-PSDB; AAR29657.		
XX			
XX	Compsn. comprising new chimeric TGF-B (TGF-beta 1-beta 2) -		
PT	inhibits proliferation of vascular endothelial cells, useful		
PT	treating cancer and to promote wound healing		
XX			
XX	Disclosure; Fig 1; 45pp; English.		
PS			
XX			
CC	The sequence given encodes the human transforming growth fa		
CC	(TGF)-beta 1. This was used within the scope of the invent		
CC	compare to a simian TGF hybrid termed TGF-beta 1/beta 2 (or		
CC	beta) (see also AAQ29177). The chimeric DNA sequence coul		
CC	under the control of Simian virus 40 (SV40) expression regu		
CC	region within an expression vector and used to transfect Ch		
CC	Hamster ovary (CHO) cells. CHO transfectants can be seen t		
CC	and secrete high levels of mature TGF-5 beta. TGF-5 beta i		
CC	effects on the proliferation of vascular endothelial cells		
CC	to those produced by TGF-beta 1.		
XX			
XX	Sequence 1565 BP; 300 A; 553 C; 439 G; 273 T; 0 other;		
SQ			

alignment_scores:

Quality: 489.00

Ratio:	4.990	Gaps:
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Percent Similarity: 87.500 Percent Identity: 75.893

alignment_block:

TGFβ3P x AAQ29178

Align seg 1/1 to: AAQ29178 from: 1 to: 1565

1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluAsnCysCysVa 17
 1106 GCCCTGGACACCAACTATTGCTTCAGAAATGTGCAGATAAATGCTGCCCT 1155
 17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTyrLysTyrValH 34
 1156 ACCTCCGCTTTACATTGATTC.....GATCTAGGGTGGAAATGGATCC 1199
 34 lsgluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
 1200 ACGAGCCCAAGGCTACCATGCCAACTTCTGCCTCGGGCCCTGCCCTAC 1249
 51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
 1250 ATTTGGAGCTGGACGCGACGACAGTACAGCAAGGTCTGTGCCCTGTACAAACCA 1299
 67 rLeuAsnProGluAlaSerAlaSerProCysValProGlnAspLeuG 84
 1300 GCATAACCGGGCGGCTCGGGCGGCGGTGCTGCTGCGCGCAGGGCGCTGG 1349
 84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
 1350 AGCCGCTGCCCATCGTGTACTACGTGGGCGCGCAAGCCCAAGGTGGAGCAG 1399
 101 LeuSerAsnMetValValLysSerCysLysCysSer 112
 1400 CTGTGCCAACATCATCGTGGCGCTCCGTCAAGTGCAGC 1435

```
seq_name: /SIDS1/gcgdata/geneseq/NA1988.DAT: AAN81084
seq_documentation_block:
ID   AAN81084 standard; cDNA; 1560 BP.
XX
AC   AAN81084;
XX
DT   09-OCT-1990 (first entry)
XX
DE   Coding sequence of simian transforming growth factor-beta 1.
XX
KW   Transforming growth factor-beta 1; tumour treatment; ss cDNA.
XX
OS   Cercopithecus aethiops.
XX
FH   Key Location/Qualifiers
FT   CDS 261..1433
FT     /*tag= a
FT   sig_peptide 282..323
FT     /*tag= b
FT   mat_peptide 1095..1433
FT     /*tag= c
XX
PN   EP293785-A.
XX
PD   07-DEC-1988.
XX
PF   27-MAY-1988; 88EP-0108528.
XX
PR   29-MAY-1987; 87US-0055662.
PR   25-JAN-1988; 88US-0147842.
XX
PA   (ONCO-) ONCOGEN.
XX
PI   Purchio AF, Gentry L, Twardzik D;
XX
DR   WPI; 1988-347488/49.
DR   P-PSDB; AAP80647.
XX
PT   Prodn. of simian transforming growth factor beta-1 - by culturing
PT   transfected eucaryotic cells, and new precursor proteins, useful for
PT   treating tumours.
XX
PS   Disclosure; ; pp; English.
XX
CC   The cDNA is prep'd. from African green monkey cell line BSC-40 and is
CC   expressed in eukaryotic cells in plasmid pSV2. There is 100% homology
CC   between mature simian and human TGF-beta 1. The plasmid also contains
CC   the SV40 promoter and a selection marker, esp. DHFR.
XX
SQ   Sequence 1560 BP; 301 A; 547 C; 445 G; 267 T; 0 other;

alignment_scores:
Quality: 487.00 Length: 112
Ratio: 5.021 Gaps: 0
Percent Similarity: 86.607 Percent Identity: 75.893
alignment_block:
TGFB3P x AAN81084 ..
Align seg 1/1 to: AAN81084 from: 1 to: 1560
1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
|||||
1095 GCCTGGACCACTACTGCTTACGCTCCACGAGAGAACTGCTGCGT 1144
|||||
17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
|||||
1145 GCGGCAGCTGTATATGACTTCGCGAAGGACCTCGGCTGGAAGTGATCC 1194
|||||
34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
```

```
|||||
1195 ACGAGCCCAAGGGTACCATGCCAACTTCTGCCTGGGGCCCTGTCCTAC 1244
XX
51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
::: ||| ||| ::||| |||:::|||||
1245 ATTTGGAGCTGGACGACGACGTACAGCAAGGTCCTGGCCCTGTACAACCA 1294
XX
67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
||||| |||||||:::||||| ||||||| |||
1295 GCATAAACCCGGCGCTCGGGGGCGCGCTGCTGCGCGAGGCGCTGG 1344
XX
84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
||||| |||:::||||| ||||||| ||||||| |||
1345 AGCCACTGCCCATGCTGTACTACGTGGGCGCGCAAGCCAAAGTGGAGCAG 1394
XX
101 LeuSerAsnMetValValLysSerCysLysCysSer 112
||||| |||||||:::||||| |||||||
1395 CTGTCCAAACATGATCGTGGCGCTCCTGGAATGCAGC 1430
XX
seq_name: /SIDS1/gcgdata/geneseq/NA1990.DAT: AAQ03508
seq_documentation_block:
ID   AAQ03508 standard; DNA; 1560 BP.
XX
AC   AAQ03508;
XX
DT   14-AUG-1990 (first entry)
XX
DE   Simian Transforming growth factor - Beta1.
XX
KW   HIV; AIDS; SIV; vaccine; AZT; CD4; cytokines; growth
KW   factors; ds.
XX
FH   Key Location/Qualifiers
FT   CDS 267..1437
FT     /*tag= a
FT   mat_peptide 1103..1437
FT     /*tag= b
XX
PN   EP356935-A.
XX
PD   07-MAR-1990.
XX
PF   25-AUG-1989; 89EP-0115719.
XX
PR   25-AUG-1988; 88US-0236698.
XX
PA   (ONCO-) ONCOGEN LTD PARTNER.
XX
PI   Brankovan V, Lioubin M, Purchio A;
XX
DR   WPI; 1990-068723/10.
DR   P-PSDB; AAR05663.
XX
PT   Compens. contg. transforming growth factor beta -
PT   used for inhibitions of HIV infection and replication in vivo.
XX
CC   TGF-beta may be used in vivo to prevent formation of synctia and
CC   inhibit HIV infection. TGF may also be used with other HIV treatments
CC   (AZT, soluble CD4 etc.).
XX
PS   Disclosure; Fig 1; 20pp; English.
XX
SQ   Sequence 1560 BP; 301 A; 547 C; 445 G; 267 T; 0 other;

alignment_scores:
Quality: 487.00 Length: 112
Ratio: 5.021 Gaps: 0
Percent Similarity: 86.607 Percent Identity: 75.893
alignment_block:
TGFB3P x AAQ03508 ..
```


89 euTyrTyrValGlyArgThrProLysValGluGlnLeuSerAsnMetVal 105
1579 TTTATATGTTGGCGCACTGTAAGTAGAGCAGCTCTTAATATGGTG 1628
106 ValLysSerCysLysCysSer 112
1629 CTAAGGCTTGCAACTGCAGC 1649

seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1991.DAT:AAQ11774

seq_documentation_block:

ID_AAQ11774 standard; DNA; 852 BP.

AC_AAQ11774;

XX 23-JUL-1991 (first entry)

XX Encodes Fb-Fb-truncated (6 Cys)-TGF-beta.

XX Transforming Growth Factor beta; AIDS; ss.

XX Synthetic.

XX Key Location/Qualifiers

FT sig_peptide 1..180

FT /*tag= a

FT /note= "modified trp-LE leader sequence"

FT 181..375

FT /*tag= b

FT /product= fragment B of Staphylococcal Protein A

FT /note= "directly linked to a second Fb fragment"

FT 376..552

FT /*tag= c

FT /product= Fragment B of Staphylococcal Protein A

FT misc_structure 553..564

FT /*tag= d

FT /product= hinge region

FT 565..843

FT /*tag= e

FT /product= truncated TGF-beta containing 6 x Cys

XX WO9105565-A.

XX 02-MAY-1991.

XX 18-OCT-1990; 90WO-US06006.

XX 18-OCT-1989; 89US-0422962.

XX (CREA-) CREATIVE BIOMOLECUL.

XX Cohen CM;

XX WPI; 1991-148530/20.

XX P-PSDB; AAR11956.

XX Recombinant truncated transforming growth factor-beta analogues -
XX capable of inducing an anti-proliferative effect in mammalian
XX epithelial cells in vitro

XX Claim 23; Fig 2; 42pp; English.

XX This synthetic gene was designed based on reported sequence data,
XX codons inferred from known amino acid sequences and observations of
XX partial homology with known genes of the TGF-beta family. It was
XX assembled from chemically synthesised oligonucleotides and can be
XX expressed in prokaryotic host cells. The truncated 6 Cys TGF-beta
XX protein is cleaved from the Fb-Fb domain at the hinge region to give
XX the truncated product.
XX See also AAQ11775, AAR11942-7 and AAR11954.

XX Sequence 852 BP; 216 A; 222 C; 225 G; 189 T; 0 other;

alignment_scores:

Quality: 412.00 Length: 93

Ratio: 5.024 Gaps: 0

Percent Similarity: 88.172 Percent Identity: 76.344

alignment_block:

TGFB3P x AAQ11774 ..

Align seg 1/1 to: AAQ11774 from: 1 to: 852

20 LeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValHisGluPr 36

|||||

565 CTGTACATCGATTCCGTTAAAGACCTGGGTTGGAAGTGGATTCATGAACC 614

|||||

36 oLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyrIleuArgS 53

|||||

615 TAAGGGTTACCATGCCAACTCTGCGCTGGGCCCTTGTCCTACATCTGGT 664

|||||

53 erAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnThrLeuAsn 69

|||||

665 CTCTGGATACCCAGTACTCCAAAGTGCTGCTGTGACATCAGCATAAC 714

|||||

70 ProGluAlaSerAlaSerProCysCysValProGlnAspLeuGluProLe 86

|||||

715 CCGGGGGCTAGCGCAGCTCGTGTGTTCCACAGGCCCTTGGAAACCGCT 764

|||||

86 uThrIleLeuTyrTyrValGlyArgThrProLysValGluGlnLeuSerA 103

|||||

765 GCGGATCGTCTATTACGTGCGCGCTAAGCCCTAAGGTTGAACAGCTGCTA 814

|||||

103 snMetValValLysSerCysLysCysSer 112

|||||

815 ACGTGATGTGCGCAGTTGCCAAGTGCTCT 843

|||||

seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1991.DAT:AAQ11775

seq_documentation_block:

ID_AAQ11775 standard; DNA; 817 BP.

XX AC_AAQ11775;

XX 23-JUL-1991 (first entry)

XX Encodes Fb-Fb-truncated " (8 Cys) "-TGF-beta.

XX Transforming Growth Factor beta; AIDS; ss.

XX Synthetic.

XX Key Location/Qualifiers

FT sig_peptide 1..180

FT /*tag= a

FT /note= "modified trp-LE leader sequence"

FT 181..375

FT /*tag= b

FT /product= fragment B of Staphylococcal Protein A

FT /note= "directly linked to a second Fb fragment"

FT 376..552

FT /*tag= c

FT /product= Fragment B of Staphylococcal Protein A

FT misc_structure 553..564

FT /*tag= d

FT /product= hinge region

FT 565..843

FT /*tag= e

FT /product= truncated TGF-beta containing 8 x Cys

FT /note= "only contains 6 Cys residues; sequence

XX disclosed in specification omits 50 bases"

XX WO9105565-A.

XX

```

PD 02-MAY-1991.
XX
PF 18-OCT-1990; 90WO-US06006.
XX
PR 18-OCT-1989; 89US-0422962.
XX
PA (CREA-) CREATIVE BIOMOLECUL.
XX
PI Cohen CM;
XX
XX WPI; 1991-148530/20.
XX P-PSDB; AAR11957.
XX
PT Recombinant truncated transforming growth factor-beta analogues -
PT capable of inducing an anti-proliferative effect in mammalian
PT epithelial cells in vitro
XX
XX Claim 23; Fig 2B; 42pp; English.
XX
XX This synthetic gene was designed based on reported sequence data,
XX codons inferred from known amino acid sequences and observations of
XX partial homology with known genes of the TGF-beta family. It was
XX assembled from chemically synthesised oligonucleotides and can be
XX expressed in prokaryotic host cells. The sequence is that given in
XX the specification, however, 50 bases should be inserted between
XX nucleotides 600 and 601 of this sequence; the two "missing" Cys
XX codons are presumably contained in the omitted sequence. The
XX truncated TGF-beta protein is cleaved from the Fb-Fb domain at the
XX hinge region to give the truncated product.
XX See also AAQ11774, AAR11942-7 and AAR11954.
XX
SQ Sequence 817 BP; 207 A; 213 C; 219 G; 178 T; 0 other;

alignment_scores:
    Quality: 302.50      Length: 99
    Ratio: 4.321        Gaps: 2
    Percent Similarity: 70.707      Percent Identity: 60.606

alignment_block:
  TGF3P x AAQ11775  ..
  Align seg 1/1 to: AAQ11775 from: 1 to: 817

15 CysValArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrp.L 31
565 TGTCTGGTGGTGCAGCTGATACATCGATTTCCTAAAGACCTGGGTGGAA 614
31 ysrpValHisGluProLysGlyTyrTyrAlaAsnPheCysSerGlyPro 47
615 GT.....
48 CysProTyrLeuArgSerAlaAspThrThrHisSerThrValLeuGlyLe 64
617 ...CCGTACATCTGGTCTCTGGATACCCAGTACTCCAAAGTCTGGTCT 663
64 uTyrAsnThrLeuAsnProGluAlaSerAlaSerProCysCysValProG 81
664 GTACAATCAGCATAAACCGGGGGCTAGCGCAGCTCCGTGCTGTTCAC 713
81 InAspLeuGluProLeuTyrIleLeuTyrTyrValGlyArgThrProLys 97
714 AGGCCCTGGAACCGCTGCCGATCGTCTATTACGTCCGCCCTAAGCCTAAG 763
98 ValGluGlnLeuSerAsnMetValValLysSerCysLysCysSer 112
764 GTTGAACAGCTGCTACAGTGATGTGCGCAGTGTGCAAGTCTCT 808

seq_name: /SIDSI/gcgdata/geneseq/geneseqn/NA1986.DAT: AAN60973
seq_documentation_block:
ID AAN60973 standard; DNA; 975 BP.
XX

```

```

AC AAN60973;
XX
XX 28-OCT-1991 (first entry)
XX
XX Genomic sequence encoding TGF-beta exon.
XX
XX Transforming growth factor beta; cancer; wound healing.
XX
XX Key Location/Qualifiers
XX Intron 1..347
XX FT /*tag= a
XX exon 348..500
XX FT /*tag= b
XX Intron 501..975
XX FT /*tag= c
XX
XX EP200341-A.
XX
XX 10-DEC-1986.
XX
XX 21-MAR-1986; 86EP-0302112.
XX
XX 22-MAR-1985; 85US-0715142.
XX
XX 13-MAR-1987; 87US-0025423.
XX
XX (GETH ) GENENTECH INC.
XX
XX Derynck RMA;
XX
XX WPI; 1986-326875/50.
XX
XX TGF-beta prodn. from transformed hosts - useful esp. for treating
XX wounds (J6 2/9/86).
XX
XX Disclosure; Fig 2; 26pp; English.
XX
XX The gene product is known to stimulate cell proliferation and
XX inhibit anchorage-dependent growth of a variety of human cancer cell
XX lines, it is esp. useful in treatment of burns and the promotion of
XX surface and internal wound healing. TGF-beta may be expressed from a
XX transformed CHO cell line.
XX See also AAN60972.
XX
XX Sequence 975 BP; 274 A; 184 C; 338 G; 179 T; 0 other;

alignment_scores:
    Quality: 237.50      Length: 60
    Ratio: 4.847        Gaps: 1
    Percent Similarity: 81.667      Percent Identity: 68.333

alignment_block:
  TGF3P x AAN60973  ..
  Align seg 1/1 to: AAN60973 from: 1 to: 975

12 GluGluAsnCysCysValArgProLeuTyrIleAspPheArgGlnAspLe 28
354 GAGAAGAACTGCTGGCTGGCAGCTGATCATTTGACTTCCCGAAGGACCT 403
28 uGlyTrpLysTrpValHisGluProLysGlyTyrTyrAlaAsnPheCysS 45
404 CGGCTTGAAGTGGATCCACGAGCCCAAGGGCTACCATTGCCAATTCTGCC 453
45 erGlyProCysProTyrLeuArgSerAlaAspThrThrHisSerThrVal 61
454 TCGGGCCCTGCCCTTACATTTGGAGCCTGGACACGACAGTACACAGGTA 503
62 .....LeuGlyLeuTyrAsnThrLeu 68
504 CGTCTGGCCACCGGGCTACGAGATGCGCTT 533

seq_name: /SIDSI/gcgdata/geneseq/geneseqn/NA1990.DAT: AAQ02815

```

```
seq_documentation_block:
ID  AAQ02815 standard; DNA; 975 BP.
XX  AC
XX  AAQ02815;
XX  31-MAY-1989 (first entry)
XX  DE
XX  Sequence of genomic fragment encoding a TGF-beta 1 exon.
XX  KW
XX  Transforming growth factor beta-3 (TGF beta 3); tumour cells; growth
XX  inhibition.
XX  FH
XX  Key Location/Qualifiers
XX  CDS 348..500
XX  FT /*tag= a
XX  FT
XX  WO8912101-A.
XX  PN
XX  PD 14-DEC-1989.
XX  PF
XX  08-JUN-1988; 88WO-US01945.
XX  PR
XX  08-JUN-1988; 88WO-U001945.
XX  PA (GETH ) GENENTECH INC.
XX  PI
XX  Derynck RM, Goeddel DV;
XX  PI
XX  WPI; 1990-007474/01.
XX  DR P-PSDB; AAR04075.
XX  DR
XX  Nucleotide sequence encoding transforming growth factor beta-3 -used as a
XX  PT probe, or to produce TGF beta 3, for inhibition of growth of normal
XX  PT and neoplastic cells, eg A549.
XX  PT
XX  Disclosure; Fig. 2; 61pp; English.
XX  PI
XX  This sequence encodes an exon of transforming growth factor-beta 1 (TGF-
XX  CC beta 1) polypeptide corresponding to AA's 288-338 of mature TGF-beta 1.
XX  CC The nucleic acid sequence encoding the second subtype of TGF-beta (TGF-
XX  CC beta 3) is useful as a probe or to produce TGF-beta 3 for both normal and
XX  CC neoplastic cell growth inhibition.
XX  CC
XX  SQ Sequence 975 BP; 274 A; 183 C; 339 G; 179 T; 0 other;
```

```
alignment_scores:
Quality: 237.50 Length: 60
Ratio: 4.847 Gaps: 1
Percent Similarity: 81.667 Percent Identity: 68.333

alignment_block:
TGFB3P x AAQ02815 ..

Align seg 1/1 to: AAQ02815 from: 1 to: 975

12 GluGluAsnCysCysValArgProLeuTyrIleAspPheArgGlnAspLe 28
|||||
354 GAGAGAACTGCTGCGTGGCAGCTGTACATTGACTTCGCGCAAGGACCT 403

28 uGlyTrpLysTrpValHisGluProLysGlyTyrTyrAlaAsnPheCysS 45
|||||
404 CGCTGGGAAGTGGATCCAGAGCCCAAGGGCTACCATGCCAACTTCTGCC 453

45 eRGlyProCysProTyrLeuArgSerAlaAspThrHisSerThrVal 61
|||||
454 TCGGGCCCTGCCCTACATTTCGAGCCTGGACAGCAGTACAGCAAGGTA 503

62 .....LeuGlyLeuTyrAsnThrLeu 68
|||||
504 GCTCTGGCCACGGGCTACGAGATGCGCTT 533
```

```
seq_name: /SIDSL/gcgdata/geneseq/geneseq/NA1996.DAT:AA15721
seq_documentation_block:
ID  AAT15721 standard; DNA; 975 BP.
XX  AC
XX  AAT15721;
XX  XX
XX  24-JUL-1997 (revised)
XX  DT 25-JAN-1980 (first entry)
XX  DE
XX  Partial pre-transforming growth factor beta 1 DNA.
XX  KW
XX  transforming growth factor beta 1; wound healing;
XX  recombinant production; ss.
XX  OS Homo sapiens.
XX  FH
XX  Key Location/Qualifiers
XX  exon 347..500
XX  FT /*tag= a
XX  FT /note= "encodes TGF beta 1 residues 252 to 302"
XX  XX
XX  PN US5482851-A.
XX  PD 09-JAN-1996.
XX  PF
XX  22-MAR-1985; 85US-0715142.
XX  PR
XX  13-MAR-1987; 87US-0025423.
XX  PR 22-MAR-1985; 85US-0715142.
XX  PR 04-AUG-1989; 89US-0389929.
XX  PR 04-MAR-1992; 92US-0845893.
XX  PR 05-NOV-1993; 93US-0147364.
XX  PA (GETH ) GENENTECH INC.
XX  PI
XX  Derynck RMA, Goeddel DV;
XX  PI
XX  WPI; 1996-076891/08.
XX  DR P-PSDB; AAR90828.
XX  DR
XX  PT New recombinant human transforming growth factor-beta prods. - produced
XX  PT using Chinese hamster ovary cells, for use in diagnostic applications
XX  PT or in therapy
XX  XX
XX  Example 2; Fig 2; 26pp; English.
XX  CC
XX  The transforming growth factor (TGF) beta 1 exon was identified using
XX  CC the "long probe" strategy used previously for TGF-alpha. Long
XX  CC oligonucleotides (T1572-23) designed on the basis of the partial protein
XX  CC sequence were used as hybridisation probes for the exon in a human
XX  CC genomic DNA library. The TGF beta 1 exon was then used as a probe for
XX  CC the isolation of TGF beta 1 cDNA (see AAT15270). DNA encoding TGF beta
XX  CC 1 is useful for the recombinant production of the protein, which is
XX  CC useful in, e.g. wound healing.
XX  CC (Revised entry submitted to correct sequence analysis breakdown.)
XX  SQ Sequence 975 BP; 274 A; 184 C; 338 G; 179 T; 0 other;
```

```
alignment_scores:
Quality: 237.50 Length: 60
Ratio: 4.847 Gaps: 1
Percent Similarity: 81.667 Percent Identity: 68.333

alignment_block:
TGFB3P x AAT15721 ..

Align seg 1/1 to: AAT15721 from: 1 to: 975

12 GluGluAsnCysCysValArgProLeuTyrIleAspPheArgGlnAspLe 28
|||||
354 GAGAGAACTGCTGCGTGGCAGCTGTACATTGACTTCGCGCAAGGACCT 403
```

28 uGlyTrpLysTrpValHisGluProLysGlyTyrTyrAlaAsnPheCys 45
 |||||
 404 CGGCTGGAAGTGGATCCACGAGCCCAAGGCTACCATGCCAATCTCTGCC 453
 45 erGlyProCysProTyrLeuArgSerAlaAspThrHisSerThrVal 61
 |||||
 454 TCGGGCCCTGCCCTACATTTGGAGCTGGACACGCGAGTACGCAAGGTA 503
 62LeuGlyLeuTyrAsnThrLeu 68
 |||||
 504 CGTCTGGCCACCGGCTACGAGATGCGCTT 533

seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1998.DAT:AAV52936

seq_documentation_block:
 ID AAV52936 standard; DNA; 975 BP.

XX AC AAV52936;

XX DT 21-DEC-1998 (first entry)

XX DE Human transforming growth factor-beta gene exon fragment.

XX KW Transforming growth factor-beta 1; TGF-beta 1; human; ss.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT Intron 1..346

FT exon /*tag= a

FT exon 347..500

FT intron /*tag= b

FT intron 501..976

FT /*tag= c

XX PN US5801231-A.

XX PD 01-SEP-1998.

XX PF 22-MAR-1985; 85US-0715142.

XX PR 13-MAR-1987; 87US-0025423.

XX PR 22-MAR-1985; 85US-0715142.

XX PR 04-AUG-1989; 89US-0389929.

XX PR 04-MAR-1992; 92US-0845893.

XX PR 05-NOV-1993; 93US-0147364.

XX PR 30-MAY-1995; 95US-0454468.

XX PA (GETH) GENENTECH INC.

XX PI Derynck RMA, Goeddel DV;

XX DR WPI; 1998-494840/42.

XX DR P-PSDB; AAW78788.

XX PT DNA encoding transforming growth factor-beta precursor sequence -
 useful for analysis to perform manipulations to increase yield of
 recombinant production of the protein

XX PS Example 2; Fig 2; 26pp; English.

XX CC This nucleotide sequence comprises a fragment of the human
 transforming growth factor-beta 1 (TGF-beta 1) gene incorporating
 an exon and flanking intron sequences. It was isolated from a
 human genomic library using probes based on a partial protein
 sequence of TGF-beta 1. The exon encodes amino acids 288-338
 (see AAW78788) of TGF-beta 1. Restriction fragments of the isolated
 exon were used as probes for the isolation of TGF-beta 1 cDNAs
 (see AAV52933). The invention relates to the recombinant production
 of TGF-beta. Nucleic acids encoding TGF-beta have been isolated
 and cloned into vectors which are replicated in bacteria and
 expressed in eukaryotic cells. TGF-beta recovered from transformed

CC cells is used in known therapeutic applications. TGF-beta nucleic
 CC acids are also useful in diagnosis and identification of TGF-beta
 CC clones.

XX SQ Sequence 975 BP; 274 A; 184 C; 338 G; 179 T; 0 other;

alignment_scores:

Quality: 237.50 Length: 60

Ratio: 4.847 Gaps: 1

Percent Similarity: 81.667 Percent Identity: 68.333

alignment_block:

TGFB3P x AAV52936 ..

Align seg 1/1 to: AAV52936 from: 1 to: 975

12 GluGluAsnCysCysValArgProLeuTyrIleAspPheArgGlnAspLe 28
 |||||
 354 GAGAAAGACTGCTGCTGCGGAGCTGTACATTGACTTCGCAAGGACCT 403

28 uGlyTrpLysTrpValHisGluProLysGlyTyrTyrAlaAsnPheCys 45
 |||||
 404 CGGCTGGAAGTGGATCCACGAGCCCAAGGCTACCATGCCAATCTCTGCC 453

45 erGlyProCysProTyrLeuArgSerAlaAspThrHisSerThrVal 61
 |||||
 454 TCGGGCCCTGCCCTACATTTGGAGCTGGACACGCGAGTACGCAAGGTA 503

62LeuGlyLeuTyrAsnThrLeu 68
 |||||

504 CGTCTGGCCACCGGCTACGAGATGCGCTT 533

seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1994.DAT:AAQ56924

seq_documentation_block:

ID AAQ56924 standard; DNA; 975 BP.

XX AC AAQ56924;

XX DT 09-JUL-1994 (first entry)

XX DE Human pre-TGF-beta-1.

XX KW TGF-beta-1; TGF-beta-2; transforming growth factor beta-1;
 transforming growth factor beta-3; recombinant; wound healing;
 XX KW vulnerable.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT exon 1..975

FT /*tag= a

FT /*codon_start= 348..350

XX PN US5284763-A.

XX PD 08-FEB-1994.

XX PF 22-MAR-1985; 85US-0715142.

XX PR 22-MAR-1985; 85US-0715142.

XX PR 13-MAR-1987; 87US-0025423.

XX PR 04-AUG-1989; 89US-0389929.

XX PR 04-MAR-1992; 92US-0845893.

XX PA (GETH) GENENTECH INC.

XX PI Derynck RMA, Goeddel DV;

XX DR WPI; 1994-056343/07.

XX DR P-PSDB; AAQ56924.

PT Nucleic acid sequences encoding transforming growth factor-beta -
PT diagnostic probes, and for use in therapeutics
XX
PS Disclosure; Fig 2; 25pp; English.
XX
CC CDNA sequences were determined for human pre-TGF-beta-1 (AAQ56923),
CC pig TGF-beta-3 (AAQ56925) and human TGF-beta-3 (AAQ56926), and the
CC corresponding amino acid sequences were determined (AAR46227-29,
CC respectively). A genomic fragment corresponding to a human TGF-
CC beta-1 exon (AAQ56924) was also isolated and its amino acid sequence
CC determined (AAR46230). The sequences have been used in the
CC construction of vectors for the expression of recombinant TGF-
CC beta.
XX
SQ Sequence 975 BP; 274 A; 181 C; 341 G; 179 T; 0 other;

alignment_scores:
Quality: 226.50 Length: 60
Ratio: 4.719 Gaps: 1
Percent Similarity: 80.000 Percent Identity: 66.667
alignment_block:
TGFB3P x AAQ56924 ..
Align seg 1/1 to: AAQ56924 from: 1 to: 975
12 GluGluAsnCysCysValArgProLeuTyrIleAspPheArgGlnAspLe 28
||||:|||||
354 GAGAGAAGTCTGCTGGCGAGCTGTACATTCAGTTCTCGCAAGGACCT 403
28 uGlyTrpLysTrpValHisGluProLysGlyTyrTyrAlaAsnPheCys 45
|||||
404 CGCTGGAGTGGATCCACGAGGCCAAGGCTACCATGCCAACTTCTGCC 453
45 eRGlyProCysProTyrLeuArgSerAlaAspThrThrHisSerThrVal 61
|||||
454 TCGGGCCCTGGCCCTACATTGGAGCGCTGGACACGCGAGTACAGCAAGGTA 503
62LeuGlyLeuTyrAsnThrLeu 68
|||||
504 CGTCTGGCCACCGGGCTACGATGCGCT 533

seq_name: /SIDS1/gcgdata/geneseq/geneseq/NA2001.DAT:AAF63556
seq_documentation_block:
ID_AAF63556 standard; cDNA; 1125 BP.
XX
AC AAF63556;
XX
DT 11-MAY-2001 (first entry)
XX
DE Zebrafish GDF-8 coding sequence.
XX
KW Gene therapy; growth differentiation factor-8; GDF-8; AIDS; cachexia;
KW neurodegenerative disease; amyotrophic lateral sclerosis; obesity;
KW muscular dystrophy; muscledenerative disease; tissue repair;
KW muscle wasting disease; neuromuscular disorder; spinal cord injury;
KW traumatic injury; congestive obstructive pulmonary disease; ss.
XX
OS Brachydanio rerio.
XX
PN WO200112777-A2.
XX
PD 22-FEB-2001.
XX
XX 17-AUG-2000; 2000WO-US22884.
XX
XX 19-AUG-1999; 99US-0378238.
XX
XX (UYJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
XX
XX Lee S, McPherron AC;

XX
DR WPI; 2001-211209/21.
DR P-PSDB; AAB73196.
XX
PT New substantially purified growth differentiation factor-8 polypeptide,
PT useful for treating muscle wasting disease, obesity, muscular
PT dystrophy, neuromuscular disorder, acquired immunodeficiency syndrome
PT and cachexia -
XX
PS Claim 39; Fig 2; 124pp; English.
XX
CC The present invention relates to growth differentiation factor-8 (GDF-8)
CC coding sequences and proteins. The present sequence is a coding sequence
CC for GDF-8, which was isolated in the present invention. GDF-8 is useful
CC for treating neurodegenerative diseases (e.g. amyotrophic lateral
CC sclerosis and muscular dystrophy), muscledenerative diseases or in
CC tissue repair due to trauma, obesity and disorders related to abnormal
CC proliferation of adipocytes. GDF-8 is also useful for treating
CC malignancies of the various organ systems, particularly cells in muscle
CC or adipose tissues and in gene therapy for the treatment of cell
CC proliferative or immunological diseases mediated by GDF-8. In addition,
CC GDF-8 is also useful for treating muscle wasting disease, neuromuscular
CC disorder, spinal cord injury, traumatic injury, congestive obstructive
CC pulmonary disease (COPD), AIDS or cachexia.
XX
SQ Sequence 1125 BP; 310 A; 285 C; 294 G; 236 T; 0 other;

alignment_scores:
Quality: 217.00 Length: 110
Ratio: 3.056 Gaps: 5
Percent Similarity: 64.545 Percent Identity: 40.000
alignment_block:
TGFB3P x AAF63556 ..
Align seg 1/1 to: AAF63556 from: 1 to: 1125
7 CysPheArgAsnLeuGluGluAsn...CysCysValArgProLeuTyrI 22
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||: |||||
811 TGGCATGAGAAATTCCTCAGAGTCTCGCTGTGTCAGGATACCTCTCAGTGT 860
22 eAspPheArgGlnAspLeuGlyTrpLysTrpValHisGluProLysGlyT 39
|||||
861 GGACTTC...GAGGACTTGGCTGGGACTGGATTATTGCTCCAAACGCT 907
39 yrTyrAlaAsnPheCysSerGlyProCysPro.....TyrLeuArgSer 53
|| |||||
908 ATAAGGCGAATTACTGTTCAGGAGATCGGACTACATGTACCTGCAGAA 957
54 AlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnThrLeuAsnPr 70
|||||
958 TATCCCCACACCCAT.....CTGCTGAACAAGGCCAGTCC 992
70 OGIuAlaSerAlaSerProCysCysValProGlnAspLeuGluProLeuT 87
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||: |||||
993 GAGAGGAACGGCTGGGCGCTGCTGCATCCCAACAGATGTCTCCATCA 1042
87 hrLeuLeuTyrTyrValGlyArgThrProLysVal...GluGlnLeuSer 102
|||||
1043 ACATGCTTTACTTTACGGCAAGAGCAGATCATCTACGGCAAGATCCCT 1092
103 AsnMetValValLysSerCysLysCysSer 112
|||||
1093 TCGATGGTAGTACCGCTGTGGCTGCTCA 1122

seq_name: /SIDS1/gcgdata/geneseq/geneseq/NA2001.DAT:AAF63558
seq_documentation_block:
ID_AAF63558 standard; cDNA; 412 BP.
XX
AC AAF63558;
XX

```

DT 11-MAY-2001 (first entry)
DE Salmon GDF-8 allele 2 coding sequence.
XX
KW Gene therapy; growth differentiation factor-8; GDF-8; AIDS; cachexia;
KW neurodegenerative disease; amyotrophic lateral sclerosis; obesity;
KW muscular dystrophy; musclogenenerative disease; tissue repair;
KW muscle wasting disease; neuromuscular disorder; spinal cord injury;
KW traumatic injury; congestive obstructive pulmonary disease; ss.
XX
OS Oncorhynchus sp.
XX
PN WO200112777-A2.
XX
PD 22-FEB-2001.
XX
PF 17-AUG-2000; 2000WO-US22884.
XX
PR 19-AUG-1999; 99US-0378238.
XX
PA (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
XX
PI Lee S, McPherron AC;
XX
DR WPI; 2001-211209/21.
DR P-PSDB; AAB73198.
XX
PT New substantially purified growth differentiation factor-8 polypeptide,
PT useful for treating muscle wasting disease, obesity, muscular
PT dystrophy, neuromuscular disorder, acquired immunodeficiency syndrome
PT and cachexia -
XX
PS Claim 39; Fig 2; 124pp; English.
XX
CC The present invention relates to growth differentiation factor-8 (GDF-8)
CC coding sequences and proteins. The present sequence is a coding sequence
CC for GDF-8, which was isolated in the present invention. GDF-8 is useful
CC for treating neurodegenerative diseases (e.g. amyotrophic lateral
CC sclerosis and muscular dystrophy), musclogenenerative diseases or in
CC tissue repair due to trauma, obesity and disorders related to abnormal
CC proliferation of adipocytes. GDF-8 is also useful for treating
CC malignancies of the various organ systems, particularly cells in muscle
CC or adipose tissues and in gene therapy for the treatment of cell
CC proliferative or immunological diseases mediated by GDF-8. In addition,
CC GDF-8 is also useful for treating muscle wasting disease, neuromuscular
CC disorder, spinal cord injury, traumatic injury, congestive obstructive
CC pulmonary disease (COPD), AIDS or cachexia.
XX
SQ Sequence 412 BP; 91 A; 134 C; 112 G; 75 T; 0 other;

alignment_scores:
  Quality: 216.50      Length: 108
  Ratio: 3.331        Gaps: 4
  Percent Similarity: 60.185      Percent Identity: 38.889

alignment_block:
TGFB3P x AAF63558 ..
Align seg 1/1 to: AAF63558 from: 1 to: 412

12 GluGluAsnCysCysValArgProLeuTyrIleAspPheArgGlnAspLe 28
116 GAGTCGCGTGTCTGCGCGGTACCCCGCTCACGCTGGACTTT...GAAGACTT 162
28 uGlyTyrLysTyrValHisGluProLysGlyTyrTyrAlaAsnPhcCysS 45
163 TGCTGGGACTGGATTATTCGCCCAAGCGCTACAGGCCCACTACTGCT 212
45 erGlyProCysProTyrLeuArgSerAlaAspThrThrHisSerThrVal 61
213 CTGCTGAGTCGAGTACATGCACCTGCAGAGTACCCCAACCC..... 256

```

```

62 LeuGlyLeuTyrAsnThrLeuAsnProGluAlaSerAlaSerProCysCy 78
257 ...CACCTGGTGACCAAGGCTAACCCCTGCGGCACCGGGGCGCTGCTG 303
78 sValProGlnAspLeuGluProLeuThrThrLeuTyrTyr..... 91
304 CACCCCAACCAAGATGTCCTCCCATCATCATGCTCTACTTCAACCGCAAG 353
92 .....ValGlyArgThrProLysValGluGlnLeuSerAsnMet 104
354 AGCAGATCATCTACGGCAAGATCCCC.....TCCATG 385
105 ValValLysSerCysLysCysSer 112
386 GTGGTGACCGCTGCGCTGCTCG 409

seq_name: /SIDSL/gcgdata/geneseq/geneseq/NA2001.DAT:AAF63557
seq_documentation_block:
ID AAF63557 standard; cDNA; 476 BP.
XX
AC AAF63557;
XX
DT 11-MAY-2001 (first entry)
XX
DE Salmon GDF-8 allele 1 coding sequence.
XX
KW Gene therapy; growth differentiation factor-8; GDF-8; AIDS; cachexia;
KW neurodegenerative disease; amyotrophic lateral sclerosis; obesity;
KW muscular dystrophy; musclogenenerative disease; tissue repair;
KW muscle wasting disease; neuromuscular disorder; spinal cord injury;
KW traumatic injury; congestive obstructive pulmonary disease; ss.
XX
OS Oncorhynchus sp.
XX
PN WO200112777-A2.
XX
PD 22-FEB-2001.
XX
PF 17-AUG-2000; 2000WO-US22884.
XX
PR 19-AUG-1999; 99US-0378238.
XX
PA (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
XX
PI Lee S, McPherron AC;
XX
DR WPI; 2001-211209/21.
DR P-PSDB; AAB73197.
XX
PT New substantially purified growth differentiation factor-8 polypeptide,
PT useful for treating muscle wasting disease, obesity, muscular
PT dystrophy, neuromuscular disorder, acquired immunodeficiency syndrome
PT and cachexia -
XX
PS Claim 39; Fig 2; 124pp; English.
XX
CC The present invention relates to growth differentiation factor-8 (GDF-8)
CC coding sequences and proteins. The present sequence is a coding sequence
CC for GDF-8, which was isolated in the present invention. GDF-8 is useful
CC for treating neurodegenerative diseases (e.g. amyotrophic lateral
CC sclerosis and muscular dystrophy), musclogenenerative diseases or in
CC tissue repair due to trauma, obesity and disorders related to abnormal
CC proliferation of adipocytes. GDF-8 is also useful for treating
CC malignancies of the various organ systems, particularly cells in muscle
CC or adipose tissues and in gene therapy for the treatment of cell
CC proliferative or immunological diseases mediated by GDF-8. In addition,
CC GDF-8 is also useful for treating muscle wasting disease, neuromuscular
CC disorder, spinal cord injury, traumatic injury, congestive obstructive
CC pulmonary disease (COPD), AIDS or cachexia.
XX
SQ Sequence 476 BP; 111 A; 145 C; 133 G; 87 T; 0 other;

```

```
alignment_scores:
  Quality: 216.50      Length: 108
  Ratio: 3.331         Gaps: 4
  Percent Similarity: 60.185  Percent Identity: 38.889

alignment_block:
  TGF3P x AAF63557 ..

Align seg 1/1 to: AAF63557 from: 1 to: 476

12 GluGluAsnCysCysValArgProLeuTyrIleAspPheArgGlnAspLe 28
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
180 GAGTCCCGCTGTTCGGCTACCCCTACCGGTAGACTTT...GAAGACTT 226
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
28 uGlyTrpLysTrpValHisGluProLysGlyTyrTyrAlaAsnPheCys 45
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
227 TGGGTGGGACTGGATTATTTGCCCCCAAGCGCTACAGGCCACTACTGCT 276
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
45 erGlyProCysProTyrLeuArgSerAlaAspThrThrHisSerThrVal 61
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
277 CTGGTGAGTGTGAGTACATGCACCTGCAGAGTACCCACACACC..... 320
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
62 LeuGlyLeuTyrAsnThrLeuAsnProGluAlaSerAlaSerProCysCy 78
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
321 ...CACCTGGTGAACAGGCTAACCTCGCGCACCGCAGGCCCTGCTG 367
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
78 sValProGlnAspLeuGluProLeuThrIleLeuTyrTyr..... 91
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
368 CACCCCAACCAAGATGTCCTCCATCAACATGCTCTACTTCAACCGCAAG 417
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
92 .....ValGlyArgThrProLysValGluGlnLeuSerAsnMet 104
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
418 AGCAGATCATCTACGGCAAGATCCCC.....TCCATG 449
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
105 ValValLysSerCysLysCysSer 112
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
450 GTGGTGACCGTTCGGGATGCTCG 473
```

seq_name: /SIDS1/gcgdata/geneseq/geneseq/NA1998.DAT:AAV45817

```
seq_documentation_block:
ID  AAV45817 standard; cDNA; 1128 BP.
XX
AC  AAV45817;
XX
DT  07-DEC-1998 (first entry)
XX
DE  Baboon growth differentiation factor-8 cDNA.
XX
KW  Growth differentiation factor-8; GDF-8; baboon; transgenic animal;
KW  transforming growth factor-beta; muscle; meat; inhibitor; obesity;
KW  neuromuscular disease; muscular dystrophy; cachexia; cancer; AIDS;
KW  therapy; ss.
XX
OS  Papio sp.
XX
PN  W09833887-A1.
XX
PD  06-AUG-1998.
XX
PF  05-FEB-1998; 98WO-US02479.
XX
PR  23-MAY-1997; 97US-0862445.
PR  05-FEB-1997; 97US-0795071.
PR  28-APR-1997; 97US-0847910.
XX
PA  (UWJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
XX
PI  Lee S, McPherron AC;
XX
DR  WPI; 1998-437444/37.
DR  P-PSDB; AAW69886.
```

```
XX
PT  Transgenic animals with gene for growth differentiation factor-8
PT  disrupted - have increased muscle and reduced cholesterol contents,
PT  also use of GDF-8 inhibitors for treating cancer, obesity,
PT  neuromuscular disease
XX
PS  Example 9; Fig 14a; 125pp; English.
XX
CC  This cDNA clone codes for baboon growth differentiation factor-8
CC  (GDF-8) (see AAW69886), a novel member of the transforming growth
CC  factor-beta superfamily that appears to relate to various cell
CC  proliferative disorders, especially those involving muscle, nerve
CC  and adipose tissue. It was isolated from a skeletal muscle cDNA
CC  library. The invention provides novel mammalian and avian GDF-8
CC  proteins (see AAW69883-92). Transgenic non-human animals are claimed
CC  in which GDF-8 expression is disrupted or interfered with. Also
CC  claimed are: (1) chicken or turkey eggs or meat, beef, milk, pork
CC  and lamb from these animals; (2) a method for increasing muscle
CC  mass in animals by administering an antibody (Ab) that binds to
CC  GDF-8; (3) inhibiting the action of GDF-8 by treating foetal or
CC  adult muscle or progenitor cells with a GDF-8 inhibitor; and (4)
CC  isolated nucleic acid encoding a GDF-8 protein truncated by loss of
CC  the C-terminal active fragment. The transgenic animals have
CC  increased muscle mass and for poultry reduced cholesterol contents.
CC  Method (3) is used to treat muscle wasting or neuromuscular
CC  diseases, muscular atrophy and aging, particularly muscular
CC  dystrophy, spinal cord or traumatic injuries, congestive or
CC  obstructive lung disease, AIDS and cachexia. Method (4) is used to
CC  treat cancer of muscle, connective tissue and bone, or obesity.
CC  Also (not claimed) GDF-8 can be used to maintain myoblasts intended
CC  for transplanting or to improve efficiency of fusion. Detection
CC  may be performed with nucleic acid probes or primers. GDF-8, or
CC  sequences encoding it, can also be used to treat cell proliferative
CC  disorders associated with underexpression of GDF-8, or expression
CC  of a mutant protein.
XX
SQ  Sequence 1128 BP; 372 A; 223 C; 238 G; 295 T; 0 other;
```

```
alignment_scores:
  Quality: 208.50      Length: 104
  Ratio: 3.159         Gaps: 4
  Percent Similarity: 63.462  Percent Identity: 40.385

alignment_block:
  TGF3P x AAV45817 ..

Align seg 1/1 to: AAV45817 from: 1 to: 1128

12 GluGluAsnCysCysValArgProLeuTyrIleAspPheArgGlnAspLe 28
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
832 GAATCGGGATGCTGCTTACCTCTAAGTGTGGATTTT...GAAGCTCT 878
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
28 uGlyTrpLysTrpValHisGluProLysGlyTyrTyrAlaAsnPheCys 45
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
879 TGGATGGGATTGGATTATCGCTCTAAAGATATAAGGCCAATTACTGCT 928
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
45 erGlyProCysPro.....TyrLeuArgSerAlaAspThrThrHisSer 59
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
929 CTGGAGAGTGTGAATTTGTATTTTACAAAAATATCTCTACTACTCAT... 975
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
60 ThrValLeuGlyLeuTyrAsnThrLeuAsnProGluAlaSerAlaSerPr 76
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
976 .....CTGGTACCAACAGCAACCCAGAGGTTTCAGCAGGCC 1013
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
76 oCysCysValProGlnAspLeuGluProLeuThrIleLeuTyrTyrValG 93
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1014 TTGCTGTACTCCCAAGATGCTCCAATTAATATGCTATATTTAATG 1063
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
93 lyArgThrProLysVal...GluGlnLeuSerAsnMetValValLysSer 108
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1064 GCAAGAACAAATAATATATATATATATATATATATATATATATATATAT 1113
```

```
109 CysLysCysSer 112
   ||| |||||
1114 TCGGGTGTCTCA 1125

seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1999.DAT:AAZ06453
seq_documentation_block:
ID  AAZ06453 standard; cDNA; 1128 BP.
XX
AC  AAZ06453;
XX
DT  08-DEC-1999 (first entry)
DE
DE  cDNA of Baboon Growth Differentiation Factor-8.
XX
KW  growth differentiation factor; tissue growth; muscle growth;
KW  cell differentiation; animal feed; muscle disorder;
KW  bone degeneration; nerve degeneration; GDF-8; development;
KW  transforming growth factor beta; TGF-beta; ds.
XX
OS  Papio anubis.
XX
PN  WO9940181-A1.
XX
PD  12-AUG-1999.
XX
PF  05-FEB-1999; 99WO-US02511.
XX
PR  28-JUL-1998; 98US-0124180.
PR  05-FEB-1998; 98US-0019070.
XX
PA  (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
XX
PI  Lee S, McPherron AC;
XX
DR  WPI; 1999-494289/41.
DR  P-PSDB; AAY33843.
XX
PT  New differentiation factor useful for treating neurodegenerative
PT  diseases
XX
PS  Example 9; Fig 14a; 138pp; English.
XX
CC  This is the cDNA nucleotide sequence of the Baboon Growth
CC  Differentiation Factor-8 (GDF-8). Skeletal muscle cDNA libraries from
CC  this species were screened with the murine GDF-8 probe, in order to
CC  isolate the GDF-8. The absolute conservation of the C-terminal region
CC  between species as evolutionarily far apart as humans and chickens,
CC  baboons and turkeys, suggests that this region will be highly conserved
CC  in many other species as well.
CC  GDF-8 has been shown to result in increased bone and muscle mass (such
CC  as ribs) when expressed in reduced amounts. GDF-8 minus transgenic
CC  animals and forms of animal feed that can inhibit/reduce production of
CC  GDF-8 are of commercial interest.
CC  GDF-8 expression may also have a role in the therapy of abnormal growth
CC  of muscle, bone or adipose tissue. A GDF-8 monoclonal antibody, GDF-8
CC  antisense molecule or dominant negative polypeptide could be used with
CC  foetal or adult muscle cells, bone cells or progenitor cells. These
CC  agents can be administered to a patient suffering from a disorder such
CC  as muscle wasting disease, neuro muscular disorder, muscle atrophy,
CC  osteoporosis, bone degenerative diseases, obesity or other adipocyte
CC  cell disorders, and aging for example.
XX
SQ  Sequence 1128 BP; 371 A; 225 C; 238 G; 294 T; 0 other;

alignment_scores:
  Quality: 208.50      Length: 104
  Ratio: 3.159        Gaps: 4
  Percent Similarity: 63.462  Percent Identity: 40.385

alignment_block:
TGFB3P x AAZ06453  ..
```

```
Align seg 1/1 to: AAZ06453 from: 1 to: 1128

12  GluGluAsnCysCysValargProLeuTyrlleAspPheArgGlnAspLe 28
   |||:||||| ||||| :|||:||||| :|||: ||
832 GAATCGCGATGCTGCTGTACCTCTAACCCTTAACCTGGATT...GAAGCTCT 878
   |||:||||| ||||| ||| |||||:|||||

28  uGlyTrpLysTrpValHisGluProLysGlyTyTyTyAlaAsnPhCysS 45
   ||||| ||||| ||||| ||| |||||:|||||
879 TGGATGGGATTGATTATCGCTCCTAAAAGATATAAGGCCAATTACTGCT 928
   ||||| ||||| ||||| |||||:|||||

45  erGlyProCysPro.....TyrlleuArgSerAlaAspThrThrHisSer 59
   ||||| ||||| ||||| |||||:|||||
929 CTGGAGAGTGTGAATTGTATTTTACAAAAATATCCTCATCTCAT... 975
   ||| :||| |||||:|||||:|||||:|||||

976 .....CTGGTACACCAACCAACCCAGAGGTTTCAGCAGGCC 1013
   ||| :||| |||||:|||||:|||||:|||||

76  oCysCysValProGlnAspLeuGluProLeuThrleLeuTyTyTyValG 93
   |||||:||||| :|||:|||||:|||||:|||||: ||
1014 TTGCTGTACTCCCAAGATGCTCCCAATTAAATATGCTATATTTTAAATG 1063
   |||: ||| :||| :|||: |||||

93  lyArgThrProLysVal...GluGlnLeuSerAsnMetValValLysSer 108
   |||: ||| :|||: |||||
1064 GCAAGAAACAAATAATATATGGGNAATTCAGCCATGGTAGTAGACGC 1113
   ||| |||||

109 CysLysCysSer 112
   ||| |||||
1114 TCGGGTGTCTCA 1125

seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1999.DAT:AAZ09366
seq_documentation_block:
ID  AAZ09366 standard; cDNA; 1128 BP.
XX
AC  AAZ09366;
XX
DT  29-OCT-1999 (first entry)
XX
DE  Baboon GDF-8 cDNA.
XX
KW  GDF-8; growth differentiation factor receptor; GDF-11; therapy; human;
KW  veterinary; medicine; treatment; muscle tissue disease; wasting disease;
KW  neuromuscular disorder; muscular atrophy; spinal cord injury; aging; fat;
KW  traumatic injury; acquired immune deficiency syndrome; cachexia; baboon;
KW  congenital obstructive pulmonary disease; transgenic animal; transgene;
KW  food animal; cholesterol; muscle mass; diagnostic; ds.
XX
OS  Papio sp.
XX
FH  Key Location/Qualifiers
FT  CDS 1..1128 /*tag= a
FT  FT /product= "GDF-8"
XX
PN  WO9906559-A1.
XX
PD  11-FEB-1999.
XX
PF  28-JUL-1998; 98WO-US15598.
XX
PR  01-AUG-1997; 97US-0054461.
XX
PA  (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
XX
PI  Lee S, McPherron A;
XX
DR  WPI; 1999-153789/13.
DR  P-PSDB; AAY31190.
XX
PT  Recombinant cells that express growth-differentiation factor
PT  receptors - and related antibodies, nucleic acids, vector,
```


seq_documentation_block:
ID AAV69286 standard; DNA; 10708 BP.
XX
AC AAV69286;
XX
DT 02-FEB-1999 (first entry)
XX
DE Sequence of mouse activin genetic loci.
XX
KW Liver activin; beta c; beta e; cell differentiation; haematopoiesis;
KW erythroid; ovarian follicular maturation; hormone; neuronal survival;
KW spermatogenesis; bone; insulin; cardiac morphogenesis; osteoporosis;
KW osteomalacia; erythropoiesis; haemophilia; cystic fibrosis; immunodassay;
KW menstrual disorder; transgenic; modulator; ss.
XX
OS Mus sp.
XX
FH Key Location/Qualifiers
FH CDS 1147..2736
FT /*tag= a
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XX
PN WO9822492-A1.
XX
PD 28-MAY-1998.
XX
PF 20-NOV-1997; 97WO-US20882.
XX
PR 20-NOV-1996; 96US-0752919.
XX
PA (UNMI) UNIV MICHIGAN.
XX
PI Bonadio J, Fang J;
XX
DR WPI; 1998-312408/27.
XX
DR P-PSDB; AAW60617, AAW60618.
XX
XX New isolated nucleic acid encoding sub-units of liver activin -
PT useful for regulating growth and differentiation of cells, e.g. for
PT treating liver, bone and haematopoietic disorders
XX

PS
XX
CC This represents the sequence of mouse activin genetic loci. The invention
CC relates to murine beta c and beta e polypeptides and the genes encoding
CC them. Disorders of cell growth or differentiation (or susceptibility to
CC them) are diagnosed by measuring liver activin gene activity or by
CC detecting a mutation in the liver activin gene. Disorders of
CC haematopoiesis, erythroid differentiation, ovarian follicular maturation,
CC hormone secretion, neuronal survival, spermatogenesis, bone formation,
CC insulin secretion or cardiac morphogenesis are some conditions that can
CC be diagnosed using the liver activin. Cell growth and differentiation can
CC be stimulated by treatment with an liver activin compound or agent that
CC upregulates the compound's expression. Antagonists can be used to treat
CC liver diseases while agonists can be used to increase growth and
CC regeneration of liver tissue. The liver activin compound may also induce
CC bone growth (e.g. for treating osteoporosis or osteomalacia) or
CC haematopoiesis, particularly erythropoiesis, e.g. for treating
CC haemophilia, cystic fibrosis or menstrual disorders. Antibodies are
CC useful in immunoassays, to generate anti-idiotypic antibodies (which bind
CC to liver activin receptors) and to inhibit liver activin. Also,
CC transgenic animals containing liver activin gene can be used to produce
CC the liver activin (in correctly processed and modified forms) proteins,
CC or the transgenic animals, are useful for screening for liver activin
CC modulators.
CC This cDNA encodes a murine liver activin beta c polypeptide. Sequences
CC derived from beta c cDNA clone is used for screening and cloning a liver
CC activin beta e gene. Disorders of cell growth or differentiation (or
CC susceptibility to them) are diagnosed by measuring liver activin gene
CC activity or by detecting a mutation in the liver activin gene. Disorders
CC of haematopoiesis, erythroid differentiation, ovarian follicular
CC maturation, hormone secretion or cardiac survival, spermatogenesis, bone
CC formation, insulin secretion or neuronal survival, are some conditions
CC that can be diagnosed using the liver activin. Cell growth and
CC differentiation can be stimulated by treatment with an liver activin
CC compound or agent that upregulates the compound's expression. Antagonists
CC can be used to treat liver diseases while agonists can be used to
CC increase growth and regeneration of liver tissue. The liver activin
CC compound may also induce bone growth (e.g. for treating osteoporosis or
CC osteomalacia) or haematopoiesis, particularly erythropoiesis, e.g. for
CC treating haemophilia, cystic fibrosis or menstrual disorders. Antibodies
CC are useful in immunoassays, to generate anti-idiotypic antibodies (which
CC bind to liver activin receptors) and to inhibit liver activin. Also,
CC transgenic animals containing liver activin gene can be used to produce
CC the liver activin (in correctly processed and modified forms) proteins,
CC or the transgenic animals, are useful for screening for liver activin
CC modulators.
XX
SQ Sequence 10708 BP; 2651 A; 2844 C; 2607 G; 2546 T; 60 other;

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31 s...TrpValHisGluProLysGlyTyrTyrAlaAsnPheCysSerGlyP 47
9269 GGATTGGATCTCGACCGGAGGATACCGAGTGAATTACTGCAGTGGCG 9318
47 roCys...ProTyrLeuArgSer.....AlaAspThrHis 58
9319 AGTGCCCGCCACCGCTGGCTGGAGTCTGGCATTTGCTGCTCTCTCAT 9368
59 SerThrValLeuGlyLeuTyrAsnThrLeuAsnProGluAlaSerAlaSe 75

PD 06-AUG-1998.
XX
PF 05-FEB-1998; 98WO-US02479.
XX
PR 23-MAY-1997; 97US-0862445.
PR 05-FEB-1997; 97US-0795071.
PR 28-APR-1997; 97US-0847910.
XX
XX
PA (UYJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
XX
PI Lee S, McPherron AC;
XX WPI: 1998-437444/37.
DR P-PSDB; AAW69889.
DR
XX Transgenic animals with gene for growth differentiation factor-8
PT disrupted - have increased muscle and reduced cholesterol contents,
PT also use of GDF-8 inhibitors for treating cancer, obesity,
PT neuromuscular disease
XX
XX Example 9; Fig 14d; 125pp; English.
XX
CC This cDNA clone codes for rat growth differentiation factor-8
CC (GDF-8) (see AAW69889), a novel member of the transforming growth
CC factor-beta superfamily that appears to relate to various cell
CC proliferative disorders, especially those involving muscle, nerve
CC and adipose tissue. It was isolated from a skeletal muscle cDNA
CC library. The invention provides novel mammalian and avian GDF-8
CC proteins (see AAW69883-92). Transgenic non-human animals are claimed
CC in which GDF-8 expression is disrupted or interfered with. Also
CC claimed are: (1) chicken or turkey eggs or meat, beef, milk, pork
CC and lamb from these animals; (2) a method for increasing muscle
CC mass in animals by administering an antibody (Ab) that binds to
CC GDF-8; (3) inhibiting the action of GDF-8 by treating foetal or
CC adult muscle or progenitor cells with a GDF-8 inhibitor; and (4)
CC isolated nucleic acid encoding a GDF-8 protein truncated by loss of
CC the C-terminal active fragment. The transgenic animals have
CC increased muscle mass and for poultry reduced cholesterol contents.
CC Method (3) is used to treat muscle wasting or neuromuscular
CC diseases, muscular atrophy and aging, particularly muscular
CC dystrophy, spinal cord or traumatic injuries, congestive or
CC obstructive lung disease, AIDS and cachexia. Method (4) is used to
CC treat cancer of muscle, connective tissue and bone, or obesity.
CC Also (not claimed) GDF-8 can be used to maintain myoblasts intended
CC for transplanting or to improve efficiency of fusion. Detection
CC may be performed with nucleic acid probes or primers. GDF-8, or
CC sequences encoding it, can also be used to treat cell proliferative
CC disorders associated with underexpression of GDF-8, or expression
CC of a mutant protein.
XX
SQ Sequence 1131 BP; 348 A; 250 C; 266 G; 267 T; 0 other;

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Ratio: 3.097 Caps: 4
Percent Similarity: 64.423 Percent Identity: 39.423
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835 GAATCGCGTGTGCTGCCTACCCCTCAGCGTGCATTTC...GAAGCCTT 881
28 uGlyTyrLysTrpValHisGluProLysGlyTyrTyrAlaAsnPheCys 45
882 TGGATGGGACTGGATTATGACCCCAAGATATAGGCTAATTACTGCT 931
45 eGlyProCysPro.....TyrLeuArgSerAlaAspThrThrHisSer 59
||||| ||| ::::: |||||

OM of: TGFB3P to: Issued_Patents_NA:* out_format : pfs

Date: Oct 30, 2001 9:12 AM

About: Results were produced by the GenCore software, version 4.5,
Copyright (c) 1993-2000 CompuGen Ltd.

Command line parameters:

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-GAPEXT=4.000 -MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000
-GAPOP=4.500 -QGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500
-FGAPOP=6.000 -FGAPEXT=7.000 -XGAPOP=10.000 -YGAPEXT=0.500
-DELOP=6.000 -DELEXT=7.000 -START=1 -MATRIX=blotsum62
-TRANS=human40.cdi -LIST=100 -DOCALIGN=200 -THR_SCORE=pct
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-NORM=ext -MINLEN=0 -MAXLEN=200000000
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-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -NO_XLPXY -WAIT -THREADS=1

Search information block:

Query: TGFB3P

Query length: 113

Database: Issued_Patents_NA:*

Database sequences: 324599

Database length: 94655562

Search time (sec): 35.810000

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;; TITLE OF INVENTION: Produced TGF-beta-like Proteins
;; NUMBER OF SEQUENCES: 43
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Henry P. No. 5650494ak
;; STREET: 520 White Plains Road, P.O. Box 2005
;; CITY: Tarrytown
;; STATE: New York
;; COUNTRY: U.S.A.
;; ZIP: 10591-9005
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/486,057B
;; FILING DATE: 07-JUN-1995
;; CLASSIFICATION: 514
;; PRIORITY APPLICATION DATA:
;; APPLICATION NUMBER: US 08/201,703
;; FILING DATE: 25-FEB-1994
;; PRIORITY APPLICATION DATA:
;; APPLICATION NUMBER: US 07/960,309
;; FILING DATE: 13-OCT-1992
;; PRIORITY APPLICATION DATA:
;; APPLICATION NUMBER: US 07/621,502
;; FILING DATE: 03-DEC-1990
;; PRIORITY APPLICATION DATA:
;; APPLICATION NUMBER: GB 8927546.5
;; FILING DATE: 06-DEC-1989
;; ATTORNEY/AGENT INFORMATION:
;; NAME: No. 5650494ak, Henry P.
;; REGISTRATION NUMBER: 33200
;; REFERENCE/DOCKET NUMBER: 4-17861/+Cont3
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (908) 277-5110
;; TELEFAX: (908) 277-4306
;; INFORMATION FOR SEQ ID NO: 3:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 339 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: double
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: 1..339
;; US-08-486-057B-3

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Ratio: 5.652 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

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51 GCGCCCCCTCTACATGTGACTCCGACAGGATCTGGGCTGGAAGTGGTCC 100
34 lsGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
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151 CTCGGAGTGCACACACACACACACACACACACACACACACACACACAC 200
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seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-470-837-33
seq_documentation_block:
; Sequence 33, Application US/08470837
; Patent No. 5800811
; GENERAL INFORMATION:
; APPLICANT: Nimni, Marcel E.
; APPLICANT: Hall, Frederick L.
; APPLICANT: Tuan, Tai-Lan
; APPLICANT: Wu, Lingtao
; APPLICANT: Cheung, David T.
; TITLE OF INVENTION: Transforming Growth Factor B Fusion
; TITLE OF INVENTION: and
; TITLE OF INVENTION: Their Use in Wound Healing
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 11150 Santa Monica Boulevard, Suite 400
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90025-3395
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,837
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharp, Janice A.
; REGISTRATION NUMBER: 34,051
; REFERENCE/DOCKET NUMBER: 30630-1US01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 310-445-1140
; TELEFAX: 310-445-9031
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 339 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..336
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; NAME/KEY: mat_peptide
; LOCATION: 1
; US-08-470-837-33

alignment_scores:
Quality: 633.00 Length: 112
Ratio: 5.652 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

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17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
|||||
51 GCGCCCTCTACATTGCTCCGACAGGATCTGGCTGGAGTGGGTCC 100
34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
|||||
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51 LeuArgSerAlaAspThrHisSerThrValLeuGlyLeuTyrAsnTh 67
|||||
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67 rLeuAsnProGluAlaSerAlaSerProCysValProGlnAspLeuG 84
|||||
201 TCTGAACCTGAAGCATCTGCCTCGCTTGCCTGGCTGCCAGGACCTGG 250
84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
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seq_documentation_block:
; Sequence 3, Application US/08789588
; Patent No. 5922846
; GENERAL INFORMATION:
; APPLICANT: Carletti, Nico
; APPLICANT: McMaster, Gary K.
; APPLICANT: Cox, David
; APPLICANT: Schmitz, Albert
; APPLICANT: Meyhack, Bernd
; TITLE OF INVENTION: Process for Refolding Recombinantly
; TITLE OF INVENTION: Produced TGF-beta-like Proteins
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Henry P. No. 5922846ak
; STREET: 520 White Plains Road, P.O. Box 2005
; CITY: Tarrytown
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10591-9005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08789,588
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/486,057
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/201,703
; FILING DATE: 25-FEB-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/960,309
; FILING DATE: 13-OCT-1992
; PRIOR APPLICATION DATA:
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seq_documentation_block:
; Sequence 5, Application US/09123233
; Patent No. 6057430
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: No. 6057430e1 process for the production of
; TITLE OF INVENTION: biologically active dimeric protein
; NUMBER OF SEQUENCES: 14
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Ratio: 5.652 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
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51 GCGCCCTCTACATTGCTCCGACAGGATCTGGCTGGAGTGGGTCC 100
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51 LeuArgSerAlaAspThrHisSerThrValLeuGlyLeuTyrAsnTh 67
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67 rLeuAsnProGluAlaSerAlaSerProCysValProGlnAspLeuG 84
|||||
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|||||
251 AGCCCTGACCATCTCTACTATGTTGGGAGGACCCCAAGTGGAGCAG 300
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301 CTCCTCAACATGGTGGTGAAGTCTTGTAAATGTAGC 336
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/123,233
FILING DATE:
CLASSIFICATION: 530
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 339 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
IMMEDIATE SOURCE:
CLONE: E. coli LC137/pPLMu.htGF-beta3 (DSM 5658)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..336
OTHER INFORMATION: /product= "human TGF-beta3"
US-09-123-233-5

alignment_scores:
Quality: 633.00 Length: 112
Ratio: 5.652 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

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34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
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51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
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151 CTCCGAGTGCAGACACACACCCAGCAGCGTGTGGGACTGTACAACAC 200

67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
|||||
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84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
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seq_documentation_block:
Sequence 1, Application PC/TUS9104541
GENERAL INFORMATION:
APPLICANT: Oncogene Science Inc.
TITLE OF INVENTION: TISSUE DERIVED TUMOR GROWTH INHIBITORS
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham

METHODS OF PR

STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/04541
FILING DATE: 19910625
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 1919/22669-F-PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)977-9550
TELEFAX: (212)664-0525
TELEX: 422523 COOP UI
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2529 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: N
ANTI-SENSE: N
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Transforming Growth Factor-Beta 3
IMMEDIATE SOURCE:
CLONE: TGF-B3
FEATURE:
NAME/KEY: CDS
LOCATION: 263..1498
OTHER INFORMATION:
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 263..1498
OTHER INFORMATION:
PCT-US91-04541-1

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Quality: 633.00 Length: 112
Ratio: 5.652 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

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17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
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1213 GCGCCCTCTCACTGATGCTCCGACAGGATCTGGGCTGGAGTGGGTCC 1262

34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
|||||
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51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
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67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
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seq_documentation_block:
;Patent No. 5262319
;APPLICANT: IWATA, KENNETH K.; FOULKES, J. GORDON; DIJKE,
;PETER T.; HALEY, JOHN D.
;TITLE OF INVENTION: METHOD FOR OBTAINING BONE MARROW FREE
;OF TUMOR CELLS USING TRANSFORMING GROWTH FACTOR B3
;NUMBER OF SEQUENCES: 9
;CURRENT APPLICATION DATA:
;APPLICATION NUMBER: US/07/543,341
;FILING DATE: 25-JUN-1990
;PRIOR APPLICATION DATA:
;APPLICATION NUMBER: 353,410
;FILING DATE: 17-MAY-1989
;APPLICATION NUMBER: 183,410
;FILING DATE: 20-APR-1988
;APPLICATION NUMBER: 111,022
;FILING DATE: 20-OCT-1987
;APPLICATION NUMBER: 922,121
;FILING DATE: 20-OCT-1986
;APPLICATION NUMBER: 847,931
;FILING DATE: 07-APR-1986
;APPLICATION NUMBER: 725,003
;FILING DATE: 19-APR-1985
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Percent Similarity: 100.000 Percent Identity: 100.000

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17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
|||||
1213 GCGCCCTCTACATTTGACTTCCGACAGGATCTGGGCTGGAAAGTGGTCC 1262

34 lsGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
|||||
1263 ATGAACCTAAGGCTACTATGCAACCTTCCGAGGAGGCTGGCCATAC 1312

51 LeuArgSerAlaAspThrHisSerThrValLeuGlyLeuTyrAsnTh 67
|||||
1313 CTCCGAGTGCACACACACACACAGCAGCAGTCTGGAGCTGTACACAC 1362

67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
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1363 TCTGAACCTGAAGCATCTGCTCGCCTTGTGGTGGCCCGAGGACCTGG 1412

84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
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1413 AGCCCTGACCATCTGTACTATGTTGGAGGACCCCAAGTGGAGCAG 1462

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seq_documentation_block:
;Patent No. 5168051
;APPLICANT: DERYNCK, RIK M.A.; GOEDEL, DAVID V.
;TITLE OF INVENTION: NUCLEIC ACID ENCODING TGF-B ITS USES
;NUMBER OF SEQUENCES: 21
;CURRENT APPLICATION DATA:
;APPLICATION NUMBER: US/07/389,929
;FILING DATE: 04-AUG-1989
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Ratio: 5.595 Gaps: 0
Percent Similarity: 99.107 Percent Identity: 98.214

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Align seg 1/1 to: 5168051-9 from: 1 to: 2671

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17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
|||||
1209 GCGCCCTCTACATTTGACTTCCGACAGGATCTGGGCTGGAAAGTGGTCC 1258

34 lsGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
|||||
1259 ATGAACCTAAGGCTACTATGCAACTTCTGCTCAGGCCCTTGCCCGTAC 1308

51 LeuArgSerAlaAspThrHisSerThrValLeuGlyLeuTyrAsnTh 67
|||||
1309 CTCCGAGTGCACACACACACAGCAGTCTGGTCTGGGCTGTACACAC 1358

67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
|||||
1359 CTTGAACCCCGAAGCCTCGGCCCTCCCGTCTCGGTCGCCCGAGGACCTGG 1408

84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
|||||
1409 AGCCCTGACCATCTGTACTAGTCTGGAGGACCCCAAGTGGAGCAG 1458

101 LeuSerAsnMetValValLysSerCysLysCysSer 112
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1459 CTCTCAACATGGTGGTGAAGTCTGCAAGTGCAGC 1494

seq_name: /cgn2_6/ptodata/2/ina/backfiles1.seq:5168051-10
seq_documentation_block:
;Patent No. 5168051
;APPLICANT: DERYNCK, RIK M.A.; GOEDEL, DAVID V.
;TITLE OF INVENTION: NUCLEIC ACID ENCODING TGF-B ITS USES
;NUMBER OF SEQUENCES: 21
;CURRENT APPLICATION DATA:
;APPLICATION NUMBER: US/07/389,929
;FILING DATE: 04-AUG-1989
;SEQ ID NO:10
;LENGTH: 2233
5168051-10

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alignment_scores:
    Quality: 600.00      Length: 112
    Ratio: 5.405         Gaps: 0
    Percent Similarity: 99.107    Percent Identity: 98.214
alignment_block:
    TGFb3P x 5168051-10
Align seg 1/1 to: 5168051-10 from: 1 to: 2173
1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluAsnCysCysVa 17
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278 GCTTTGGACCAATACATGCTTCCCAACTTGGAGGAACTGCTGTGT 327
17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
|||||
328 GGGCCCCCTCTACATGACTTCGGACAGGATCTGGGCTGGAAGTGGGTCC 377
34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
|||||
378 ATGAACCTAAGGCTACTA.GCCAACTTCTGCTCAGGCCCTTGCCCATAC 426
51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
|||||
427 CTCCCGAGTGCAGACACAAACCCACAGCAGCGTCTGGGACTGTACAACAC 476
67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
|||||
477 TCTGAACCTCGAAGCATCTGCTCGCCTTGTGCAATGCCCGAGGACCTGG 526
84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
|||||
527 AGCCCTTGACCATCTGTACTATGTTGGAGGACCCCAAGTGGAGCAG 576
101 LeuSerAsnMetValLysSerCysLysCysSer 112
|||||
577 CTCTCCACATGGTGGTGAAGTCTTGTAAATGTAGC 612
seq_name: /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-09-123-233-7

seq_documentation_block:
; Sequence 7, Application US/09123233
; Patent No. 6057430
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: No. 6057430el process for the production of
; biologically active dimeric protein
; NUMBER OF SEQUENCES: 14
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/123.233
; FILING DATE:
; CLASSIFICATION: 530
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 336 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "recombinant hybrid DNA of
; TGF-beta1 and TGF-beta3 DNA"
; IMMEDIATE SOURCE:
; CLONE: E. coli LC137/pPLMu.TGF-beta1(44/45)beta3
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 1..132

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; OTHER INFORMATION: /product= "N-terminal 44 amino
; OTHER INFORMATION: acids of human TGF-beta1"
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 133..336
; OTHER INFORMATION: /product= "C-terminal 68 amino
; OTHER INFORMATION: acids of human TGF-beta3"
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..336
; OTHER INFORMATION: /product= "hybrid TGF-beta named
; OTHER INFORMATION: TGF-beta1-3"
; US-09-123-233-7

alignment_scores:
    Quality: 595.00      Length: 112
    Ratio: 5.459         Gaps: 0
    Percent Similarity: 97.321    Percent Identity: 92.857
alignment_block:
    TGFb3P x US-09-123-233-7
Align seg 1/1 to: US-09-123-233-7 from: 1 to: 336
1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluAsnCysCysVa 17
|||||
1 GCCTGGACACCAACTATTGCTTCAGCTCCACGGAGAACTGCTGCGT 50
17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
|||||
51 GCGGCACTGTACATGACTTCCGCAAGGACCTCGGCTGGAAGTGGATCC 100
34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
|||||
101 ACAGCCCAAGGCTACCATGCCAACTTCTGCTCAGGCCCTTGCCCATAC 150
51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
|||||
151 CTCCGAGTGCAGACACACACCCACAGCAGCGTCTGGGACTGTACAACAC 200
67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
|||||
201 TCTGAACCTCGAAGCATCTGCTCGCCTTGTGCTGCCCGAGGACCTGG 250
84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
|||||
251 AGCCCTTGACCATCTGTACTATGTTGGAGGACCCCAAGTGGAGCAG 300
101 LeuSerAsnMetValLysSerCysLysCysSer 112
|||||
301 CTCTCCACATGGTGGTGAAGTCTTGTAAATGTAGC 336
seq_name: /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-09-123-233-9

seq_documentation_block:
; Sequence 9, Application US/09123233
; Patent No. 6057430
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: No. 6057430el process for the production of
; biologically active dimeric protein
; NUMBER OF SEQUENCES: 14
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/123.233
; FILING DATE:
; CLASSIFICATION: 530
; INFORMATION FOR SEQ ID NO: 9:

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101 LeuSerAsnMetValVallYsserCysLysCysSer 112
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301 CTTTCTAATGATTGAAGCTTGCAGGATGAGC 336

seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-486-057B-2
seq_documentation_block:
; Sequence 2, Application US/08486057B
; Patent No. 5650494
; GENERAL INFORMATION:
; APPLICANT: Cerletti, Nico
; APPLICANT: McMaster, Gary K.
; APPLICANT: Cox, David
; APPLICANT: Schmitz, Albert
; APPLICANT: Meyhack, Bernd
; TITLE OF INVENTION: Process for Refolding Recombinantly
; Produced TGF-beta-like Proteins
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Henry P. No. 5650494ak
; STREET: 520 White Plains Road, P.O. Box 2005
; CITY: Tarrytown
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10591-9005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,057B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/201,703
; FILING DATE: 25-FEB-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/960,309
; FILING DATE: 13-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/621,502
; FILING DATE: 03-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 8927546.5
; FILING DATE: 06-DEC-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5650494ak, Henry P.
; REGISTRATION NUMBER: 33200
; REFERENCE/DOCKET NUMBER: 4-17861/+/Cont3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 277-5110
; TELEFAX: (908) 277-4306
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 339 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..339
US-08-486-057B-2

alignment_scores:
Quality: 535.00 Length: 112
Ratio: 5.095 Gaps: 0
Percent Similarity: 93.750 Percent Identity: 79.464

alignment_block:
TGFB3P x US-08-486-057B-2
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Align seq 1/1 to: US-08-486-057B-2 from: 1 to: 339

1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
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1 GCITTTGGATGGCGCTATTGCTTTAGAAATGTGCAGGATAAATTGCTGCCT 50

17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTyrLysTrpValH 34
|||||:|||||:|||||:|||||:|||||:|||||:
51 ACGTCCACTTTACATTGATTTCGAAGAGGGATCTAGGTGGAAATGGATAC 100

34 iGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
|||||:|||||:|||||:|||||:|||||:|||||:
101 ACGAACCCAAAGGGTACAATGCCCAACTTCTGCTGGAGCATGCCCGTAT 150

51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
|||||:|||||:|||||:|||||:|||||:|||||:
151 TTATGGAGTTCACACTCAGCACAGGAGGTCTGAGCTTATATAATAC 200

67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
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201 CATAAATCCAGAGCATCTGCTTCTCCTGCTGCTGCCAAGATTAG 250

84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
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251 AACCTCTAACCATTTCTACTACTATTGGCAAAACACCCCAAGATTGAACAG 300

101 LeuSerAsnMetValVallYsserCysLysCysSer 112
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seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-470-837-31
seq_documentation_block:
; Sequence 31, Application US/08470837
; Patent No. 5800811
; GENERAL INFORMATION:
; APPLICANT: Nimni, Marcel E.
; APPLICANT: Hall, Frederick L.
; APPLICANT: Tuan, Tai-Lan
; APPLICANT: Wu, Lingtao
; APPLICANT: Cheung, David T.
; TITLE OF INVENTION: Transforming Growth Factor B Fusion
; TITLE OF INVENTION: and
; TITLE OF INVENTION: Their Use in Wound Healing
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 11150 Santa Monica Boulevard, Suite 400
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90025-3395
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,837
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharp, Janice A.
; REGISTRATION NUMBER: 34,051
; REFERENCE/DOCKET NUMBER: 30630-1US01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 310-445-1140
; TELEFAX: 310-445-9031
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 339 base pairs
; TYPE: nucleic acid
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251 AACCTCTAACCAATTCCTACTACATTGGCAAAACACCCCAAGATTGAACAG 300
101 LeuSerAsnMetValVallySerCysLysCysSer 112
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seq_name: /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-09-123-233-3

seq_documentation_block:
; Sequence 3, Application US/09123233
; Patent No. 6057430
; GENERAL INFORMATION:
; APPLICANT: Mu-En Lee
; TITLE OF INVENTION: No. 6057430el process for the production of
; biologically active dimeric protein
; NUMBER OF SEQUENCES: 14
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/123,233
; FILING DATE:
; CLASSIFICATION: 530
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 339 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cdna to mRNA
; IMMEDIATE SOURCE:
; CLONE: E. coli LC137/pPLMu.htGF-beta2 (DSM5657)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..336
; OTHER INFORMATION: /product= "human TGF-beta2"
US-09-123-233-3

alignment_scores:
Quality: 535.00 Length: 112
Ratio: 5.095 Gaps: 0
Percent Similarity: 93.750 Percent Identity: 79.464

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1 GCCTTTGGATGCGGCCTATTGCTTTAGAAATGTGCAAGGATAATGCTGCCT 50
17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
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51 ACCTCCACTTTACATGATTTCAGAGGGATCTAGGGTGAATGGATAC 100
34 lGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
|||||
101 ACGAACCCAAAGGGTACAATGCCACTTCTGTGTGGAGCATGCCCGTAT 150
51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
|||||
151 TTATGGAGTTCAGACACTCAGACAGAGGGTCCCTGAGCTTATATAATAC 200
67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
|:|||||
201 CATAAATCCAGAGGATCGCTTCCTTCCTGCTGCTGCCAGGATTAG 250
84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
|||||

251 AACCTCTAACCAATTCCTACTACATTGGCAAAACACCCCAAGATTGAACAG 300
101 LeuSerAsnMetValVallySerCysLysCysSer 112
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seq_name: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:PCT-US94-03705-4

seq_documentation_block:
; Sequence 4, Application PC/TUS9403705
; GENERAL INFORMATION:
; APPLICANT: Mu-En Lee
; TITLE OF INVENTION: FACTOR- INHIBITS
; TITLE OF INVENTION: TRANSFORMING GROWTH
; TITLE OF INVENTION: INDUCIBLE NITRIC OXIDE
; TITLE OF INVENTION: SYNTHASE GENE
; TITLE OF INVENTION: TRANSCRIPTION
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/03705
; FILING DATE: 5 April 1994
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Janis K. Fraser
; REGISTRATION NUMBER: Reg. No. 34,819
; REFERENCE/DOCKET NUMBER: 05433/007001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
PCT-US94-03705-4

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Quality: 535.00 Length: 112
Ratio: 5.095 Gaps: 0
Percent Similarity: 93.750 Percent Identity: 79.464

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17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
:|||||
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1707 AACCTTAACCATTCCTATTATTTGGCAAAACACCAGAATTGAACAG 1756
      101 LeuSerAsnMetValVallySerCysLysCysSer 112
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seq_name: /cgn2_6/ptodata/2/ina/backfiles1.seq:5221620-3
seq_documentation_block:
; Patent No. 5221620
; APPLICANT: PURCHIO; ANTHONY F.; MADISEN, LINDA; WEBB, NANCY
; TITLE OF INVENTION: CLONING AND EXPRESSION OF TRANSFORMING
; GROWTH FACTOR BETA-2
; NUMBER OF SEQUENCES: 16
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/446,020
; FILING DATE: 05-DEC-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 285,140
; FILING DATE: 16-DEC-1988
; APPLICATION NUMBER: 234,065
; FILING DATE: 18-AUG-1988
; APPLICATION NUMBER: 148,267
; FILING DATE: 25-JAN-1988
; APPLICATION NUMBER: 106,752
; FILING DATE: 06-OCT-1987
; SEQ ID NO:3:
; LENGTH: 2207
; 5221620-3

alignment_scores:
    Quality: 532.00      Length: 112
    Ratio: 5.115        Gaps: 0
Percent Similarity: 92.857 Percent Identity: 79.464

alignment_block:
TGFB3P x 5221620-3 ..
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1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluuAsnCysCysVa 17
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1095 GCTTTGGATCCGGCCTATTGCTTTTACAAATGTCAGCATAAATGCTGCCT 1144

17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTyrLpLysTrpValH 34
|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
1145 AGCTGCACCTTTACATTGATTTCAAGAGGATCTTAGGTGGAAATGGATAC 1194

34 lSgluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
1195 AGCAACCCAAAGGGTACAATGGCAACTCTGTCTGGAGCATGCCCGTAT 1244

51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
1245 TTATGGAGTTCAGACACTCAGCACACGAGGTCCTGAGCTTATATATATAC 1294

67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
1295 CATAAATCCAGAAGCATCTGCTTCTCTTGGTGGGTGCCCAAGATTAG 1344

84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
1345 AACCTCTAACCATTTCTCTACTACATTGGCAAAACACCCAGATTGAACAG 1394

101 LeuSerAsnMetValValLysSerCysLysCysSer 112
|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
1395 CTTTCTAATATGATTGTAAAGTCTTGCAATGCAGC 1430

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seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-07-669-171-3

seq_documentation_block:
; Sequence 3, Application US/07669171
; Patent No. 530451
; GENERAL INFORMATION:
; APPLICANT: PURCHIO, ANTHONY F.
; APPLICANT: MADISEN, LINDA
; APPLICANT: MERWIN, JUNE RAE
; TITLE OF INVENTION: TGF-b1/D2: A NOVEL CHIMERIC TRANSFORMING
; TITLE OF INVENTION: GROWTH FACTOR-BETA
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS
; STREET: 1155 AVENUE OF THE AMERICAS
; CITY: NEW YORK
; STATE: N.Y.
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/669,171
; FILING DATE: 19910314
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MISROCK, S. LESLIE
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 5624-159-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1569 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-07-669-171-3

alignment_scores:
Quality: 513.00 Length: 112
Ratio: 5.079 Gaps: 0
Percent Similarity: 90.179 Percent Identity: 76.786

alignment_block:
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17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTyrLysTyrValH 34
1154 AGTCGCGCTTACATTGATTTCAAGAGGATCTAGGCTGGAAGTGGATCC 1203
34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
1204 ACGAGCCCAAGGCTACCATGCCAACTTGCCTCGGCGCTCCGCCCTAC 1253
51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnH 67
1254 ATTTGAGCGCTGACGACGAGTACAGCAAGGTCTGGCCCTGTACAACCA 1303
67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84

1304 GCATAACCCGGCGCCTCGGCGCGCGTGTGCGTCCGCGAGCGCTGG 1353
84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
1354 AGCGCTGCGCCATCGTGTACTACGTGGCGCGCAAGCCCAAGGTGGAGCAG 1403
101 LeuSerAsnMetValValLysSerCysLysCysSer 112
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seq_documentation_block:
; Sequence 1, Application US/08486057B
; Patent No. 5650494
; GENERAL INFORMATION:
; APPLICANT: Cerletti, Nico
; APPLICANT: McMaster, Gary K.
; APPLICANT: Cox, David
; APPLICANT: Schmitz, Albert
; APPLICANT: Meyhack, Bernd
; TITLE OF INVENTION: Process for Refolding Recombinantly
; TITLE OF INVENTION: Produced TGF-beta-like Proteins
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Henry P. No. 5650494ak
; STREET: 520 White Plains Road, P.O. Box 2005
; CITY: Tarrytown
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10591-9005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,057B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/201,703
; FILING DATE: 25-FEB-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/960,309
; FILING DATE: 13-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/621,502
; FILING DATE: 03-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 8927546.5
; FILING DATE: 06-DEC-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5650494ak, Henry P.
; REGISTRATION NUMBER: 33200
; REFERENCE/DOCKET NUMBER: 4-17861/+/Cont3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 277-5110
; TELEFAX: (908) 277-4306
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 339 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..339
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..339

US-08-486-057B-1

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  Quality: 500.00      Length: 112
  Ratio: 5.102        Gaps: 0
  Percent Similarity: 87.500  Percent Identity: 76.786

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  Align seg 1/1 to: US-08-486-057B-1 from: 1 to: 339

1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
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1 GCCCTGGACACCAACTATTCTTCAGCTCCACGAGAGAAGAACTGCTGCGT 50

17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
|||||
51 GCGGACGCTGTACATTGACTTCCGCAAGGACCTCGGCTGGAAGTGGATCC 100

34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
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101 ACAGGCCAAGGCTACCATGCAACTTCTGCTCGGGCCCTGCCCTAC 150

51 LeuArgSerAlaAspThrHisSerThrValLeuGlyLeuTyrAsnTh 67
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151 ATTTGGAGCTGGACAGCGACGTACAGCAAGTCTTGCCCTGTACAACCA 200

67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
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201 GCATAACCGGGCGCTCGGCGCGCGCTGCTGCTGCGCGCGCGCTGG 250

84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
|||||
251 AGCGCTGCCCATCGTACTACGTGGGCGCGCAAGGCCAAGGTGGAGCAG 300

101 LeuSerAsnMetValValLysSerCysLysCysSer 112
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301 CTGTCCAACATGATCGTGGCTCTGCAAGTGGCAGC 336
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seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-470-837-29

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seq_documentation_block:
; Sequence 29, Application US/08470837
; Patent No. 5800811
; GENERAL INFORMATION:
; APPLICANT: Nimni, Marcel E.
; APPLICANT: Hall, Frederick L.
; APPLICANT: Tuan, Tai-Lan
; APPLICANT: Wu, Lingtao
; APPLICANT: Cheung, David T.
; TITLE OF INVENTION: Transforming Growth Factor B Fusion
; TITLE OF INVENTION: and
; TITLE OF INVENTION: Their Use in Wound Healing
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 11150 Santa Monica Boulevard, Suite 400
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90025-3395
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,837
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
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; NAME: Sharp, Janice A.
; REGISTRATION NUMBER: 34,051
; REFERENCE/DOCKET NUMBER: 30630-1US01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 310-445-1140
; TELEFAX: 310-445-9031
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 339 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..333
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alignment_scores:
  Quality: 500.00      Length: 112
  Ratio: 5.102        Gaps: 0
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1 AlaLeuAspThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysVa 17
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1 GCCCTGGACACCAACTATTCTTCAGCTCCACGAGAGAAGAACTGCTGCGT 50

17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
|||||
51 GCGGACGCTGTACATTGACTTCCGCAAGGACCTCGGCTGGAAGTGGATCC 100

34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
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101 ATGAGCCCAAGGCTTACCATGCAACTTCTGCTCGGGCCCTGCCCTAC 150

51 LeuArgSerAlaAspThrHisSerThrValLeuGlyLeuTyrAsnTh 67
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151 ATTTGGAGCTGGACACGACGTACAGCAAGTCTTGCCCTGTACAACCA 200

67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
|||||
201 GCATAACCGGGCGCTCGGCGCGCGCTGCTGCTGCGCGCGCGCTGG 250

84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
|||||
251 AGCGCTGCCCATCGTACTACGTGGGCGCGCAAGGCCAAGGTGGAGCAG 300

101 LeuSerAsnMetValValLysSerCysLysCysSer 112
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301 CTGTCCAACATGATCGTGGCTCTGCAAGTGGCAGC 336
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seq_name: /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-789-588-1

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seq_documentation_block:
; Sequence 1, Application US/08789588
; Patent No. 5922846
; GENERAL INFORMATION:
; APPLICANT: Cerletti, Nico
; APPLICANT: McMaster, Gary K.
; APPLICANT: Cox, David
; APPLICANT: Schmitz, Albert
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51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
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67 rLeuAsnProGluAlaSerAlaSerProCysValProGlnAspLeuG 84
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1876 GCATAACCCGGCGCGCTCGCGCGCGGTGCTGCGCGCAGGCGCTGG 1925
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84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
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1926 AGCGCGTCCCATCGTGTACTAGTGGCGCGCAAGCCCAAGGTGGAGCAG 1975
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101 LeuSerAsnMetValLysSerCysLysCysSer 112
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seq_name: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq: PCT-US94-03705-3

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seq_documentation_block:
; Sequence 3, Application PC/TUS9403705
; GENERAL INFORMATION:
; APPLICANT: Mu-En Lee
; APPLICANT: Mark A. Perrella
; TITLE OF INVENTION: TRANSFORMING GROWTH
; TITLE OF INVENTION: FACTOR- INHIBITS
; TITLE OF INVENTION: INDUCIBLE NITRIC OXIDE
; TITLE OF INVENTION: SYNTHASE GENE
; TITLE OF INVENTION: TRANSCRIPTION
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/03705
; FILING DATE: 5 April 1994
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Janis K. Fraser
; REGISTRATION NUMBER: Reg. No. 34,819
; REFERENCE/DOCKET NUMBER: 05433/007001
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2745
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
PCT-US94-03705-3

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  Ratio: 5.102        Gaps: 0
Percent Similarity: 87.500 Percent Identity: 76.786

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17 lArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpValH 34
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1729 GCGCAGCTGTACATTGACTTCGCCAAGGACCTCGGTGGAAGTGGATCC 1778
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34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
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51 LeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAsnTh 67
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67 rLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspLeuG 84
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1879 GCATAACCCGGCGCGCTCGCGCGCGGTGCTGCTGCGCGCAGGCGCTGG 1928
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
84 luProLeuThrIleLeuTyrTyrValGlyArgThrProLysValGluGln 100
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1929 AGCGCGTCCCATCGTGTACTAGTGGCGCGCAAGCCCAAGGTGGAGCAG 1978
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101 LeuSerAsnMetValLysSerCysLysCysSer 112
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seq_name: /cgn2_6/ptodata/2/ina/backfiles1.seq: 5168051-3

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seq_documentation_block:
; Patent No. 5168051
; APPLICANT: DERYNCK, RIK M.A.; GOEDDEL, DAVID V.
; TITLE OF INVENTION: NUCLEIC ACID ENCODING TGF-B ITS USES
; NUMBER OF SEQUENCES: 21
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/389,929
; FILING DATE: 04-AUG-1989
; SEQ ID NO:3:
; LENGTH: 975
5168051-3

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alignment_scores:
  Quality: 231.50      Length: 60
  Ratio: 4.724        Gaps: 1
Percent Similarity: 81.667 Percent Identity: 66.667

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Align seg 1/1 to: 5168051-3 from: 1 to: 975

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12 GluGluAsnCysCysValArgProLeuTyrIleAspPheArgGlnAspLe 28
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354 GAGAAGAACTGCTGCGTGGCGGACGCTGTACATTGACTTCCGCAAGGACCT 403
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28 uGlyTrpLysTrpValHisGluProLysGlyTyrTyrAlaAsnPheCys 45
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404 CGCTGGAAGTGGATCCACGAGCCCAAGGCTACCATGCCACCTTCGCCC 453
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
45 erGlyProCysProTyrLeuArgSerAlaAspThrThrHisSerThrVal 61
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454 TCGGGCCCTGCCCTACATTGGAGCGCTGGACACGACGACGACGCAAGSTA 503
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62 .....LeuGlyLeuTyrAsnThrLeu 68
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504 CGTGTGCCACCGGGCTACGAGATGCGCTT 533

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; Sequence 11, Application US/08274215A
; Patent No. 5831054
; GENERAL INFORMATION:
; APPLICANT: Lee, Se-Jin
; APPLICANT: Esqueda, Aurora F.
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-12
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: US
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/274,215A
; FILING DATE: 13-JUL-1994
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Ph.D., Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07265/040001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-678-5070
; TELEFAX: 619-68-5099
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 360 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 1...357
; US-08-274-215A-11

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Ratio: 2.784 Gaps: 6
Percent Similarity: 69.811 Percent Identity: 41.509

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31 s...TrpValHisGluProLysGlyTyrtYrAlaAsnPheCysSerGlyp 47
: ||| : : ||| : : ||| : : ||| : : ||| : : ||| :
93 GGACTGGATACTGCAGCCGAGGGGTACCAGCTGAATTACGACGTGGGC 142

47 roCys...ProTyrlleuArgSer.....AlaAspThrThrHis 58
||| ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
143 AGTGCCTCCCCACCTGGCTGCAGCCAGCCAGCATGTGCTCTTTCCAT 192

59 SerThrValLeuGlyLeuTyrtYrAsnThrLeuAsnProGluAlaSerAlaSe 75
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alignment_scores:
  Quality: 206.00
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  Percent Similarity: 69.811
  Length: 106
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  Percent Identity: 41.509

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31 s...TrpValHisGluProLysGlyTyrTyrAlaAsnPheCysSerGlyP 47
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93 GGACTGGATACGACGCGGAGGGGTACCAAGTGAATTAATGCACTGGGCG 142

47 roCys...ProTyrLeuArgSer.....AlaAspThrThrHis 58
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143 AGTGGCCCTCCACCTGGCTGGCAGCCAGGAGTGTCTCTCTCTTTCAT 192

59 SerThrValLeuGlyLeuTyrAsnThrLeuAsnProGluAlaSerAlaSe 75
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193 TCTGCGCTCTTCAAGCTCTCTCAAGGCAACATCTCTGGCTGCCAGTAC 242

75 rProCysValProGlnAspLeuGluProLeuThrIleLeuTyr... 90
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243 CTCCTGTTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 292

91 ...TyrValGlyArgThrProLysValGluGlnLeuSerAsnMetValVal 106
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293 ATCAATATGGCAATGTGTCAAGACGGAT...GTGCCAGATATGTTGGTG 339

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seq_documentation_block:
; Sequence 11, Application US/09184933
; Patent No. 6130050
; GENERAL INFORMATION:
; APPLICANT: Lee, Se-Jin
; APPLICANT: Esquela, Aurora F.
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-12
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: US
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/184,933
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/274,215
; FILING DATE: 13-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Ph.D., Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07265/040001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-678-5070
; TELEFAX: 619-68-5099
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 360 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
;
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 1...357
; US-09-184-933-11

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Quality: 206.00 Length: 106
Ratio: 2.784 Gaps: 6
Percent Similarity: 69.811 Percent Identity: 41.509

alignment_block:
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Align seg 1/1 to: US-09-184-933-11 from: 1 to: 360

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46 TGTTCAGCGGAGAGACCATACGTAGACTTC...CAGGAACCTGGGATGGCG 92

31 s...TrpValHisGluProLysGlyTyrTyrAlaAsnPheCysSerGlyP 47
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93 GGACTGGATACGACGCGGAGGGGTACCAAGTGAATTAATGCACTGGGCG 142

47 roCys...ProTyrLeuArgSer.....AlaAspThrThrHis 58
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
143 AGTGGCCCTCCACCTGGCTGGCAGCCAGGAGTGTCTCTCTCTTTCAT 192

59 SerThrValLeuGlyLeuTyrAsnThrLeuAsnProGluAlaSerAlaSe 75
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193 TCTGCGCTCTTCAAGCTCTCTCAAGGCAACATCTCTGGCTGCCAGTAC 242

75 rProCysValProGlnAspLeuGluProLeuThrIleLeuTyr... 90
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91 ...TyrValGlyArgThrProLysValGluGlnLeuSerAsnMetValVal 106
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
293 ATCAATATGGCAATGTGTCAAGACGGAT...GTGCCAGATATGTTGGTG 339

107 LysSerCysLysCysSer 112
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340 GAGGCGCTGTGGCTGCAGC 357

seq_name: /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-09-184-933-11

seq_documentation_block:
; Sequence 11, Application PC/TUS9508745
; GENERAL INFORMATION:
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-12
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/08745
; FILING DATE: 12-JUL-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Ph.D., Lisa A.
; REGISTRATION NUMBER: 38,347
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> ADDRESS: Legal Affairs, Genetics Institute, Inc.
> STREET: 87 Cambridgepark Drive
> CITY: Cambridge
> STATE: MA
> COUNTRY: USA
> ZIP: 02140
> COMPUTER READABLE FORM:
> MEDIUM TYPE: Floppy disk
> COMPUTER: IBM PC compatible
> OPERATING SYSTEM: PC-DOS/MS-DOS
> SOFTWARE: PatentIn Release #1.0, Version #1.25
> CURRENT APPLICATION DATA:
> APPLICATION NUMBER: US/07/764,731B
> FILING DATE: 19910924
> CLASSIFICATION: 435
> ATTORNEY/AGENT INFORMATION:
> NAME: Kapinos, Ellen J.
> REGISTRATION NUMBER: 32,245
> REFERENCE/DOCKET NUMBER: G15159B
> TELECOMMUNICATION INFORMATION:
> TELEPHONE: 617-876-1170
> TELEFAX: 617-876-5851
> INFORMATION FOR SEQ ID NO: 5:
> SEQUENCE CHARACTERISTICS:
> LENGTH: 400 base pairs
> TYPE: NUCLEIC ACID
> STRANDEDNESS: double
> TOPOLOGY: circular
> MOLECULE TYPE: cDNA to mRNA
> HYPOTHETICAL: NO
> FRAGMENT TYPE: C-terminal
> ORIGINAL SOURCE:
> ORGANISM: Homo sapiens
> CELL LINE: U2-OS Osteosarcoma
> IMMEDIATE SOURCE:
> LIBRARY: U2-OS human osteosarcoma cDNA library
> CLONE: U2-7
> POSITION IN GENOME:
> UNITS: bp
> FEATURE:
> NAME/KEY: CDS
> LOCATION: 1..399
> FEATURE:
> NAME/KEY: mat_peptide
> LOCATION: 1..400
> FEATURE:
> NAME/KEY: mRNA
> LOCATION: 1..400
> US-07-764-731B-5

alignment_scores:
    Quality: 206.00      Length: 113
    Ratio: 2.822         Gaps: 4
Percent Similarity: 64.602      Percent Identity: 37.168

alignment_block:
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4 ThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysValArgProLe 20
   ::::::::::: ::::::::::: ::::::::::: :::::::::::
58 TCAGATTACAACAGCAGCTGAATTGAAACACGCCCTGCAGGAAGCATGAGCT 107
   uUyrIlleAspPheArgGlnAspLeuGlyTyrPlys...TrrValHisGluP 36
   ::::::::::: ::::::::::: ::::::::::: :::::::::::
108 GRATGTGAGTTTC...CAAGACCTGGGATGCGCAGGACTGGATCATGTCAC 154

36 roLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyrLeuArg 52
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53 SerAlaAsp.....ThrThrHisSerThrValLeuGlyLeuTyraS 66
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205 AAGCACACATGAATGCAACCAACGAGTGTGCAGACCTTGGTTCA 254
: : : : : | | | | | : : : : : | | | | |
66 nThrLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspL 83
: : : : : | | | | | : : : : : | | | | |
255 CCTATGAACCCGAGTATGCCCAACCGTCTGTGCGCCAACCTAAGC 304
: : : : : | | | | | : : : : : | | | | |
83 euGlupProLeuThrIleLeuTyTyValGlyArgThrProLysVal... 98
: : : : : | | | | | : : : : : | | | | |
305 TAAATGCCATCTCGGTTCTTACTTGTGATGACAACCTCAATGTCATTCTG 354
: : : : : | | | | | : : : : : | | | | |
99 GluGlnLeuSerAsnMetValValLysSerCysLysCys 111
: : : : : | | | | | : : : : : | | | | |
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seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-163-877-7

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seq_documentation_block:
; Sequence 7, Application US/08163877
; Patent No. 5399677
; GENERAL INFORMATION:
; APPLICANT: McCoy, John
; APPLICANT: Murray, Beth
; APPLICANT: Wolfman, Neil
; TITLE OF INVENTION: MUTANTS OF BONE MORPHOGENIC PROTEINS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc - Legal Affairs
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/163,877
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Lazar, Steven R.
; REGISTRATION NUMBER: 32,618
; REFERENCE/DOCKET NUMBER: GI 5219
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617 876-1170 x 8260
; TELEFAX: 617 876-5851
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 406 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: bmp-6
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..396
; US-08-163-877-7
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Ratio: 2.822 Gaps: 4
Percent Similarity: 64.602 Percent Identity: 37.168

alignment_block:
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58 TCAGATTACAAACAGCAGTGAATTGAAACAGCCTGCAGGAAGCATGAGCT 107
: : : : : | | | | | : : : : : | | | | |
20 uTyriLeAspPheArgGlnAspLeuGlyTrpLys...TrpValHisGluP 36
: : : : : | | | | | : : : : : | | | | |
108 GTATGTGAGTTTC...CAAGACCTGGGATGCGAGGACTGGATCATTCAC 154
: : : : : | | | | | : : : : : | | | | |
36 roLysGlyTyTyTyAlaAsnPheCysSerGlyProCysProTyTyLeuArg 52
: : : : : | | | | | : : : : : | | | | |
155 CCAAGGCTATGTCGCAATTACTGTGTGAGAAATGCTCTCTCCCATC 204
: : : : : | | | | | : : : : : | | | | |
53 SerAlaAsp.....ThrThrHisSerThrValLeuGlyLeuTyraS 66
: : : : : | | | | | : : : : : | | | | |
205 AAGCACACATGAATGCAACCAACGAGTGTGCAGACCTTGGTTCA 254
: : : : : | | | | | : : : : : | | | | |
66 nThrLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspL 83
: : : : : | | | | | : : : : : | | | | |
255 CCTATGAACCCGAGTATGCCCAACCGTCTGTGCGCCAACCTAAGC 304
: : : : : | | | | | : : : : : | | | | |
83 euGlupProLeuThrIleLeuTyTyValGlyArgThrProLysVal... 98
: : : : : | | | | | : : : : : | | | | |
305 TAAATGCCATCTCGGTTCTTACTTGTGATGACAACCTCAATGTCATTCTG 354
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99 GluGlnLeuSerAsnMetValValLysSerCysLysCys 111
: : : : : | | | | | : : : : : | | | | |
355 AAAAAATACAGGAATATGTTGTAAGAGCTTGTGGATGC 393
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seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-360-914B-7

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seq_documentation_block:
; Sequence 7, Application US/08360914B
; Patent No. 5756308
; GENERAL INFORMATION:
; APPLICANT: Neil M. Wolfman and John McCoy
; TITLE OF INVENTION: MUTANTS OF BONE MORPHOGENIC PROTEINS
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc - Legal Affairs
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/360,914B
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/163,877
; FILING DATE: December 7, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Lazar, Steven R.
; REGISTRATION NUMBER: 32,618
; REFERENCE/DOCKET NUMBER: GI 5219B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617 498-8260
; TELEFAX: 617 876-5851
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 406 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; ORIGINAL SOURCE:
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; ORGANISM: bmp-6
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..396
US-08-360-914B-7

alignment_scores:
  Quality: 206.00      Length: 113
  Ratio: 2.822         Gaps: 4
Percent Similarity: 64.602 Percent Identity: 37.168

alignment_block:
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Align seg 1/1 to: US-08-360-914B-7 from: 1 to: 406

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58 TCAGATTACACACAGCAGTGAATTGAAACACGCTGCAGGAAGCATGAGCT 107
20 uTyrIleAspPheArgGlnAspLeuGlyTrpLys...TrpValHisGluP 36
108 GTATGTGAGTTTC...CAAGACCTGGGATGGCAGACTGGATCATTCAC 154
36 roLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyrLeuArg 52
155 CCAAGGCGTATGCTGCCAATTACTGTGATGGAGAATGCTCTTCCCACTC 204
53 SerAlaAsp.....ThrThrHisSerThrValLeuGlyLeuTyrAs 66
205 AACGCACACATGAATGCAACCAACACCGGATTTGCGAGACCTTGGTTCA 254
66 nThrLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspL 83
255 CCTTATGAACCCGAGTATGCTCCCAACCGTGTGTGCGCCAACTAAGC 304
83 euGluProLeuThrIleLeuTyrValGlyArgThrProLysVal... 98
305 TAAATGCCATCTCGGTTCTTACTTTGATGACACAACTCCAATGTCATCTG 354
99 GluGlnLeuSerAsnMetValLysSerCysLysCys 111
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seq_name: /cqn2_6/ptodata/2/ina/5A_COMB.seq:US-08-741-589A-7

seq_documentation_block:
; Sequence 7, Application US/08741589A
; Patent No. 5804416
; GENERAL INFORMATION:
; APPLICANT: Neil M. WOLFMAN and John MCCOY
; TITLE OF INVENTION: MUTANTS OF BONE MORPHOGENIC PROTEINS
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc - Legal Affairs
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/741,589A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/163,877
; FILING DATE: December 7, 1993
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; ATTORNEY/AGENT INFORMATION:
; NAME: Lazar, Steven R.
; REGISTRATION NUMBER: 32,618
; REFERENCE/DOCKET NUMBER: GI 5219B-DIV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617 498-8260
; TELEFAX: 617 876-5851
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 406 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; ORIGINAL SOURCE:
; ORGANISM: bmp-6
; NAME/KEY: CDS
; LOCATION: 1..396
US-08-741-589A-7

alignment_scores:
  Quality: 206.00      Length: 113
  Ratio: 2.822         Gaps: 4
Percent Similarity: 64.602 Percent Identity: 37.168

alignment_block:
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Align seg 1/1 to: US-08-741-589A-7 from: 1 to: 406

4 ThrAsnTyrCysPheArgAsnLeuGluGluAsnCysCysValArgProLe 20
58 TCAGATTACACACAGCAGTGAATTGAAACACGCTGCAGGAAGCATGAGCT 107
20 uTyrIleAspPheArgGlnAspLeuGlyTrpLys...TrpValHisGluP 36
108 GTATGTGAGTTTC...CAAGACCTGGGATGGCAGACTGGATCATTCAC 154
36 roLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyrLeuArg 52
155 CCAAGGCGTATGCTGCCAATTACTGTGATGGAGAATGCTCTTCCCACTC 204
53 SerAlaAsp.....ThrThrHisSerThrValLeuGlyLeuTyrAs 66
205 AACGCACACATGAATGCAACCAACACCGGATTTGCGAGACCTTGGTTCA 254
66 nThrLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspL 83
255 CCTTATGAACCCGAGTATGCTCCCAACCGTGTGTGCGCCAACTAAGC 304
83 euGluProLeuThrIleLeuTyrValGlyArgThrProLysVal... 98
305 TAAATGCCATCTCGGTTCTTACTTTGATGACACAACTCCAATGTCATCTG 354
99 GluGlnLeuSerAsnMetValLysSerCysLysCys 111
355 AAAAAATACAGGAATATGGTTGTAAGAGCTTGTGGATGC 393

seq_name: /cqn2_6/ptodata/2/ina/PCTUS_COMB.seq:PCT-US94-13181-7

seq_documentation_block:
; Sequence 7, Application PC/TUS9413181
; GENERAL INFORMATION:
; APPLICANT: GENETICS INSTITUTE, INC.
; TITLE OF INVENTION: MUTANTS OF BONE MORPHOGENIC PROTEINS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc - Legal Affairs
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: Massachusetts
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> COUNTRY.: USA
> ZIP: 02140
> COMPUTER READABLE FORM:
> MEDIUM TYPE: Floppy disk
> COMPUTER: IBM PC compatible
> OPERATING SYSTEM: PC-DOS/MS-DOS
> SOFTWARE: Patentin Release #1.0, Version #1.25
> CURRENT APPLICATION DATA:
> APPLICATION NUMBER: PCT/US94/13181
> FILING DATE:
> CLASSIFICATION:
> PRIOR APPLICATION DATA:
> APPLICATION NUMBER: US 08/163,877
> FILING DATE: December 7, 1993
> ATTORNEY/AGENT INFORMATION:
> NAME: Lazar, Steven R.
> REGISTRATION NUMBER: 32,618
> REFERENCE/DOCKET NUMBER: GI 5219-PCT
> TELECOMMUNICATION INFORMATION:
> TELEPHONE: 617 498-8260
> TELEFAX: 617 876-5851
> INFORMATION FOR SEQ ID NO: 7:
> SEQUENCE CHARACTERISTICS:
> LENGTH: 406 base pairs
> TYPE: nucleic acid
> STRANDEDNESS: double
> TOPOLOGY: linear
> MOLECULE TYPE: DNA
> ORIGINAL SOURCE:
> ORGANISM: bmp-6
> FEATURE:
> NAME/KEY: CDS
> LOCATION: 1..396
> PCT-US94-13181-7

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    Quality: 206.00      Length: 113
    Ratio: 2.822        Gaps: 4
Percent Similarity: 64.602 Percent Identity: 37.168

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58 TCAGATTACAACAGCAGTGGAATTCGAAACAGCGCTGCAGGAAGCATGACT107
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20 uTyriLeaspPheArgGlnAspLeuGlyTrpLys...TrpValHisGlu36
   : :::::|||||
108 GTATGTGAGTTTC...CAAGACCTGGGATGGCAGGACTGGATCATTCAC154
   : :::::|||||
36 roLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyrLeuArg52
   : |||||:::|||||
155 CCAAGGGCTATGCTGCCAATTAAGTGTGATGGAGAATGCTCTTCCCACCTC204
   : |||||:::|||||
53 SerAlaasp.....ThrThrHisSerThrValLeuGlyLeuTyrAs66
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205 AACGCACACATGAATGCAACCACACCGCATGTTGCAGAGACCTTGGTTCA254
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83 euGluProLeuThrIleLeuTyrTyrValGlyArgThrProLysVal...98
   : |||||:::|||||
305 TAAATGGCATCTCGGTCTTACTTTTTCATGATGACAACTCCAATGTCATCTG354
   : :::::|||||
99 GluGlnLeuSerAsnMetValValLysSerCysLysCys 111
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355 AAAAAATACAGGAATATGGTTGTGAAGAGCTTGTGGATCG 393

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; FILING DATE: 23-JUN-1989
; APPLICATION NUMBER: 347,559
; FILING DATE: 04-MAY-1989
; APPLICATION NUMBER: 329,610
; FILING DATE: 28-MAR-1989
; APPLICATION NUMBER: 179,100
; FILING DATE: 08-APR-1988
; APPLICATION NUMBER: 179,101
; FILING DATE: 08-APR-1988
; APPLICATION NUMBER: 179,197
; FILING DATE: 08-APR-1988
; APPLICATION NUMBER: 28,285
; FILING DATE: 20-MAR-1987
; APPLICATION NUMBER: 31,346
; FILING DATE: 26-MAR-1987
; APPLICATION NUMBER: 943,322
; FILING DATE: 17-DEC-1986
; APPLICATION NUMBER: 880,776
; FILING DATE: 01-JUL-1986
; SEQ ID NO:5
; LENGTH: 2923
5187076-5

alignment_scores:
  Quality: 206.00      Length: 113
  Ratio: 2.822         Gaps: 4
Percent Similarity: 64.602 Percent Identity: 37.168

alignment_block:
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Align seg 1/1 to: 5187076-5 from: 1 to: 2923

4 ThrAsnTyrCysPheArgAsnLeuGluAsnCysCysValArgProLe 20
1360 TCAGATTACACAGCAGTGAATGAAACAGCCTGCAGGAGCATGAGT 1409
20 uTyrIleAspPheArgGlnAspLeuGlyTrpLys...TyrValHisGluP 36
1410 GTATGTGAGTTTC...CAAGACCTGGGATGGCAGGACTGGATCATGTCAC 1456
36 rOlySGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyrLeuArg 52
1457 CCAAGGCGTATGCTGCCAATCTACTGTGATGGAGAATGCTCTCTCCCACTC 1506
53 SerAlaAsp.....ThrThrHisSerThrValLeuGlyLeuTyrAs 66
1507 AAGCGACACATGAATGCAACCAACCGCGATTGTGCAGACCTTGGTTCA 1556
66 nThrLeuAsnProGluAlaSerAlaSerProCysCysValProGluAspL 83
1557 CCTTATGAACCCCGATGTGTCCTCCCAACCGTGTGTGCGCCCAACTAAGC 1606
83 euGluProLeuThrIleLeuTyrTyrValGlyArgThrProLysVal... 98
1607 TAAATCCCATCTCGGTCTTACTTTGATGACACACTCCAATGTCATTCTG 1656
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seq_documentation_block:
; Sequence 5, Application US/08525596B
; Patent No. 5827733
; GENERAL INFORMATION:
; APPLICANT: Huynh, Thanh
; APPLICANT: Lee, Se-Jin
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
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```
;
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: US
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/525,596B
; FILING DATE: 19-SEP-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/07762
; FILING DATE: 08-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Wetherell, Jr., Ph.D, John R.
; REGISTRATION NUMBER: 31,678
; REFERENCE/DOCKET NUMBER: 07265/075001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-678-5070
; TELEFAX: 619-678-5099
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 550 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: mouse GDF-8
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 59...436
; US-08-525-596B-5

alignment_scores:
  Quality: 204.50      Length: 104
  Ratio: 3.098         Gaps: 4
Percent Similarity: 63.462 Percent Identity: 39.423

alignment_block:
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Align seg 1/1 to: US-08-525-596B-5 from: 1 to: 550

12 GluGluAsnCysCysValArgProLeuTyrIleAspPheArgGlnAspLe 28
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28 uGlyTrpLysTrpValHisGluProLysGlyTyrTyrAlaAsnPheCys 45
190 TGGATGGGACTGGATTATCGCACCAAAAGATATAAGGCCAATTACTGCT 239
45 erGlyProCysPro.....TyrLeuArgSerAlaAspThrThrHisSer 59
240 CAGGAGAGTGTGAATTTGTGTTTACAAAAATATCCGCATCTCAT... 286
60 ThrValLeuGlyLeuTyrAsnThrLeuAsnProGluAlaSerAlaSerPr 76
287 .....CTGTGCACCAACCAACCCAGAGGCTCAGCAGGCC 324
76 oCysCysValProGlnAspLeuGluProLeuThrIleLeuTyrValG 93
325 TTGCTGCACCTCGACAAAAATGCTCTCCCATTAATATGCTATATTTAATG 374
93 lyArgThrProLysVal...GluGlnLeuSerAsnMetValLysSer 108
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seq_documentation_block:
; Sequence 5, Application US/09177860A
; Patent No. 6096506
; GENERAL INFORMATION:
; APPLICANT: Huynh, Thanh
; APPLICANT: Lee, Se-Jin
; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR GROWTH DIFFERENTIATION FACTOR-8 AN
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Gray Cary Ware & Freidenrich LLP
; STREET: 4365 Executive Drive, Suite 1600
; CITY: San Diego
; STATE: CA
; COUNTRY: US
; ZIP: 92121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/177,860A
; FILING DATE: 23-OCT-1998
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/525,596
; FILING DATE: 19-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Halle, Ph.D, Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07265/075003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 858-677-1456
; TELEFAX: 858-677-1465
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 550 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: mouse GDF-8
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 59...436
US-09-177-860A-5

alignment_scores:
Quality: 204.50 Length: 104
Ratio: 3.098 Gaps: 4
Percent Similarity: 63.462 Percent Identity: 39.423

alignment_block:
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143 GAATCCCGGTGTCTGCGGTACCCCTCCAGGTCGATTTT...GAAGCCTT 189

28 uGlyTrpLysTrpValHisGlyProLysGlyTyrTyrAlaAsnPheCys 45
|||||
190 TGGATGGGACTGGATTATCGCACCAAGATATAGGCCAATTACTGCT 239

45 erGlyProCysPro.....TyrLeuArgSerAlaAspThrThrHisSer 59
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||||| ||| ::|||::|::| |||||
240 CAGGAGAGTGTGAATTGTGTTTTTACAAATATATCCGCATCAT... 286

60 ThrValLeuGlyLeuTyrAsnThrLeuAsnProGluAlaSerAlaSerPr 76
||| ::| |||||::|::|::|::|::|::|::|
287 .....CTGTGTCACCAAGCAACCCAGAGGCTCAGCAGGCC 324

76 oCysCysValProGlnAspLeuGluProLeuThrIleLeuTyrTyrValG 93
|||||::|::|::|::|::|::|::|::|::|::|::|::|
325 TTGCTGCATCCGACAAAAATGTCCTCCATTATATGCTATATTTAATG 374

93 lyArgThrProLysVal...GluGlnLeuSerAsnMetValValLysSer 108
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375 GCAAGAACAAATAATATATATGGGAAATTCAGCCATGGTAGTAGACCGC 424

109 CysLysCysSer 112
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seq_name: /cgn2_6/ptodata/2/1na/5A_COMB.seq:US-08-525-596B-11

seq_documentation_block:
; Sequence 11, Application US/08525596B
; Patent No. 5827733
; GENERAL INFORMATION:
; APPLICANT: Huynh, Thanh
; APPLICANT: Lee, Se-Jin
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: US
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/525,596B
; FILING DATE: 19-SEP-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/07762
; FILING DATE: 08-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Wetherell, Jr., Ph.D, John R.
; REGISTRATION NUMBER: 31,678
; REFERENCE/DOCKET NUMBER: 07265/075001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-678-5070
; TELEFAX: 619-678-5099
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2676 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
; IMMEDIATE SOURCE:
; CLONE: Murine GDF-8
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 104...1231
US-08-525-596B-11

alignment_scores:
Quality: 204.50 Length: 104
Ratio: 3.098 Gaps: 4
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938 GAATCCCGGTGCTGCGCTACCCCTCAGCGTCGATTTT...GAAGCCTT 984
28 uGlyTrpLysTrpValHisGluProLysGlyTyrTyrAlaAsnPheCysS 45
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
985 TGGATGGGACTGGATTATCCACCAAGATATAAGGCCAATTACTGCT 1034
45 erGlyProCysPro.....TyrLeuArgSerAlaAspThrThrHisSer 59
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60 ThrValLeuGlyLeuTyrAsnThrLeuAsnProGluAlaSerAlaSerPr 76
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1170 GCAAGAACAAATAATATATGGGAAAATTCACGCCATGGTAGACCGC 1219
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seq_name: /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-09-177-860A-11
seq_documentation_block:
; Sequence 11, Application US/09177860A
; Patent No. 6096506
; GENERAL INFORMATION:
; APPLICANT: Huynh, Thanh
; APPLICANT: Lee, Se-Jin
; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR GROWTH DIFFERENTIATION FACTOR-8 AN
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Gray Cary Ware & Freidenrich LLP
; STREET: 4365 Executive Drive, Suite 1600
; CITY: San Diego
; STATE: CA
; COUNTRY: US
; ZIP: 92121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/177,860A
; FILING DATE: 23-OCT-1998
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/525,596
; FILING DATE: 19-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Ph.D. Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07265/075003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 858-677-1456
; TELEFAX: 858-677-1465
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
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; LENGTH: 2676 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
; IMMEDIATE SOURCE: Murine GDF-8
; CLONE: Murine GDF-8
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 104...1231
US-09-177-860A-11
alignment_scores:
Quality: 204.50 Length: 104
Ratio: 3.098 Gaps: 4
Percent Similarity: 63.462 Percent Identity: 39.423
alignment_block:
TGFB3P x US-09-177-860A-11 ..
Align seg 1/1 to: US-09-177-860A-11 from: 1 to: 2676
12 GluGluAsnCysCysValArgProLeuTyrIleAspPheArgGlnAspLe 28
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
938 GAATCCCGGTGCTGCGCTACCCCTCAGCGTCGATTTT...GAAGCCTT 984
28 uGlyTrpLysTrpValHisGluProLysGlyTyrTyrAlaAsnPheCysS 45
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
985 TGGATGGGACTGGATTATCGCACCAAGATATAAGGCCAATTACTGCT 1034
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1035 CAGGAGAGTGTGAATTTGTTTACAAAAATATCCGCATCAT... 1081
60 ThrValLeuGlyLeuTyrAsnThrLeuAsnProGluAlaSerAlaSerPr 76
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1082 .....CTGTGCACCAAGCAAAACCCAGAGGCTCAGCAGGCC 1119
76 oCysCysValProGlnAspLeuGluProLeuThrIleLeuTyrTyrValG 93
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1120 TTGCTGCACCTCCGACAAAAATGCTCCCATTAATATGCTATATTTAATG 1169
93 lYArgThrProLysVal...GluGlnLeuSerAsnMetValValLysSer 108
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1170 GCAAGAACAAATAATATATGGGAAAATTCACGCCATGGTAGACCGC 1219
109 CysLysCysSer 112
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1220 TGTGGGTGCTCA 1231
seq_name: /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-891-789B-5
seq_documentation_block:
; Sequence 5, Application US/08891789B
; Patent No. 6103466
; GENERAL INFORMATION:
; APPLICANT: Grobet, Luc; Georges, Michel
; TITLE OF INVENTION: Double-Muscling in Mammals
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Blake, Cassels & Graydon
; STREET: Box 25, Commerce Court West
; CITY: Toronto
; STATE: Ontario
; ZIP: M5L 1A9
; COUNTRY: Canada
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3 1/2 inch, 1.4 Mb storage
; COMPUTER: COMPAQ, IBM PC compatible
; OPERATING SYSTEM: MS-DOS 5.1
; SOFTWARE: WORD PERFECT
; CURRENT APPLICATION DATA:
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; APPLICATION NUMBER: US/08/891,789B
; FILING DATE: July 14, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunt, John C.
; REGISTRATION NUMBER: 36,424
; REFERENCE/DOCKET NUMBER: 52836/00004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 863-4344
; TELEFAX: (416) 863-2653
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2676 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-891-789B-5
..
alignment_scores:
    Quality: 204.50      Length: 104
    Ratio: 3.098        Gaps: 4
    Percent Similarity: 63.462    Percent Identity: 39.423
alignment_block:
TGFB3P x US-08-891-789B-5
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Align seg 1/1 to: US-08-891-789B-5 from: 1 to: 2676
12 GluGluAsnCysCysValArgProLeuTyrIleAspPheArgGlnAspLe 28
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938 GAATCCCGGTGTCGGCTACCCCTCAGCGTCGATTTT...GAAGCCTT 984
28 uGlyTrpLysTrpValHisGluProLysGlyTyrTyrAlaAsnPheCys 45
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
985 TGGATGGGACTGGATTATCGCACCAAAAGATATAGGCCAATTACTGCT 1034
45 erGlyProCysPro.....TyrLeuArgSerAlaAspThrThrHisSer 59
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1035 CAGGAGAGTGAATTTGTGTTTTACAAAAATATCCGCATCAT... 1081
60 ThrValLeuGlyLeuTyrAsnThrLeuAsnProGluAlaSerAlaSerPr 76
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1082 .....CTGTGCACCAAGCAACCCAGAGGCTCAGCAGGCC 1119
76 oCysCysValProGlnAspLeuGluProLeuThrIleLeuTyrValG 93
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1120 TTGCTGCTACTCCGACAAAATGCTCCCAATTAATATGCTATATTTAATG 1169
93 lyArgThrProLysVal...GluGlnLeuSerAsnMetValValLysSer 108
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1170 GCAAGAACAATAATATATGCAAAATTCACGCGATGGTAGACCGC 1219
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seq_documentation_block:
; Sequence 13, Application US/08525596B
; Patent No. 5827733
; GENERAL INFORMATION:
; APPLICANT: Huynh, Thanh
; APPLICANT: Lee, Se-Jin
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: US
; ZIP: 92037
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/525,596B
; FILING DATE: 19-SEP-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/07762
; FILING DATE: 08-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Wetherell, Jr., Ph.D, John R.
; REGISTRATION NUMBER: 31,678
; REFERENCE/DOCKET NUMBER: 07265/075001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-678-5070
; TELEFAX: 619-678-5099
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2743 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
; IMMEDIATE SOURCE:
; CLONE: Human GDF-8
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; NAME/KEY: CDS
; LOCATION: 59...1183
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US-08-525-596B-13
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890 GAATCAGATGCTGCTTACCTCTAAAGATATAGGCCAATTACTGCT 936
28 uGlyTrpLysTrpValHisGluProLysGlyTyrTyrAlaAsnPheCys 45
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937 TGGATGGGATTGGATTATCGCTCTAAAGATATAGGCCAATTACTGCT 986
45 erGlyProCysPro.....TyrLeuArgSerAlaAspThrThrHisSer 59
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60 ThrValLeuGlyLeuTyrAsnThrLeuAsnProGluAlaSerAlaSerPr 76
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1072 TTGCTGCTACTCCCAAGATGCTCCAATTAATATGCTATATTTAATG 1121
93 lyArgThrProLysVal...GluGlnLeuSerAsnMetValValLysSer 108
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1122 GCAAGAACAATAATATATATGCAAAATTCACGCGATGGTAGACCGC 1171
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  296 CGGATATCTCTCACAGTGGACTTT...GAGCTTTTGGCTGGGACTGGA 342
  33 alHisGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysPro 49
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  343 TCATCGCACCTAAGCGCTACAAGGCCAACTACTGCTCGGCCAGTGCAG 392
  50 TyrLeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAs 66
  ||||| : : |||||
  393 TACATGTTTCATGCAAAAGTATCCACACACC.....CACTTGTGTGCA 433
  66 nThrLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspL 83
  : ||||| : : ||||| : : ||||| : : ||||| : : |||||
  434 ACAGGCCAACCCAGAGGCTCTGCTGGGCCCTGCTGCACCCCTACCAAGA 483
  83 euGluProLeuThrIleLeuTyrTyr.....Val 92
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  484 TGTCCCAATCAACATGCTCTACTTCAATGACAAAGCAGCAGATTATCTAC 533
  93 GlyArgThrProLysValGluGlnLeuSerAsnMetValValLysSerCy 109
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  534 GGCAGATCCCT.....GGCATGGTGTGTGATGATG 565
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  seq_documentation_block:
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  ; Patent No. 6008434
  ; GENERAL INFORMATION:
  ; APPLICANT: Se-Jin Lee and Alexandra McPherron
  ; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-11
  ; NUMBER OF SEQUENCES: 9
  ; CORRESPONDENCE ADDRESS:
  ; ADDRESSEE: Fish & Richardson P.C.
  ; STREET: 4225 Executive Square, Suite 1400
  ; CITY: La Jolla
  ; STATE: California
  ; COUNTRY: US
  ; ZIP: 92037
  ; COMPUTER READABLE FORM:
  ; MEDIUM TYPE: Floppy disk
  ; COMPUTER: IBM PC compatible
  ; OPERATING SYSTEM: PC-DOS/MS-DOS
  ; SOFTWARE: PatentIn Release #1.0, Version #1.25
  ; CURRENT APPLICATION DATA:
  ; APPLICATION NUMBER: US/08/795,671
  ; FILING DATE: February 6, 1997
  ; CLASSIFICATION: 800
  ; ATTORNEY/AGENT INFORMATION:
  ; NAME: HAILE, PH.D., LISA A.
  ; REGISTRATION NUMBER: 38,347
  ; REFERENCE/DOCKET NUMBER: 07265/106001
  ; TELECOMMUNICATION INFORMATION:
  ; TELEPHONE: 619/678-5070
  ; TELEFAX: 619/678-5099
  ; INFORMATION FOR SEQ ID NO: 3:
  ; SEQUENCE CHARACTERISTICS:
  ; LENGTH: 630 base pairs
  ; TYPE: nucleic acid
  ; STRANDEDNESS: single
  ; TOPOLOGY: linear
  ; MOLECULE TYPE: DNA (genomic)
  ; IMMEDIATE SOURCE:
  ; CLONE: MOUSE GDF-11
  ; FEATURE:
  ; NAME/KEY: CDS
  ; LOCATION: 198..575
  ; US-08-795-671-3
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  |||||
  246 CGGAACCTAGGCTCGAGTGCATGAACTCGAGTGCAGTCCCGCTGCTG 295
  16 sValArgProLeuTyrIleAspPheArgGlnAspLeuGlyTyrLysTrpV 33
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  33 alHisGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysPro 49
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  ||||| : : |||||
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  ; Patent No. 6008434
  ; GENERAL INFORMATION:
  ; APPLICANT: Se-Jin Lee and Alexandra McPherron
  ; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-11
  ; NUMBER OF SEQUENCES: 9
  ; CORRESPONDENCE ADDRESS:
  ; ADDRESSEE: Fish & Richardson P.C.
  ; STREET: 4225 Executive Square, Suite 1400
  ; CITY: La Jolla
  ; STATE: California
  ; COUNTRY: US
  ; ZIP: 92037
  ; COMPUTER READABLE FORM:
  ; MEDIUM TYPE: Floppy disk
  ; COMPUTER: IBM PC compatible
  ; OPERATING SYSTEM: PC-DOS/MS-DOS
  ; SOFTWARE: PatentIn Release #1.0, Version #1.25
  ; CURRENT APPLICATION DATA:
  ; APPLICATION NUMBER: US/08/795,671
  ; FILING DATE: February 6, 1997
  ; CLASSIFICATION: 800
  ; ATTORNEY/AGENT INFORMATION:
  ; NAME: HAILE, PH.D., LISA A.
  ; REGISTRATION NUMBER: 38,347
  ; REFERENCE/DOCKET NUMBER: 07265/106001
  ; TELECOMMUNICATION INFORMATION:
  ; TELEPHONE: 619/678-5070
  ; TELEFAX: 619/678-5099
  ; INFORMATION FOR SEQ ID NO: 3:
  ; SEQUENCE CHARACTERISTICS:
  ; LENGTH: 630 base pairs
  ; TYPE: nucleic acid

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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/247.907A
; FILING DATE: May 20, 1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: LAZAR, Steven R.
; REGISTRATION NUMBER: 32,618
; REFERENCE/DOCKET NUMBER: G15205-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617 876-1170
; TELEFAX: 617 876-5851
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 789 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Bos Taurus
; STRAIN: Bovine Activin WC
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 324..704
; NAME/KEY: misc feature
; LOCATION: 322..323
; OTHER INFORMATION: /note= "putative 3' end of intron"
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 375..701
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US-08-247-907A-1

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Percent Similarity: 55.000 Percent Identity: 36.667

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372 CGGAACCTGGCGCTGGACTGCGATGAACATTCAGTGAGTCCCGCTGTTG 421

16 sValArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpV 33
|||||
422 CGCTACCCCTCAGTGTGGACTTT...GAGGCTTTTGGCTGGGACTGGA 468

33 alHisGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysPro 49
:: |||||
469 TCATCGCTCTTAACCTACAGGCCAATACGTCTCCGGCCAGTCGGAG 518

50 TyrLeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAs 66
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519 TACATGTTTATGCAAAAGTATCCGCACACC.....CAGTTGGTGCA 559

66 nThrLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspL 83
: |||||
560 ACAGGCTAACCCCAAGAGGCTCTCGGGGCCCTGCTGCACACCCACCAAGA 609

83 euCluProLeuThrIleLeuTyrTyr.....Val 92
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610 TGTCCTCAATCAACATGCTCTACTTCAATGACAGCAGCATATTATCTAC 659

93 GlyArgThrProLysValGluGlnLeuSerAsnMetValValLysSerCy 109
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660 GCCAAGATCCCT.....GGCATGGTGGTGGATCGCTG 691

109 sLysCysSer 112
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seq_documentation_block:
; Sequence 1, Application US/08452772
; Patent No. 5700911
; GENERAL INFORMATION:
; APPLICANT: WOZNEY, John
; APPLICANT: CELESTE, Anthony J.
; TITLE OF INVENTION: BMP-II COMPOSITIONS
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENETICS INSTITUTE, INC.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/452,772
; FILING DATE: 30-MAY-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/247,907
; FILING DATE: 20-MAY-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: LAZAR, Steven R.
; REGISTRATION NUMBER: 32,618
; REFERENCE/DOCKET NUMBER: G15205-CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617 876-1170
; TELEFAX: 617 876-5851
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 789 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Bos Taurus
; STRAIN: Bovine Activin WC
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 324..704
; NAME/KEY: misc feature
; LOCATION: 322..323
; OTHER INFORMATION: /note= "putative 3' end of intron"
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; NAME/KEY: mat_peptide
; LOCATION: 375..701
;
US-08-452-772-1

alignment_scores:
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Percent Similarity: 55.000 Percent Identity: 36.667

alignment_block:
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Align seg 1/1 to: US-08-452-772-1 from: 1 to: 789
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9 ArgAsnLeu.....GluGluAsnCysCy 16
|||||
372 CGGAACCTGGCGCTGGACTCGGATGACATTCAGTGAGTCCCGCTGTG 421

16 sValArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpV 33
|
422 CCGCTACCCCTCCTACTGTGGACTTT...GAGGCTTTTGGCTGGGACTGGA 468

33 aHisGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysPro 49
|||
469 TCATCGCTCTCTAAACGCTACAAGGCCAACTACTGCTCCGGCCAGTGGAG 518

50 TyrLeuArgSerAlaAspThrHisSerThrValLeuGlyLeuTyrAs 66
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519 TACATGTTTATGCAAAAGTATCCGCACACC.....CACTTGGTGCA 559

66 nThrLeuAsnProGluAlaSerProCysValProGlnAspL 83
|
560 ACAGGCTAACCCCAAGAGGCTCTCGGGGGCCCTGCTGCACACCCACCAAGA 609

83 euGluProLeuThrIleLeuTyrTyr.....Val 92
|||||
610 TGTCCCAATCAACATGCTCTACTTCAATGACAAGCAGCAGATTATCTAC 659

93 GlyArgThrProLysValGluGlnLeuSerAsnMetValValLysSerCy 109
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109 sLysCysSer 112
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692 TGGCTGCTCC 701

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seq_documentation_block:
; Sequence 1, Application PC/TUS9405288
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: BMP-11 COMPOSITIONS
; NUMBER OF SEQUENCES: 11
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/05288
; FILING DATE:
; CLASSIFICATION:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 789 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Bos Taurus
; STRAIN: Bovine Activin WC
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 324..704
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 322..323
; OTHER INFORMATION: /note= "putative 3' end of intron"
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 375..701
; PCT-US94-05288-1

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alignment_scores:
Quality: 203.00      Length: 120
Ratio: 3.076        Gaps: 5
Percent similarity: 55.000 Percent Identity: 36.667

alignment_block:
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Align seg 1/1 to: PCT-US94-05288-1 from: 1 to: 789

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372 CGGAACCTGGCGCTGGACTCGGATGACATTCAGTGAGTCCCGCTGTG 421

16 sValArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpV 33
|
422 CCGCTACCCCTCCTACTGTGGACTTT...GAGGCTTTTGGCTGGGACTGGA 468

33 aHisGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysPro 49
|||
469 TCATCGCTCTCTAAACGCTACAAGGCCAACTACTGCTCCGGCCAGTGGAG 518

50 TyrLeuArgSerAlaAspThrHisSerThrValLeuGlyLeuTyrAs 66
|||||
519 TACATGTTTATGCAAAAGTATCCGCACACC.....CACTTGGTGCA 559

66 nThrLeuAsnProGluAlaSerProCysValProGlnAspL 83
|
560 ACAGGCTAACCCCAAGAGGCTCTCGGGGGCCCTGCTGCACACCCACCAAGA 609

83 euGluProLeuThrIleLeuTyrTyr.....Val 92
|||||
610 TGTCCCAATCAACATGCTCTACTTCAATGACAAGCAGCAGATTATCTAC 659

93 GlyArgThrProLysValGluGlnLeuSerAsnMetValValLysSerCy 109
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seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-247-907A-10

seq_documentation_block:
; Sequence 10, Application US/08247907A
; Patent No. 5639638
; GENERAL INFORMATION:
; APPLICANT: WOZNEY, John
; APPLICANT: CELESTE, Anthony J.
; TITLE OF INVENTION: BMP-11 COMPOSITIONS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENETICS INSTITUTE, INC.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/247,907A
; FILING DATE: May 20, 1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: LAZAR, Steven R.
; REGISTRATION NUMBER: 32,618
; REFERENCE/DOCKET NUMBER: GI5205-A
; TELECOMMUNICATION INFORMATION:

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;
; TELEPHONE: 617 876-1170
; TELEFAX: 617 876-5851
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1270 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Human BMP-11
; IMMEDIATE SOURCE:
; CLONE: FB30.5
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1086
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 760..1086
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US-08-247-907A-10
..

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Align seg 1/1 to: US-08-247-907A-10 from: 1 to: 1270

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16 sValArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpV 33
|||||
807 CCGATATCCCTCACAGTGGACTTT...GAGGCTTTCGGCTGGGACTGGA 853

33 alHisGluProLysGlyTyrTyraAlaAsnPheCysSerGlyProCysPro 49
:|||||
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50 TyrLeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAs 66
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:|||||
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:|||||
995 TGTCCCAATCAACATGCTCTACTTCAATGACAAGCAGCAGATTATCTAC 1044

93 GlyArgThrProLysValGluGlnLeuSerAsnMetValValLysSerCy 109
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; Sequence 10, Application US/08452772
; Patent No. 5700911
; GENERAL INFORMATION:
; APPLICANT: WOZNEY, John
; APPLICANT: CELESTE, Anthony J.
; TITLE OF INVENTION: BMP-11 COMPOSITIONS
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; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENETICS INSTITUTE, INC.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/452.772
; FILING DATE: 30-MAY-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/247,907
; FILING DATE: 20-MAY-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: LAZAR, Steven R.
; REGISTRATION NUMBER: 32,618
; REFERENCE/DOCKET NUMBER: G15205-CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617 876-1170
; TELEFAX: 617 876-5851
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1270 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Human BMP-11
; IMMEDIATE SOURCE:
; CLONE: FB30.5
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1086
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 760..1086
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US-08-452-772-10
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    Percent Similarity: 55.000    Percent Identity: 36.667
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16 sValArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLysTrpV 33
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807 CCGATATCCCTCACAGTGGACTTT...GAGGCTTTCGGCTGGGACTGGA 853

33 alHisGluProLysGlyTyrTyraAlaAsnPheCysSerGlyProCysPro 49
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854 TCATCGACCTAAGCGCTACAGGCCAACTACTGCTCCGCCAGTGGCAG 903

50 TyrLeuArgSerAlaAspThrThrHisSerThrValLeuGlyLeuTyrAs 66
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  Ratio: 3.076         Gaps: 5
  Percent Similarity: 55.000  Percent Identity: 36.667

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33 alHisGluProLysGlyTyriTyriAlaAsnPheCysSerGlyProCysPro 49
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66 nThrLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspL 83
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83 euGluProLeuThrIleLeuTyriTyri.....Val 92
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1183 TGTCCCAATCAACATGCTCTACTTCAATGACAGCAGCAGATATCTAC 1232

93 GlyArgThrProLysValGluGlnLeuSerAsnMetValValLysSerCy 109
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109 sLysCysSer 112
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seq_name: /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-795-671-1

seq_documentation_block:
; Sequence 1, Application US/08795671
; Patent No. 6008434
; GENERAL INFORMATION:
; APPLICANT: Se-Jin Lee and Alexandra McPherron
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-11
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: California
; COUNTRY: US
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/795,671
; FILING DATE: February 6, 1997
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: HAILE, PH.D., LISA A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07265/106001

TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1393 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; IMMEDIATE SOURCE:
; CLONE: HUMAN GDF-11
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 54..1274
; US-08-795-671-1

alignment_scores:
  Quality: 203.00      Length: 120
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alignment_block:
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Align seg 1/1 to: US-08-795-671-1 from: 1 to: 1393

9 ArgAsnLeu.....GluGluAsnCysCy 16
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16 sValArgProLeuTyriLeAspPheArgGlnAspLeuGlyTrpLysTrpV 33
|||||
995 CCGATATCCCTCACAGTGGACTTT...GAGGCTTTCGGCTGGGACTGGA 1041

33 alHisGluProLysGlyTyriTyriAlaAsnPheCysSerGlyProCysPro 49
|||||
1042 TCATCGCACCTAAGCGCTACAAGCCCACTACTGCTCCGGCCAGTGGCGAG 1091

50 TyrLeuArgSerAlaAspThrHisSerThrValLeuGlyLeuTyriAs 66
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1092 TACATGTTTCATGCAAAAATATCCGCATACC.....CATTTGGTGCA 1132

66 nThrLeuAsnProGluAlaSerAlaSerProCysCysValProGlnAspL 83
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93 GlyArgThrProLysValGluGlnLeuSerAsnMetValValLysSerCy 109
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seq_documentation_block:
; Sequence 1, Application US/08795671
; Patent No. 6008434
; GENERAL INFORMATION:
; APPLICANT: Se-Jin Lee and Alexandra McPherron
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-11
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: California
; COUNTRY: US
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/795,671
; FILING DATE: February 6, 1997
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: HAILE, PH.D., LISA A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07265/106001
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; STATE: Ontario
; ZIP: M5L 1A9
; COUNTRY: Canada
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3 1/2 inch, 1.4 Mb storage
; COMPUTER: COMPAQ, IBM PC compatible
; OPERATING SYSTEM: MS-DOS 5.1
; SOFTWARE: WORD PERFECT
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/891,789B
; FILING DATE: July 14, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunt, John C.
; REGISTRATION NUMBER: 36,424
; REFERENCE/DOCKET NUMBER: 52836/00004
; TELEPHONE: (416) 863-4344
; TELEFAX: (416) 863-2653
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1240 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-891-789B-3

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    Quality: 202.50      Length: 104
    Ratio: 3.022        Gaps: 4
Percent Similarity: 64.423 Percent Identity: 39.423

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alignment_block:
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28 uGlyTrpLysTrpValHisGluProLysGlyTyrTyrAlaAsnPheCys 45
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914 TGGATGGGATGGATTTATTCACCTAAAGATATAAGGCCAATTACTGCT 963

45 erGlyProCysPro.....TyrLeuArgSerAlaAspThrThrHisSer 59
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109 CysLysCysSer 112
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seq_documentation_block:
; Sequence 1, Application US/08891789B
; Patent No. 6103466
; GENERAL INFORMATION:
; APPLICANT: Grobet, Luc; Georges, Michel
; TITLE OF INVENTION: Double-Muscling in Mammals

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; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Blake, Cassels & Graydon
; STREET: Box 25, Commerce Court West
; CITY: Toronto
; STATE: Ontario
; ZIP: M5L 1A9
; COUNTRY: Canada
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3 1/2 inch, 1.4 Mb storage
; COMPUTER: COMPAQ, IBM PC compatible
; OPERATING SYSTEM: MS-DOS 5.1
; SOFTWARE: WORD PERFECT
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/891,789B
; FILING DATE: July 14, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunt, John C.
; REGISTRATION NUMBER: 36,424
; REFERENCE/DOCKET NUMBER: 52836/00004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 863-4344
; TELEFAX: (416) 863-2653
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1196 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-891-789B-1

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alignment_scores:
    Quality: 201.50      Length: 104
    Ratio: 3.053        Gaps: 4
Percent Similarity: 63.462 Percent Identity: 39.423

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alignment_block:
TGFB3P x US-08-891-789B-1 ..

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Align seg 1/1 to: US-08-891-789B-1 from: 1 to: 1196

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12 GluGluAsnCysValArgProLeuTyrIleAspPheArgGlnAspLe 28
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878 GAATCTCGATGCTGCTTACCTCTAAGTGGATTT...GAAGCTTT 924

28 uGlyTrpLysTrpValHisGluProLysGlyTyrTyrAlaAsnPheCys 45
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
925 TGGATGGGATGGATTTATTCACCTAAAGATATAAGGCCAATTACTGCT 974

45 erGlyProCysPro.....TyrLeuArgSerAlaAspThrThrHisSer 59
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975 CTGGAGAATGTGAATTTGATTTTTCGAAAGTATCCTCATACCCAT... 1021

60 ThrValLeuGlyLeuTyrAsnThrLeuAsnProGluAlaSerAlaSerPr 76
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1022 .....CTGTGCACCAAGCAACCCAGAGGTTACGCCGCC 1059

76 oCysValProGlnAspLeuGluProLeuThrIleLeuTyrTyrValG 93
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1060 CTGCTACTCTACAAAGATGTCCTCAATTAATATGCTATATTTAATG 1109

93 lyArgThrProLysVal...GluGlnLeuSerAsnMetValValLysSer 108
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109 CysLysCysSer 112
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seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-455-550-2
seq_documentation_block:

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; APPLICATION NUMBER: 06/783910
; FILING DATE: 03-OCT-1985
; ATTORNEY/AGENT INFORMATION:
; NAME: Hasak, Janet E.
; REGISTRATION NUMBER: 28,616
; REFERENCE/DOCKET NUMBER: 297P2D4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1896
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3588 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-197-792-32

alignment_scores:
    Quality: 200.00      Length: 107
    Ratio: 2.703        Gaps: 5
    Percent Similarity: 69.159      Percent Identity: 37.383

alignment_block:
TGFB3P x US-08-197-792-32

Align seg 1/1 to: US-08-197-792-32 from: 1 to: 3588

15 CysCysValArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpGly 31
988 TGTGTGAAGACAGTCTTTGTGCACTTCAAG...GACATCGGCTGGAA 1034

31 s...TrpValHisGluProLysGlyTyrTyrAlaAsnPheCysSerGlyp 47
: : : : : : : : : : : : : : : : : : : : : : : : : : :
1035 CGACTGGATCATCGCTCCGCTGCTACCAGGCCAACTACTGCGAGGCG 1084

47 roCysPro.....TyrLeuArgSerAlaAspThrHis 58
: : : : : : : : : : : : : : : : : : : : : : : : : :
1085 AGTGCCCGCCAGCACATGAGCGGCGACGTCGCTCTGCTGCCAC 1134

59 SerThrValLeuGlyLeuTyrAsnThrLeu.....AsnProGluAlaSe 73
: : : : : : : : : : : : : : : : : : : : : : : : : :
1135 TCGAGGTCATCAACACATACGATGCGCGGCGCCAGCCCTTCGCCAA 1184

73 rAlaSerProCysCysValProGlnAspLeuGluProLeuThrIleLeuT 90
: : : : : : : : : : : : : : : : : : : : : : : : : :
1185 CCTCAAGTCGTGCTGCTGCCCTCCACCAAGCTGAGGCCCATGCTCCATG 1234

90 yTyr...ValGlyArgThrProLysValGluGlnLeuSerAsnMetVal 105
: : : : : : : : : : : : : : : : : : : : : : : : : :
1235 ACTACGACGCGGCGAGAACATCATCAAGAAGACATCCAGAACATGATC 1284

106 ValLysSerCysLysCysSer 112
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1285 GTGAGGAGTGGCGGTGCTCC 1305

seq_name: /cgn2_5/ptodata/2/ina/5A_COMB.seq:US-08-459-850-32

seq_documentation_block:
; Sequence 32, Application US/08459850
; Patent No. 5665568
; GENERAL INFORMATION:
; APPLICANT: Anthony J. Mason
; APPLICANT: Peter H. Seaburg
; TITLE OF INVENTION: Nucleic Acid Encoding the Alpha or
; TITLE OF INVENTION: Beta Chains of Inhibin and Method for Synthesizing Polypeptide
; TITLE OF INVENTION: Using such Nucleic Acid
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco

```

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; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,850
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/197792
; FILING DATE: 17-FEB-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/958414
; FILING DATE: 08-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/744207
; FILING DATE: 12-AUG-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/215466
; FILING DATE: 05-JUL-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 06/906729
; FILING DATE: 31-DEC-1986
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 06/827710
; FILING DATE: 07-FEB-1986
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 06/783910
; FILING DATE: 03-OCT-1985
; ATTORNEY/AGENT INFORMATION:
; NAME: Hasak, Janet E.
; REGISTRATION NUMBER: 28,616
; REFERENCE/DOCKET NUMBER: 297P2D5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1896
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3588 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-459-850-32

alignment_scores:
    Quality: 200.00      Length: 107
    Ratio: 2.703        Gaps: 5
    Percent Similarity: 69.159      Percent Identity: 37.383

alignment_block:
TGFB3P x US-08-459-850-32

Align seg 1/1 to: US-08-459-850-32 from: 1 to: 3588

15 CysCysValArgProLeuTyrIleAspPheArgGlnAspLeuGlyTrpGly 31
988 TGTGTGAAGACAGTCTTTGTGCACTTCAAG...GACATCGGCTGGAA 1034

31 s...TrpValHisGluProLysGlyTyrTyrAlaAsnPheCysSerGlyp 47
: : : : : : : : : : : : : : : : : : : : : : : : : :
1035 CGACTGGATCATCGCTCCGCTGCTACCAGGCCAACTACTGCGAGGCG 1084

47 roCysPro.....TyrLeuArgSerAlaAspThrHis 58
: : : : : : : : : : : : : : : : : : : : : : : : : :
1085 AGTGCCCGCCAGCACATGAGCGGCGACGTCGCTCTGCTGCCAC 1134

59 SerThrValLeuGlyLeuTyrAsnThrLeu.....AsnProGluAlaSe 73

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/056,564
; FILING DATE: 30-APR-1993
; APPLICATION NUMBER: 07/577,892
; FILING DATE: 05-SEP-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Eisenstein, Ronald I
; REGISTRATION NUMBER: 30628
; REFERENCE/DOCKET NUMBER: 40302-FWC-DIV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-523-3400
; TELEFAX: 617-523-6440
; TELEX: 200291
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1667 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; US-08-455-550-1
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alignment_scores:
    Quality: 199.00      Length: 108
    Ratio: 2.689         Gaps: 6
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alignment_block:
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Align seg 1/1 to: US-08-455-550-1 from: 1 to: 1667
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723 TGTTCAGAGAGCATTTCTACGTCAGCTTCAAA...GACATTGGTTGGAG 769
;
31 s...TrpValHisGluProLysGlyTyrIleAsnPheCysSerGlyP 47
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770 TGATTGGATCATAGACCTCTCGGTACCATGCCAATTATTGTGAGGAG 819
;
47 roCysProTyrLeuArgSerAlaAspThr... : : : : : : : : : : : : : : : : : : : : : : : :
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58 HisSerThrValLeuGlyLeuTyrAsnThr.....LeuAsnProGluAl 72
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72 aserAlaSerProCysValProGlnAspLeuGluProLeuThrIleL 89
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917 CAGCATCAATCCTGCTGTGTCCTCTAAGCTTAGAGCTATGTCCTCATG 966
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89 euTyrTyr...ValGlyArgThrProLysValGluGlnLeuSerAsnMet 104
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967 TGTACTATCATGACGGTCAGATATATAATCAAAAGGATATTCAAATATG 1016
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105 ValValLysSerCysLysCysSer 112
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1017 ATTGTGGAGGAATGTGGCTGCTCA 1040
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seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-278-729A-24
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seq_documentation_block:
; Sequence 24, Application US/08278729A
; Patent No. 5650276
; GENERAL INFORMATION:
; APPLICANT: SMART, JOHN
; APPLICANT: OPPERMANN, HERMAN
```

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;
; APPLICANT: OZKAYNAK, ENGIN
; APPLICANT: KUBERASAMPATH, THANGAVEL
; APPLICANT: RUEGER, DAVID C.
; APPLICANT: PANG, ROY H.L.
; APPLICANT: COHEN, CHARLES M.
; TITLE OF INVENTION: MORPHOGENIC PROTEIN SCREENING METHOD
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES
; STREET: 45 SOUTH STREET
; CITY: HOPKINTON
; STATE: MA
; COUNTRY: USA
; ZIP: 01748
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/278,729A
; FILING DATE: 20-JUL-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: PITCHER Esq., EDMUND R.
; REGISTRATION NUMBER: 27,829
; REFERENCE/DOCKET NUMBER: CRP-058CPEW
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (508) 435-9001
; TELEFAX: (508) 435-6951
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1368 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1365
; US-08-278-729A-24
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alignment_scores:
    Quality: 195.00      Length: 103
    Ratio: 2.868         Gaps: 4
    Percent Similarity: 66.019      Percent Identity: 39.806
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alignment_block:
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Align seg 1/1 to: US-08-278-729A-24 from: 1 to: 1368
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46 lyProCysProTyrLeuArgSerAlaAsp.....ThrThrHisSer 59
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76 ocCysCysValProGlnAspLeuGluProLeuThrIleLeuTyrTyrValG 93
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1104 GCATGACTGGATCATGCACACAGAGGCGCTATGGCGCCTTCTACTGCACGC 1153
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46  lyProCysProTyrLeuArgSerAlaAsp.....ThrThrHisSer 59
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1154 GCGAGTGCAATTTCGCGCTCAATGCGCACATGAAGCCACCAACCATCGC 1203
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60  ThrValLeuGlyLeuTyrAsnThrLeuAsnProGluAlaSerAlaSerPr 76
      |||  |||  :::|||||  |||:::|||||
1204 ATCGTCCAGACCCTGGTGCACCTGCTGGAGGCCAAGAAGTGCCCAAGCC 1253
      |||  |||  :::|||||  |||:::|||||
76  cCysValProGluAspLeuGluProLeuThrIleLeuTyrTyrValG 93
      |||  |||  :::|||||  |||  |||  |||  |||  :::
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93  ly...ArgThrProLysValGluGlnLeuSerAsnMetValValLysSer 108
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1204 ATCGTCAGACCCCTGGTCCACCTGCTGGAGCCCAAGAAGGTGCCCAAGCC
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76 OcysCysValProGlnAspLeuGluProLeuThrIleLeuTyrTyrValG
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1254 CTGCTCGCTCCACCACCGAGGTGGGAGCACTACCCGTTCTGTACCACCTGA
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93 Iy...ArgThrProLysValGluGlnLeuSerAsnMetValValLysSer
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1304 AGCAGCAGAAATGTGAACCTGAAAAGATATAGAAACATGATTGTGAATCC
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109 CysLysCys 111
      |||      |||
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seq.name: /cqn2_6/ptodata/2/ina/5A_COMB_seq:US-08-406-672-24

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76 ocCysValProGlnAspLeuGluProLeuThrIleLeuTyrTyrValG 93
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seq_name: /cgn2_6/ptodata/2/Ina/5A_COMB.seq:US-08-406-672-24

seq_documentation_block:
; Sequence 24, Application US/08406672
; Patent No. 56744844
; GENERAL INFORMATION:
; APPLICANT: KUBERASAMPATH, THANGAVEL
; APPLICANT: COHEN, CHARLES M.
; APPLICANT: OPPERMANN, HERMANN
; APPLICANT: OZKAYNAK, ENGIN
; APPLICANT: RUEGER, DAVID C.
; APPLICANT: PANG, ROY H.L.
; TITLE OF INVENTION: TREATMENT TO PREVENT LOSS OF AND/OR
; INCREASE BONE MASS IN METABOLIC BONE DISEASES
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES
; STREET: 45 SOUTH STREET

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PRIOR APPLICATION DATA: US 667,274

ATTORNEY/AGENT INFORMATION:
NAME: FENTON Esq., GILLIAN

REGISTRATION NUMBER: 36,508
REFERENCE/DOCKET NUMBER: CRP-060CN
TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 248-7360
TELEFAX: (617) 248-7100

INFORMATION FOR SEQ ID NO. 24:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1368 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear

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; MOLECULE TYPE:  CDS
; FEATURE:
; NAME/KEY:  CDS
; LOCATION:  1..1365
US-08-406-672-24

alignment_scores:
  Quality: 195.00      Length: 103
  Ratio: 2.868        Gaps: 4
  Percent Similarity: 66.019      Percent Identity: 39.806

alignment_block:
  TGF3P x US-08-406-672-24

  Align seg 1/1 to: US-08-406-672-24 from: 1 to: 1368

14 AsnCysCysValArgProLeuTyrIleAspPheArgGlnAspLeuGlyTr 30
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1057 AGCTGCCAGATGCAGACCCCTGTACATAGACTTCAAG...GATCTGGGCTG 1103
  30 p...LysTrpValHisGluProLysGlyTyrTyrAlaAsnPheCysSerG 46
  | ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
1104 GCATGACTGCATCCACCGACGAGGGCTATGGCGCTTCTACTGCAGCG 1153

46 lyProCysProTyrLeuArgSerAlaAsp.....ThrThrHisSer 59
  || ||| ::::: ::::: ::::: ::::: ::::: ::::: :::::
1154 GCGAGTGCAATTTCCTCCGCTCAATGCCGACATGAACGCCACCAACCATGCG 1203

60 ThrValLeuGlyLeuTyrAsnThrLeuAsnProGluAlaSerAlaSerPr 76
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76 oCysCysValProGlnAspLeuGluProLeuThrIleLeuTyrTyrValG 93
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109 CysLysCys 111
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seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-643-563A-24

seq_documentation_block:
; Sequence 24, Application US/08643563A
; Patent No. 5707810
; GENERAL INFORMATION:
; APPLICANT: SMART, JOHN
; APPLICANT: OPPERMAN, HERMAN
; APPLICANT: OZKAYNAK, ENGIN
; APPLICANT: KUBERASAMPATH, THANGAVEL
; APPLICANT: RUEGER, DAVID C.
; APPLICANT: PANG, ROY H.L.
; APPLICANT: COHEN, CHARLES M.
; TITLE OF INVENTION: MORPHOGENIC PROTEIN SCREENING METHOD
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES
; STREET: 45 SOUTH STREET
; CITY: HOPKINTON
; STATE: MA
; COUNTRY: USA
; ZIP: 01748
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

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; APPLICATION NUMBER:  US/08/643,563A
; FILING DATE: 06-MAY-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: TWOMEY ESQ., MICHAEL J.
; REGISTRATION NUMBER: 38,349
; REFERENCE/DOCKET NUMBER: CRP-058CN2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (508) 435-9001
; TELEFAX: (508) 435-6951
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1368 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDS
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1365
US-08-643-563A-24

alignment_scores:
  Quality: 195.00      Length: 103
  Ratio: 2.868        Gaps: 4
  Percent Similarity: 66.019      Percent Identity: 39.806

alignment_block:
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1057 AGCTGCCAGATGCAGACCCCTGTACATAGACTTCAAG...GATCTGGGCTG 1103
  30 p...LysTrpValHisGluProLysGlyTyrTyrAlaAsnPheCysSerG 46
  ||||| ::::: ::::: ::::: ::::: ::::: ::::: :::::
1104 GCATGACTGCATCCACCGACGAGGGCTATGGCGCTTCTACTGCAGCG 1153

46 lyProCysProTyrLeuArgSerAlaAsp.....ThrThrHisSer 59
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seq_documentation_block:
; Sequence 24, Application US/08643763A
; Patent No. 5733878
; GENERAL INFORMATION:
; APPLICANT: KUBERASAMPATH, THANGAVEL
; APPLICANT: RUEGER, DAVID C.
; APPLICANT: OPPERMAN, HERMAN
; APPLICANT: COHEN, CHARLES M.
; APPLICANT: PANG, ROY H.L.
; TITLE OF INVENTION: MORPHOGENIC-INDUCED PERIODONTAL TISSUE

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; TITLE OF INVENTION: REGENERATION.
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES
; STREET: 45 SOUTH STREET
; CITY: HOPKINTON
; STATE: MA
; COUNTRY: USA
; ZIP: 01748
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/643,763A
; FILING DATE: 06-MAY-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: FENTON Esq., GILLIAN M.
; REGISTRATION NUMBER: 36,508
; REFERENCE/DOCKET NUMBER: CRP-067CN
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7560
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1368 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1365
; US-08-643-763A-24

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  Percent Similarity: 66.019  Percent Identity: 39.806

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; Patent No. 5739107
; GENERAL INFORMATION:
; APPLICANT: COHEN, CHARLES M.
; APPLICANT: CHARETTE, MARC F.
; APPLICANT: KUBERASAMPATH, THANGAVEL
; APPLICANT: RUEGER, DAVID C.
; APPLICANT: OPPERMANN, HERMANN
; APPLICANT: PANG, ROY H.L.
; APPLICANT: OZKAYNAK, ENGIN
; APPLICANT: SMART, JOHN E.
; TITLE OF INVENTION: MORPHOGEN TREATMENT OF GASTROINTESTINAL
; TITLE OF INVENTION: ULCERS.
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES
; STREET: 45 SOUTH STREET
; CITY: HOPKINTON
; STATE: MA
; COUNTRY: USA
; ZIP: 01748
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/462,623
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/445,882
; FILING DATE: 22-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: FENTON Esq., GILLIAN M.
; REGISTRATION NUMBER: 36,508
; REFERENCE/DOCKET NUMBER: CRP-074CN
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (508) 435-9001
; TELEFAX: (508) 435-6951
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1368 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1365
; US-08-462-623-24

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; Patent No. 5849686
; GENERAL INFORMATION:
; APPLICANT: KUBERASAMPATH, THANGAVEL
; APPLICANT: RUEGER, DAVID C.
; APPLICANT: OPPERMANN, HERMAN
; APPLICANT: PANG, ROY H.L.
; APPLICANT: COHEN, CHARLES M.
; TITLE OF INVENTION: MORPHOGEN-INDUCED LIVER REGENERATION
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES
; STREET: 45 SOUTH STREET
; CITY: HOPKINTON
; STATE: MA
; COUNTRY: USA
; ZIP: 01748
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/445,468A
; FILING DATE: 22-MAY-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: FENTON ESQ., GILLIAN M.
; REGISTRATION NUMBER: 36,508
; REFERENCE/DOCKET NUMBER: CRP-072FW2

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; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7560
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1368 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1365
; US-08-445-468A-24

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46 lyProCysProTyrLeuArgSerAlaAsp.....ThrThrHisSer 59
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; Sequence 24, Application US/08461397A
; Patent No. 5972884
; GENERAL INFORMATION:
; APPLICANT: COHEN, CHARLES M.
; APPLICANT: CHARETTE, MARC F.
; APPLICANT: KUBERASAMPATH, THANGAVEL
; APPLICANT: RUEGER, DAVID C.
; APPLICANT: OPPERMANN, HERMANN
; APPLICANT: PANG, ROY H. L.
; APPLICANT: OZKANAK, ENGIN
; APPLICANT: SMART, JOHN E.
; TITLE OF INVENTION: MORPHOGEN TREATMENT FOR LIMITING
; TITLE OF INVENTION: PROLIFERATION OF EPITHELIAL CELLS.
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES
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; STREET: 45 SOUTH STREET
; CITY: HOPKINTON
; STATE: MA
; COUNTRY: USA
; ZIP: 01748
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,397A
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: PITCHER ESQ, EDMUND R.
; REGISTRATION NUMBER: 27,829
; REFERENCE/DOCKET NUMBER: CRP-074FW2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/248-7000
; TELEFAX: 617/248-7100
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1368 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1365
; US-08-461-397A-24

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; GENERAL INFORMATION:
; APPLICANT: SMART, JOHN
; APPLICANT: OPPERMAN, HERMAN
; APPLICANT: OZKAYNAK, ENGIN
; APPLICANT: KUBERASAMPATH, THANGAVEL
; APPLICANT: RUEGER, DAVID C.
; APPLICANT: PANG, ROY H.L.
; APPLICANT: COHEN, CHARLES M.
; TITLE OF INVENTION: MORPHOGENIC PROTEIN SCREENING METHOD
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES
; STREET: 45 SOUTH STREET
; CITY: HOPKINTON
; STATE: MA
; COUNTRY: USA
; ZIP: 01748
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/912.088
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/278,729
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: PITCHER ESQ., EDMUND R.
; REGISTRATION NUMBER: 27,829
; REFERENCE/DOCKET NUMBER: CRP-058CPFW
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (508) 433-9001
; TELEFAX: (508) 435-6951
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1368 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1365
; US-08-912-088-24

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Ratio: 2.868 Gaps: 4
Percent Similarity: 66.019 Percent Identity: 39.806

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; GENERAL INFORMATION:
; APPLICANT: KUBERASAMPATH, THANGAVEL
; APPLICANT: COHEN, CHARLES M.
; APPLICANT: RUEGER, DAVID C.
; APPLICANT: OPPERMAN, HERMAN
; APPLICANT: PANG, ROY H.L.
; TITLE OF INVENTION: MORPHOGENIC-ENRICHED DIETARY COMPOSITION
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES
; STREET: 45 SOUTH STREET
; CITY: HOPKINTON
; STATE: MA
; COUNTRY: USA
; ZIP: 01748
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; SOFTWARE: PatentIn Release #1.0, Version #1.30
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; FILING DATE: 20-JULY-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: FENTON ESQ., GILLIAN M.
; REGISTRATION NUMBER: 36,508
; REFERENCE/DOCKET NUMBER: CRP-071FW
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7560
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 24:
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; LENGTH: 1368 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
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; LOCATION: 1..1365
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; Patent No. 6077823
; GENERAL INFORMATION:
; APPLICANT: KUBERASAMPATH, THANGAVEL
; APPLICANT: PANG, ROY HL
; APPLICANT: OPPERMANN, HERMANN
; APPLICANT: RUEGER, DAVID C
; APPLICANT: COHEN, CHARLES M
; APPLICANT: OZKAYNAK, ENGIN
; APPLICANT: SMART, JOHN E
; TITLE OF INVENTION: MORPHOGEN-INDUCED MODULATION OF
; OPERATING SYSTEM: PC-DOS/MS-DOS
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CREATIVE BIOMOLECULES, INC.
; STREET: 35 SOUTH STREET
; CITY: HOPKINTON
; STATE: MA
; COUNTRY: USA
; ZIP: 01748
; COMPUTER READABLE FORM:
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; SOFTWARE: PatentIn Release #1.0, Version #1.25
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; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/165,511
; FILING DATE:
; APPLICATION NUMBER: US/07/938,336
; FILING DATE:
; APPLICATION NUMBER: US 07/667,274
; FILING DATE: 11-MAR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/753,059
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; FILING DATE: 30-AUG-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/752,764
; FILING DATE: 30-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: PITCHER ESQ, EDMUND R
; REGISTRATION NUMBER: 27,829
; REFERENCE/DOCKET NUMBER: CRP-059CP.APP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/248-7000
; TELEFAX: 617/248-7100
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1368 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1368
; US-08-445-467-24

alignment_scores:
Quality: 195.00 Length: 103
Ratio: 2.868 Gaps: 4
Percent Similarity: 66.019 Percent Identity: 39.806

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30 p...LysTrpValHisGluProLysGlyTyrTyrAlaAsnPheCysSerG 46
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1104 GCATGACTGGATCATCGCACAGAGGCTATGGCGCTTCTACTGCAGCG 1153
46 lyProCysProTyrLeuArgSerAlaAsp.....ThrThrHisSer 59
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1154 GCGAGTGCAATTTCCCGCTCAATGCCACATGAAGCCACCAACCATGCG 1203
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1204 ATCGTCCAGACCCCTGGTCCACCTGCTGGAGCCCAAGAGGTGCCCAAGCC 1253
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1254 CTGCTGGCTCCGACCGAGGCTGGAGCAGCTACCCGCTTCTGTACCACCTGA 1303
93 ly...ArgThrProLysValGluGlnLeuSerAsnMetValValLysSer 108
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seq_name: /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-480-515A-24

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; Sequence 24, Application US/08480515A
; Patent No. 6090776
; GENERAL INFORMATION:
; APPLICANT: KUBERASAMPATH, THANGAVEL
; APPLICANT: PANG, ROY H.L.
; APPLICANT: OPPERMANN, HERMANN
; APPLICANT: RUEGER, DAVID C.
; APPLICANT: COHEN, CHARLES M.
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; APPLICANT: SMART, JOHN E.
; TITLE OF INVENTION: MORPHOGEN TREATMENT OF ORGAN TRANSPLANTS
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES
; STREET: 45 SOUTH STREET
; CITY: HOPKINTON
; STATE: MA
; COUNTRY: USA
; ZIP: 01748
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,515A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: FENTON ESQ., GILLIAN M.
; REGISTRATION NUMBER: 36,508
; REFERENCE/DOCKET NUMBER: CRP-068FWC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7560
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1368 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1365
; US-08-480-515A-24

alignment_scores:
    Quality: 195.00      Length: 103
    Ratio: 2.868         Gaps: 4
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alignment_block:
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Align seg 1/1 to: US-08-480-515A-24 from: 1 to: 1368

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1104 GCATGACTGGATGCAGCGACAGAGGGCTATGGCGCTTCTACTGCAGCG 1153

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60 ThrValLeuGlyLeuTyrAsnThrLeuAsnProGluAlaSerAlaSerPr 76
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76 oCysCysValProGlnAspLeuGluProLeuThrIleLeuTyrTyrValG 93
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93 Ly...ArgThrProLysValGluGlnLeuSerAsnMetValValLysSer 108
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109 CysLysCys 111
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seq_documentation_block:
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; Patent No. 6211146
; GENERAL INFORMATION:
; APPLICANT: KUBERASAMPATH, THANGAVEL
; APPLICANT: PANG, ROY HL
; APPLICANT: OPPERMAN, HERMANN
; APPLICANT: RUEGER, DAVID
; APPLICANT: COHEN, CHARLES M
; TITLE OF INVENTION: 60A PROTEIN-INDUCED MORPHOGENESIS
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CREATIVE BIOMOLECULES, INC
; STREET: 45 SOUTH STREET
; CITY: HOPKINTON
; STATE: MA
; COUNTRY: USA
; ZIP: 01748
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/271,556A
; FILING DATE: 07-JUL-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/945,292
; FILING DATE: 15-SEP-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/667,274
; FILING DATE: 11-MAR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/753,059
; FILING DATE: 30-AUG-1991
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; APPLICATION NUMBER: US 07/752,764
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/752,857
; FILING DATE: 30-AUG-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/923,780
; FILING DATE: 31-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/922,813
; FILING DATE: 31-JUL-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: FENTON, GILLIAN M
; REGISTRATION NUMBER: 36,508
; REFERENCE/DOCKET NUMBER: CRP-066FW
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7000
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1368 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1365
; US-08-271-556A-1
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; TOPOLOGY: linear
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; . NAME/KEY: CDS
; . LOCATION: 1..1368
PCT-US93-07190-24

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    Quality: 195.00      Length: 103
    Ratio: 2.868        Gaps: 4
    Percent Similarity: 66.019    Percent Identity: 39.806

alignment_block:
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||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
1104 GCATGACTGGATCATCGCCAGCAGAGGCTATGGCGCTTCTTACTGCACGC 1153

46 lyProCysProTyrLeuArgSerAlaAsp.....ThrThrHisSer 59
||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
1154 GCGAGTGCAGTAATTTCCCGCTCAATGCGGCACATGACGCCCAACCATCGC 1203

60 ThrValLeuGlyLeuTyrAsnThrLeuAsnProGluAlaSerAlaSerPr 76
||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
1204 ATCGTCCAGACCCCTGGTCCACCTGCTGGAGCCCAAGAAGGTGCCCAAGCC 1253

76 cCysCysValProGlnAspLeuGluProLeuThrIleLeuTyrTyrValG 93
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93 ly...ArgThrProLysValIcIuLeuSerAsnMetValValLysSer 108
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1304 ACGACCAAGATGTGAACCTGAAAAAGTATAGAAACATGATTGTGNAATCC 1353

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; GENERAL INFORMATION:
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; APPLICANT:
; TITLE OF INVENTION: MORPHOGEN-INDUCED NERVE REGENERATION AND
; TITLE OF INVENTION: REPAIR
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CREATIVE BIOMOLECULES, INC.
; STREET: 35 SOUTH STREET
; CITY: HOPKINTON
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 01748
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/07231
; FILING DATE: 19930729
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: KELLEY, ROBIN D.

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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/08742
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: KELLEY ESQ, ROBIN D.
; REGISTRATION NUMBER: 34,637
; REFERENCE/DOCKET NUMBER: CRP-067
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/248-7477
; TELEFAX: 617/248-7100
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1368 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1368
PCT-US93-08742-24

alignment_scores:
    Quality: 195.00      Length: 103
    Ratio: 2.868        Gaps: 4
Percent Similarity: 66.019    Percent Identity: 39.806

alignment_block:
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30 p...LysTrpValHisGluProLysGlyTyrrTyrrAlaAsnPheCysSerG 46
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1104 GCAATGACTGGATCATGCCACGAGGGCTTGCCTTCTACTGCAGCG 1153

46  lyProCysProTyrrLeuArgSerAlaAsp.....ThrThrHisSer 59
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1154 GCGAGTGCATTTCCCGCTCAATGCCACATGAACGCCACGACCATCGG 1203

60  ThrValLeuGlyLeuTyrrAsnThrLeuAsnProGluAlaSerAlaSerPr 76
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1204 ATCGTCCAGACCCGTGCTCCACCTGCTGGAGCCCCAAGAAGTGCCCAAGCC 1253

76  oCysCysValProGlnAspLeuGluProLeuThrIleLeuTyrrTyrrValG 93
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; GENERAL INFORMATION:

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;; APPLICANT:
;; TITLE OF INVENTION: MORPHOGEN-INDUCED LIVER REGENERATION
;; NUMBER OF SEQUENCES: 33
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: CREATIVE BIOMOLECULES, INC.
;; STREET: 45 SOUTH STREET
;; CITY: HOPKINTON
;; STATE: MA
;; COUNTRY: USA
;; ZIP: 01748
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
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;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER:
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: KELLEY ESQ, ROBIN D.
;; REGISTRATION NUMBER: 34,637
;; REFERENCE/DOCKET NUMBER: CRP-072
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 617/248-7477
;; TELEFAX: 617/248-7100
;; INFORMATION FOR SEQ ID NO: 24:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1368 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: CDNA
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: 1..1368
PCT-US93-08808-24

alignment_scores:
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  Ratio: 2.868        Gaps: 4
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alignment_block:
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Align seg 1/1 to: PCT-US93-08808-24 from: 1 to: 1368

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46 lyProCysProTyrLeuArgSerAlaAsp.....ThrThrHisSer 59
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1154 GCGAGTGCAATTTCCCGCTCAATGCGCACATGAACGCCACGACCACTGCG 1203

60 ThrValLeuGlyLeuTyrAsnThrLeuAsnProGluAlaSerAlaSerPr 76
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1204 ATGCTCCAGACCTGGTCCACCTGCTGGAGCCCAAGAGGTGCCCAAGCC 1253

76 oCysCysValProGlnAspLeuGluProLeuThrIleLeuTyrTyrValG 93
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93 ly...ArgThrProLysValGluGlnLeuSerAsnMetValValLysSer 108
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seq_documentation_block:
; Sequence 24, Application PC/TUS9308885
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: MORPHOGEN TREATMENT OF GASTROINTESTINAL
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CREATIVE BIOMOLECULES, INC.
; STREET: 45 SOUTH STREET
; CITY: HOPKINTON
; STATE: MA
; COUNTRY: USA
; ZIP: 01748
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/08885
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: KELLEY ESQ, ROBIN D.
; REGISTRATION NUMBER: 34,637
; REFERENCE/DOCKET NUMBER: CRP-074
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/248-7477
; TELEFAX: 617/248-7100
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1368 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1368
PCT-US93-08885-24

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  Quality: 195.00      Length: 103
  Ratio: 2.868        Gaps: 4
  Percent Similarity: 66.019  Percent Identity: 39.806

alignment_block:
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Align seg 1/1 to: PCT-US93-08885-24 from: 1 to: 1368

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1104 GCATGACTGGATCATCGCACCGAGGCTATGGCGCTTCTACTGCAGCG 1153
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; TELEFAX: 617 876-5851
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 417 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: bmp-7
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..417
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    Ratio: 2.662        Gaps: 5
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73 AACGTGGCAGACACACAGCAGCGCAGCGCCTGTAAGAGCA 122
18 gProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLys...TrpValH 34
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123 CGAGCTGTATGTCAGCTCCGA...GACCTGGGCTGGCAGGACTGGATCA 169
34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
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170 TCGCGCTGAAGGCTACGCCCTACTACTGTGAGGGGAGTGTGCCTTC 219
51 LeuArgSerAla.....AspThrThrHisSerThrValLeuGlyLe 64
: |||||: |||||: |||||: |||||: |||||: |||||: |||||: ||
220 CCTGTGAACCTCTACATGAACGCCACCAACCGCCATCTGTGACAGCGCT 269
64 uTyrAsnThrLeuAsnProGluAlaSerAlaSerProCysCysValProG 81
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270 GTTCCACTTCATCAACCGGAACGGTGCCCAAGCCCTGCTGTGCGGCCA 319
81 lnAspLeuGluProLeuThrIleLeuTyrTyrValGlyArgThrProLys 97
: |||||: |||||: |||||: |||||: |||||: |||||: |||||: ||
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98 val...GluGlnLeuSerAsnMetValValLysSerCysLysCys 111
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seq_documentation_block:
; Sequence 1, Application US/08149106
; Patent No. 5411941
; GENERAL INFORMATION:
; APPLICANT: Grinna, Lynn
; APPLICANT: Parsons, Thomas F.
; APPLICANT: Theofan, Georgia
; TITLE OF INVENTION: Osteogenic Factor
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell
; STREET: Two First National Plaza, 20 South Clark
; STREET: Street
; CITY: Chicago
; STATE: Illinois

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; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/149,106
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/415,555
; FILING DATE: 04-OCT-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/256,034
; FILING DATE: 11-OCT-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharp, Jeffrey S.
; REGISTRATION NUMBER: 31,879
; REFERENCE/DOCKET NUMBER: 27129/9430
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 346-5750
; TELEFAX: (312) 984-9740
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 417 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
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18 gProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLys...TrpValH 34
: |||||:|||||:|||||:|||||:|||||:|||||:|||||: |||
123 CGAGCTGTATGTCAGCTCCGA...GACCTGGGCTGGCAGGACTGGATCA 169
34 isGluProLysGlyTyrTyrAlaAsnPheCysSerGlyProCysProTyr 50
|||||:|||||: ||| :|||||: ||| :|||||: ||| :||| :||| :
170 TCGCGCTGAAGGCTACGCCCTACTACTGTGAGGGGAGTGTGCCTTC 219
51 LeuArgSerAla.....AspThrThrHisSerThrValLeuGlyLe 64
: |||||: |||||: |||||: |||||: |||||: |||||: |||||: ||
220 CCTGTGAACCTCTACATGAACGCCACCAACCGCCATCTGTGACAGCGCT 269
64 uTyrAsnThrLeuAsnProGluAlaSerAlaSerProCysCysValProG 81
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  Percent Similarity: 61.739      Percent Identity: 34.783

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; APPLICATION NUMBER: PCT/US94/13181
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/163,877
; FILING DATE: December 7, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Lazar, Steven R.
; REGISTRATION NUMBER: 32,618
; REFERENCE/DOCKET NUMBER: GI 5219-PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617 498-8260
; TELEFAX: 617 876-5851
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 417 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; ORIGINAL SOURCE:
; ORGANISM: bmp-7
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; NAME/KEY: CDS
; LOCATION: 1..417
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Align seg 1/1 to: PCT-US94-13181-9 from: 1 to: 417

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73 AACGTGGCAGAGAACAGCAGCAGCAGCAGCGAGCGCTGTGAAGAAGCA 122

18 gProLeuTyrIleAspPheArgGlnAspLeuGlyTrpLys...TrpValH 34
: |||||:|||||: |||||:|||||: |||||:
123 CGAGCTGTATGTACAGCTTCCGA...GACCTGGGCTGGCAGGACTGGATCA 169

34 isGluProLysGlyTyrTyrAlaAspPheCysSerGlyProCysProTyr 50
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98 Val...GluGlnLeuSerAsnMetValValLysSerCysLysCys 111
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; Patent No. 5851802
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; TITLE OF INVENTION: Methods for Recombinant Microbial Production of
; TITLE OF INVENTION: Fusion Proteins and BPI-Derived Peptides
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
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; APPLICATION NUMBER: US/08/621,803
; FILING DATE: 22-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Borun, Michael F.
; REGISTRATION NUMBER: 25,447
; REFERENCE/DOCKET NUMBER: 27129/33199
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
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; ORGANISM:
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GenCore version 4.5
 Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

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 (without alignments)
 511.755 Million cell updates/sec

Title: TGFB3P
 Perfect score: 634
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 Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues
 Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 100 summaries

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 1: piri:*
 2: pir2:*
 3: pir3:*
 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	633	99.8	412	2 A36169	transforming growth
3	630	99.4	410	2 A55706	transforming growth
4	629	99.2	412	2 A34939	transforming growth
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10	535	84.4	442	2 B31249	transforming growth
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47	186.5	29.4	408	2 S50899	betaB inhibin prec
48	184.5	29.1	255	2 I48235	inhibin beta-B cha
49	184.5	29.1	393	2 I50103	activin beta B - z
50	184.5	29.1	411	2 B41398	inhibin beta-B cha
51	183.5	28.9	115	2 PN0505	activin beta B-1 c
52	183	28.9	115	2 PN0504	activin beta A cha
53	183	28.9	430	2 JQ1184	osteogenic protein
54	182.5	28.8	393	2 S37073	bone morphogenetic
55	182.5	28.8	394	2 S45355	bone morphogenetic
56	182.5	28.8	396	1 BMH02	bone morphogenetic
57	182.5	28.8	398	2 JH0688	bone morphogenetic
58	182.5	28.8	398	2 JH0687	bone morphogenetic
59	182	28.7	495	2 S43294	bone morphogenetic
60	182	28.7	501	2 A55452	cartilage-derived
61	182	28.7	501	2 JC2347	growth/differentia
62	181.5	28.6	115	2 PN0506	activin beta B-2 c
63	181	28.5	461	2 S52408	SPDVRL protein - s
64	180	28.4	352	2 JC2466	inhibin beta-C cha
65	180	28.4	352	2 JC5366	activin beta C - m
66	180	28.4	352	2 S70580	activin beta C pre
67	179	28.2	125	2 S43295	bone morphogenetic
68	179	28.2	452	2 I49542	bone morphogenetic
69	179	28.2	454	1 BMH05	bone morphogenetic
70	176	27.8	151	2 S43296	bone morphogenetic
71	175	27.6	436	2 B55452	cartilage-derived
72	174	27.4	372	2 C39364	GDF-1 embryonic gr
73	172	27.1	588	2 A26158	decapentaplegic pr
74	171.5	27.1	102	2 A36192	inhibin beta-A cha
75	171.5	27.1	353	2 I50607	bone morphogenetic
76	171	27.0	34	2 C42320	transforming growth
77	170.5	26.9	405	2 I50608	bone morphogenetic
78	170.5	26.9	408	1 BMH04	bone morphogenetic
79	170.5	26.9	408	2 S38343	bone morphogenetic
80	170.5	26.9	408	2 S58791	bone morphogenetic
81	170.5	26.9	420	2 I49541	bone morphogenetic
82	170	26.8	101	2 B36192	inhibin beta-B1 ch
83	169	26.7	101	2 C36192	inhibin beta-B2 ch
84	168	26.5	402	2 A45056	osteogenic protein
85	165.5	26.1	400	2 A49147	bone morphogenetic
86	165.5	26.1	401	2 JH0689	bone morphogenetic
87	164.5	25.9	357	2 A39364	GDF-1 embryonic gr
88	163.5	25.8	408	2 JH0801	bone morphogenetic
89	162.5	25.6	366	2 A46607	growth/differentia
90	160.5	25.3	366	2 A45402	transforming growth
91	159	25.1	373	2 PN0042	activin - fruit fl
92	158.5	25.0	472	1 BMH03	bone morphogenetic
93	156.5	24.7	360	2 I53032	bone morphogenetic
94	149.5	23.6	350	2 T25451	transforming growth
95	148	23.3	366	2 T03907	TGF-beta-related p
96	140	22.1	427	2 A40735	TGF beta homolog d
97	135.5	21.4	309	2 JC5697	placental transfer
98	135.5	21.4	476	2 JC4646	bone morphogenetic
99	133.5	21.1	354	2 S29718	gene nodal protein
100	133.5	21.1	478	2 JC4838	bone morphogenetic

ALIGNMENTS

```
RESULT 1
A41397
transforming growth factor beta-3 precursor - mouse
C:Species: Mus musculus (house mouse)
C>Date: 03-Apr-1992 #sequence_revision 03-Apr-1992 #text_change 16-Jul-1999
C:Accession: A41397; A61039; A61225
R:Miller, D.A.; Lee, A.; Matsui, Y.; Chen, E.Y.; Moses, H.L.; Derynck, R.
Mol. Endocrinol. 3, 1926-1934, 1989
A:Title: Complementary DNA cloning of the murine transforming growth factor-beta3 (TGFB3)
t tissues.
A:Reference number: A41397; MUID:90190650
A:Accession: A41397
A:Molecule type: mRNA
A:Residues: 1-410 <MIL>
A:Cross-references: GB:M32745; NID:g201949; PIDN:AAA0422.1; PID:g201950
R:Denhez, F.; Lafyatis, R.; Kondaliah, P.; Roberts, A.B.; Sporn, M.B.
Growth Factors 3, 139-146, 1990
A:Title: Cloning by polymerase chain reaction of a new mouse TGF-beta, mTGF-beta3.
A:Reference number: A61039; MUID:91000714
A:Accession: A61039
A:Molecule type: mRNA
A:Residues: 1-410 <DEN>
R:Watrin, F.; Scotto, L.; Assolian, R.K.; Wolgemuth, D.J.
Cell Growth Differ. 2, 77-83, 1991
A:Title: Cell lineage specificity of expression of the murine transforming growth factor
A:Reference number: A61225; MUID:91299576
A:Accession: A61225
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 285-410 <WAT>
C:Superfamily: inhibin
C:Keywords: glycoprotein; growth factor; growth regulation
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-298/Domain: propeptide #status predicted <PRO>
F:299-461/Region: cell attachment (R-G-D) motif
F:299-410/Product: transforming growth factor beta-3 #status predicted <WAT>
F:72,133,140/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 99.8%; Score 633; DB 2; Length 410;
Best Local Similarity 100.0%; Pred. No. 7.2e-57;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALDTNYCFRNLENCVRLPYIDFRODLGKWKVHEPKGYANFCSGPCPYLRSADTTHT 60
|||||
Db 299 ALDTNYCFRNLENCVRLPYIDFRODLGKWKVHEPKGYANFCSGPCPYLRSADTTHT 358

QY 61 VLGLYNTLNPEASAPCCVPQDLEPLTILYYVGRTPKVEQLSNMVKSKCS 112
|||||
Db 359 VLGLYNTLNPEASAPCCVPQDLEPLTILYYVGRTPKVEQLSNMVKSKCS 410

RESULT 2
A36169
transforming growth factor beta-3 precursor - human
C:Species: Homo sapiens (man)
C>Date: 14-Dec-1990 #sequence_revision 14-Dec-1990 #text_change 20-Jun-2000
C:Accession: A36169; A41262; S01824
R:ten Dijke, P.; Hansen, P.; Iwata, K.K.; Pieler, C.; Foulkes, J.G.
Proc. Natl. Acad. Sci. U.S.A. 85, 4715-4719, 1988
A:Title: Identification of another member of the transforming growth factor type beta ge
A:Reference number: A36169; MUID:88263019
A:Accession: A36169
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-412 <TEN>
A:Cross-references: GB:J03241; NID:g339551; PIDN:AAA61161.1; PID:g339552
R:Arick, B.A.; Lee, A.L.; Grendell, R.L.; Derynck, R.
Mol. Cell. Biol. 11, 4306-4313, 1991
A:Title: Inhibition of translation of transforming growth factor-beta3 mRNA by its 5' un
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```
A:Reference number: A41262; MUID:91342629
A:Accession: A41262
A:Molecule type: DNA
A:Residues: 1-48 <ARR>
A:Cross-references: GB:M58524
R:Derynck, R.; Lindquist, P.B.; Lee, A.; Wen, D.; Tamm, J.; Graycar, J.L.; Rhee, L.;
EMBO J. 7, 3737-3743, 1988
A:Title: A new type of transforming growth factor-beta, TGF-beta3.
A:Reference number: S01824; MUID:89091120
A:Accession: S01824
A:Molecule type: mRNA
A:Residues: 3-412 <DER>
A:Cross-references: EMBL:X14885; NID:g37075; PIDN:CAA33024.1; PID:g1200236
C:Genetics:
A:Gene: GDB:TGFEB3
A:Cross-references: GDB:120437; OMIM:190230
A:Map position: 14Q24-14Q24
A:Introns: 118/1; 172/3; 216/1; 252/1; 309/2; 360/3
C:Superfamily: inhibin
C:Keywords: growth factor; homodimer
F:1-27/Domain: signal sequence #status predicted <SIG>
F:28-300/Domain: propeptide #status predicted <PRO>
F:301-412/Product: transforming growth factor beta-3 #status predicted <WAT>

Query Match 99.8%; Score 633; DB 2; Length 412;
Best Local Similarity 100.0%; Pred. No. 7.2e-57;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALDTNYCFRNLENCVRLPYIDFRODLGKWKVHEPKGYANFCSGPCPYLRSADTTHT 60
|||||
Db 301 ALDTNYCFRNLENCVRLPYIDFRODLGKWKVHEPKGYANFCSGPCPYLRSADTTHT 360

QY 61 VLGLYNTLNPEASAPCCVPQDLEPLTILYYVGRTPKVEQLSNMVKSKCS 112
|||||
Db 361 VLGLYNTLNPEASAPCCVPQDLEPLTILYYVGRTPKVEQLSNMVKSKCS 412

RESULT 3
A55706
transforming growth factor beta-3 precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 03-Mar-1995 #sequence_revision 03-Mar-1995 #text_change 16-Jul-1999
C:Accession: A55706; B40699; S36042
R:Wang, J.; Kuliszewski, M.; Yee, W.; Sedlackova, L.; Xu, J.; Tseu, I.; Post, M.
J. Biol. Chem. 270, 2722-2728, 1995
A:Title: Cloning and expression of glucocorticoid-induced genes in fetal rat lung fib
A:Reference number: A55706; MUID:95155340
A:Accession: A55706
A:Molecule type: mRNA
A:Residues: 1-410 <WAN>
A:Cross-references: GB:U03491
A:Note: it is uncertain whether Met-1 is the initiator
R:McKinnon, R.D.; Piras, G.; Ida Jr., J.A.; Dubois-Dalcq, M.
J. Cell Biol. 121, 1397-1407, 1993
A:Title: A role for TGF-beta in oligodendrocyte differentiation.
A:Reference number: A40699; MUID:93286190
A:Accession: B40699
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 157-211 <MCK>
A:Cross-references: EMBL:X71903; NID:g311326; PIDN:CAA50722.1; PID:g311327
C:Superfamily: inhibin

Query Match 99.4%; Score 630; DB 2; Length 410;
Best Local Similarity 99.1%; Pred. No. 1.4e-56;
Matches 111; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALDTNYCFRNLENCVRLPYIDFRODLGKWKVHEPKGYANFCSGPCPYLRSADTTHT 60
|||||
Db 299 ALDTNYCFRNLENCVRLPYIDFRODLGKWKVHEPKGYANFCSGPCPYLRSADTTHT 358
```

QY 61 VLGLYNTLNPEASASPCCVQDLEPLTILYVGRTPKVEQLSNMVKSKCS 112
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 359 VLGLYNTLNPEASASPCCVQDLEPLTILYVGRTPKVEQLSNMVKSKCS 410

RESULT 4

A34939
 transforming growth factor beta-3 precursor - chicken
 C:Species: Gallus gallus (chicken)
 C>Date: 13-Jul-1990 #sequence_revision 13-Jul-1990 #text_change 16-Jul-1999
 C:Accession: A34939; S25850; S36124; I51181
 R:Jakowlew, S.B.; Dillard, P.J.; Kondalah, P.; Sporn, M.B.; Roberts, A.B.
 Mol. Endocrinol. 2, 747-755, 1988
 A:Title: Complementary deoxyribonucleic acid cloning of a novel transforming growth factor
 A:Reference number: A34939; MUID:89096966
 A:Accession: A34939
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-412 <JAK>
 A:CROSS-references: GB:M31154; NID:G212758; PIDN:AAA49089.1; PID:G212759
 R:Burt, D.W.; Paton, I.R.; Dev, B.R.
 J. Mol. Endocrinol. 7, 175-183, 1991
 A:Title: Comparative analysis of human and chicken transforming growth factor-beta-2 and
 A:Reference number: S25850; MUID:92134496
 A:Accession: S25850
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-117 <BUR>
 A:CROSS-references: EMBL:X58127; NID:G63815; PIDN:CAA41128.1; PID:G63816
 A:Accession: S36125
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 119-172 <BU2>
 A:CROSS-references: EMBL:X60055; NID:G396688; PIDN:CAA42653.1; PID:G396689
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1991
 A:Accession: S36124
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 173-322, 'ELPT', 327-412 <BU3>
 A:CROSS-references: EMBL:X60091
 A:Note: The nucleotide sequence was submitted to the EMBL Data Library, June 1991
 R:Jakowlew, S.B.; Lechleider, R.; Geiser, A.G.; Kim, S.J.; Santa-Coloma, T.A.; Cubert, J.
 Mol. Endocrinol. 6, 1285-1298, 1992
 A:Title: Identification and characterization of the chicken transforming growth factor-
 A:Reference number: I51181; MUID:93024487
 A:Accession: I51181
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-117 <JAK2>
 A:CROSS-references: GB:S46000; NID:G257172; PIDN:AAB23575.1; PID:G257173
 C:Genetics:
 A:Introns: 216/1; 252/1; 309/2; 360/3
 A:Note: list of introns may be incomplete
 C:Superfamily: inhibin
 C:Keywords: glycoprotein; growth factor; growth regulation; homodimer; mitogen
 F:1-22/Domain: signal sequence #status predicted <SIG>
 F:23-300/Domain: propeptide #status predicted <PRO>
 F:301-412/Product: transforming growth factor beta-3 #status predicted <MAT>
 F:74,142/Binding site: carbohydrate (Asn) (covalent)

Query Match 99.2%; Score 629; DB 2; Length 412;
 Best Local Similarity 99.1%; Pred. No. 1.8e-56;
 Matches 111; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALDTNYCFRNLEENCCVRPLYIDFQDLGKWKVHEPKGYANFCSCGPCPYLRSADTTHST 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 301 ALDTNYCFRNLEENCCVRPLYIDFQDLGKWKVHEPKGYANFCSCGPCPYLRSADTTHST 360

QY 61 VLGLYNTLNPEASASPCCVQDLEPLTILYVGRTPKVEQLSNMVKSKCS 112

Db 361 VLGLYNTLNPEASASPCCVQDLEPLTILYVGRTPKVEQLSNMVKSKCS 412

RESULT 5

S01825
 transforming growth factor beta-3 precursor - pig
 C:Species: Sus scrofa domestica (domestic pig)
 C>Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 16-Jul-1999
 C:Accession: S01825
 R:Derynck, R.; Lindquist, P.B.; Lee, A.; Wen, D.; Tamm, J.; Graycar, J.L.; Rhee, L.;
 EMBO J. 7, 3737-3743, 1988
 A:Title: A new type of transforming growth factor-beta, TGF-beta3.
 A:Reference number: S01824; MUID:89091120
 A:Accession: S01825
 A:Molecule type: mRNA
 A:Residues: 1-409 <DER>
 A:CROSS-references: EMBL:X14150; NID:G2127; PIDN:CAA32363.1; PID:G2128
 C:Superfamily: inhibin
 C:Keywords: growth factor
 F:1-25/Domain: signal sequence #status predicted <SIG>
 F:26-297/Domain: propeptide #status predicted <PRO>
 F:298-409/Product: transforming growth factor beta-3 #status predicted <MAT>

Query Match 97.9%; Score 621; DB 2; Length 409;
 Best Local Similarity 98.2%; Pred. No. 1.2e-55;
 Matches 110; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ALDTNYCFRNLEENCCVRPLYIDFQDLGKWKVHEPKGYANFCSCGPCPYLRSADTTHST 60

Db 298 ALDTNYCFRNLEENCCVRPLYIDFQDLGKWKVHEPKGYANFCSCGPCPYLRSADTTHST 357

QY 61 VLGLYNTLNPEASASPCCVQDLEPLTILYVGRTPKVEQLSNMVKSKCS 112

Db 358 VLGLYNTLNPEASASPCCVQDLEPLTILYVGRTPKVEQLSNMVKSKCS 409

RESULT 6

A39489
 transforming growth factor beta-2 precursor - chicken
 N:Alternate names: TGF-beta2
 C:Species: Gallus gallus (chicken)
 C>Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 16-Jul-1999
 C:Accession: A39489; A61018; S25849
 R:Burt, D.W.; Paton, I.R.
 DNA Cell Biol. 10, 723-734, 1991
 A:Title: Molecular cloning and primary structure of the chicken transforming growth f
 A:Reference number: A39489; MUID:92075163
 A:Accession: A39489
 A:Molecule type: DNA
 A:Residues: 1-412 <BUR>
 A:CROSS-references: GB:X58071; NID:G63810; PIDN:CAA41101.1; PID:G833616; GB:X59082; G
 R:Jakowlew, S.B.; Dillard, P.J.; Sporn, M.B.; Roberts, A.B.
 Growth Factors 2, 123-133, 1990
 A:Title: Complementary deoxyribonucleic acid cloning of an mRNA encoding transforming
 A:Reference number: A61018; MUID:90253805
 A:Accession: A61018
 A:Status: not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-94, 'G', 96-244, 'L', 246-412 <JAK>
 C:Genetics:
 A:Introns: 115/1; 169/3; 214/1; 251/1; 309/2; 360/3
 C:Superfamily: inhibin
 C:Keywords: growth factor; growth regulation; mitogen; transformation
 F:1-26/Domain: signal sequence #status predicted <SIG>
 F:27-300/Domain: propeptide #status predicted <PRO>
 F:301-412/Product: transforming growth factor beta-2 #status predicted <MAT>

Query Match 85.0%; Score 539; DB 2; Length 412;
 Best Local Similarity 79.5%; Pred. No. 2.6e-47;
 Matches 89; Conservative 15; Mismatches 8; Indels 0; Gaps 0;

QY 1 ALDTNYCFRNLEENCCVRPLYIDFQDLGKWKVHEPKGYANFCSCGPCPYLRSADTTHST 60

||||| |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

A;Reference number: A34005; MUID:88124824
A;Accession: A34005
A;Molecule type: mRNA
A;Residues: 1-414 <HAN>
A;Cross-references: GB:J03585; NID:g176495; PIDN:AAA35358.1; PID:g176496
A;Note: part of this sequence, including the amino end of the active peptide, confirm
R;Webb, N.R.; Madisen, L.; Rose, T.M.; Purchio, A.F.
DNA 7, 493-497, 1988
A;Title: Structural and sequence analysis of TGF-beta-2 cDNA clones predicts two diff
A;Reference number: A90960; MUID:89090808
A;Contents: annotation
A;Note: although they do not show the sequences, a clone identical yielding a sequence
with that in the long form of the human sequence
C;Superfamily: Inhibin
C;Keywords: alternative splicing; glycoprotein; growth factor; growth regulation; hom
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-302/Domain: propeptide #status predicted <PRO>
F;303-414/Product: transforming growth factor beta-2 #status predicted <MAT>
F;72,140,241/Binding site: carboxydrate (Asn) (covalent) #status predicted

Query Match 84.4%; Score 535; DB 1; Length 414;
Best Local Similarity 79.8%; Pred. No. 6.7e-47;
Matches 89; Conservative 14; Mismatches 9; Indels 0; Gaps 0;

QY 1 ALDITNYCFRNLNECCVRPLYIDFRODLGNKWKVHEPKGYVANFCGPGPYLRSADTTHTST 60
DB 303 ALDAAYCFRNVQDNCRLRPLYIDFKRDLGNKWKVHEPKGYVANFCGAGCPYLWSSDTQHSR 362
QY 61 VLGLYNTLNPEASAPCCVPQDLEPLTILYVGRTPKVEQLSNMVKSKCS 112
DB 363 VLSLYNTINPEASAPCCVSGDLEPLTILYVIGTKPIEQLSNMIVKSKCS 414

RESULT 9
A31249
transforming growth factor beta-2 precursor, short form - human
N;Alternate names: glioblastoma-derived T-cell suppressor factor
C;Species: Homo sapiens (man)
C;Date: 01-Dec-1989 #sequence_revision 19-Oct-1995 #text_change 16-Jul-1999
C;Accession: S06216; A31249
R;de Martin, R.; Haendler, B.; Hofer-Warbinek, R.; Gaugitsch, H.; Wrann, M.; Schlues
EMBO J. 6, 3673-3677, 1987
A;Title: Complementary DNA for human glioblastoma-derived T cell suppressor factor, a
A;Reference number: S06216; MUID:88115555
A;Accession: S06216
A;Molecule type: mRNA
A;Residues: 1-414 <DEM>
A;Cross-references: EMBL:Y00083; NID:g31959; PIDN:CAA68279.1; PID:g31960
R;Webb, N.R.; Madisen, L.; Rose, T.M.; Purchio, A.F.
DNA 7, 493-497, 1988
A;Title: Structural and sequence analysis of TGF-beta-2 cDNA clones predicts two diff
A;Reference number: A90960; MUID:89090808
A;Accession: A31249
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 101-130 <WEB>
C;Genetics:
A;Gene: GDB:TCF82
A;Cross-references: GDB:120436; OMIM:190220
A;Map position: 1q41-1q41
C;Superfamily: Inhibin
C;Keywords: alternative splicing; growth factor
F;1-20/Domain: signal sequence #status predicted <SIG>
F;31-302/Domain: propeptide #status predicted <PRO>
F;303-414/Product: transforming growth factor beta-2 #status experimental <MAT>

Query Match 84.4%; Score 535; DB 2; Length 414;
Best Local Similarity 79.8%; Pred. No. 6.7e-47;
Matches 89; Conservative 14; Mismatches 9; Indels 0; Gaps 0;

QY 1 ALDITNYCFRNLNECCVRPLYIDFRODLGNKWKVHEPKGYVANFCGPGPYLRSADTTHTST 60


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QY 1 ALDNTYCFRNLENCVVRPLYIDFRDLGKWKVHPKGYANFCGPGCPYLRSADTTHST 60
  ||| |||||:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 302 ALDAYCFRNVDNCCRLPLYIDFRKDLGKWKIHPKGYANFCAGACPYLWSSDTQHRSR 361
  ||| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 VLGLYNTLNPEASAPCCVPQDLEPLTILYVGRTPKVEQLSNMVKSKCS 112
  ||| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 362 VLSLYNTLNPEASAPCCVQDLSLTILYIGNKPKTEQLSNMVKSKCS 413
  ||| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 13
WFM52
transforming growth factor beta-1 precursor - mouse
N:Alternate names: TGF type 2; TGF-beta
C:Species: Mus musculus (house mouse)
C>Date: 04-Dec-1986 #sequence_revision 04-Dec-1986 #text_change 24-Nov-1999
C:Accession: A01396
R:Derynck, R.; Jarrett, J.A.; Chen, E.Y.; Goeddel, D.V.
J. Biol. Chem. 261, 4377-4379, 1986
A:Title: The murine transforming growth factor-beta precursor.
A:Reference number: A01396; MUID:86168129
A:Accession: A01396
A:Molecule type: mRNA
A:Residues: 1-390 <DER>
A:Cross-references: GB:M13177; NID:g201952; PIDN:AAA40423.1; PID:g201953
A:Note: The authors suggest that residues 8-23 could represent the hydrophobic core of a
C:Comment: The mature protein is the carboxyl-terminal segment of a precursor polypeptide
C:Superfamily: inhibin
C:Keywords: glycoprotein; growth factor; growth regulation; homodimer; mitogen; transform
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-278/Domain: propeptide #status predicted <PRO>
F:244-246/Region: cell attachment (R-G-D) motif
F:279-390/Product: transforming growth factor beta-1 #status predicted <MAT>
F:82,136,176/Binding site: transforming growth factor beta-1 #status predicted
F:82,136,176/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 79.3%; Score 503; DB 1; Length 390;
Best Local Similarity 77.7%; Pred. No. 1.le-43;
Matches 87; Conservative 10; Mismatches 15; Indels 0; Gaps 0;

QY 1 ALDNTYCFRNLENCVVRPLYIDFRDLGKWKVHPKGYANFCGPGCPYLRSADTTHST 60
  |||||:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 279 ALDNTYCFSTSEKNCVRLYIDFRKDLGKWKIHPKGYANFCGLGCPYIWSLDTQYSK 338
  ||| ||| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 VLGLYNTLNPEASAPCCVPQDLEPLTILYVGRTPKVEQLSNMVKSKCS 112
  || ||| || |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 339 VLALYNQHNPGASAPCCVPQALEPLPIVYVGRPKVEQLSNMIVRSCKCS 390
  || ||| || |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 15
transforming growth factor beta-1 precursor - bovine (fragment)
N:Alternate names: beta-TGF; cartilage-inducing factor-A; EGF-dependent TGF or dEGF;
C:Species: Bos primigenius taurus (cattle)
C>Date: 28-Feb-1992 #sequence_revision 28-Feb-1992 #text_change 16-Jul-1999
C:Accession: A40057; A05284; A24322; B61439
R:Van Obberghen-Schilling, E.; Kondaiah, P.; Ludwig, R.L.; Sporn, M.B.; Baker, C.C.
Mol. Endocrinol. 1, 693-698, 1987
A:Title: Complementary deoxyribonucleic acid cloning of bovine transforming growth fa
A:Reference number: A40057; MUID:91042552
A:Accession: A40057
A:Molecule type: mRNA
A:Residues: 1-315 <VAN>
A:Cross-references: GB:M36271; NID:g163747; PIDN:AAA30778.1; PID:g163748
R:Ogawa, Y.; Schmidt, D.K.; Dasch, J.R.; Chang, R.J.; Glaser, C.B.
J. Biol. Chem. 267, 2325-2328, 1992
A:Title: Purification and characterization of transforming growth factor-beta2.3 and
A:Reference number: A42320; MUID:92129307
A:Accession: A42320
A:Molecule type: protein
A:Residues: 204-209,'X',211-217 <OGA>
R:Roberts, A.B.; Anzano, M.A.; Meyers, C.A.; Wideman, J.; Blacher, R.; Pan, Y.C.E.; S
Biochemistry 22, 5692-5698, 1983
A:Title: Purification and properties of a type beta transforming growth factor from b
A:Reference number: A05284; MUID:84104793
A:Accession: A05284
A:Molecule type: protein
A:Residues: 204-218 <ROB>
R:Seyedin, S.M.; Thompson, A.Y.; Bentz, H.; Rosen, D.M.; McPherson, J.M.; Conti, A.;
J. Biol. Chem. 261, 5693-5695, 1986
A:Title: Cartilage-inducing factor-A. Apparent identity to transforming growth factor
A:Reference number: A24322; MUID:86195954
A:Accession: A24322
A:Molecule type: protein
A:Residues: 204-233 <SEY>
R:Jin, Y.; Cox, D.A.; Knecht, R.; Raschdorf, F.; Cerletti, N.
J. Protein Chem. 10, 565-575, 1991
A:Title: Separation, purification, and sequence identification of TGF-beta1 and TGF-b
A:Reference number: A61439; MUID:92189724
A:Accession: B61439
A:Molecule type: protein
A:Residues: 204-209,'X',211-217,'XX',220-232 <JIN>
C:Comment: This polypeptide is composed of two polypeptide chains cross-linked by dis
C:Comment: Type II TGF does not bind to the EGF receptor and lacks intrinsic mitogeni
ion. Cells grown in monolayer do not respond in a similar manner to these growth fact
```

```
A:Title: One of two subunits of masking protein in latent TGF-beta is a part of pro-T
A:Reference number: S02267; MUID:89121078
A:Accession: S02267
A:Molecule type: protein
A:Residues: 30-32,'X',34-38,'Q',40-42,'X',44 <OK2>
C:Superfamily: inhibin
C:Keywords: glycoprotein; growth factor; integrin binding
F:1-29/Domain: signal sequence #status predicted <SIG>
F:30-278/Domain: propeptide #status experimental <PRO>
F:244-246/Region: cell attachment (R-G-D) motif
F:279-390/Product: transforming growth factor beta-1 #status predicted <MAT>
F:82,136,176/Binding site: transforming growth factor beta-1 #status predicted
F:82,136,176/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 79.3%; Score 503; DB 2; Length 390;
Best Local Similarity 77.7%; Pred. No. 1.le-43;
Matches 87; Conservative 10; Mismatches 15; Indels 0; Gaps 0;

QY 1 ALDNTYCFRNLENCVVRPLYIDFRDLGKWKVHPKGYANFCGPGCPYLRSADTTHST 60
  |||||:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 279 ALDNTYCFSTSEKNCVRLYIDFRKDLGKWKIHPKGYANFCGLGCPYIWSLDTQYSK 338
  ||| ||| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 VLGLYNTLNPEASAPCCVPQDLEPLTILYVGRTPKVEQLSNMVKSKCS 112
  || ||| || |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 339 VLALYNQHNPGASAPCCVPQALEPLPIVYVGRPKVEQLSNMIVRSCKCS 390
  || ||| || |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 15
transforming growth factor beta-1 precursor - bovine (fragment)
N:Alternate names: beta-TGF; cartilage-inducing factor-A; EGF-dependent TGF or dEGF;
C:Species: Bos primigenius taurus (cattle)
C>Date: 28-Feb-1992 #sequence_revision 28-Feb-1992 #text_change 16-Jul-1999
C:Accession: A40057; A05284; A24322; B61439
R:Van Obberghen-Schilling, E.; Kondaiah, P.; Ludwig, R.L.; Sporn, M.B.; Baker, C.C.
Mol. Endocrinol. 1, 693-698, 1987
A:Title: Complementary deoxyribonucleic acid cloning of bovine transforming growth fa
A:Reference number: A40057; MUID:91042552
A:Accession: A40057
A:Molecule type: mRNA
A:Residues: 1-315 <VAN>
A:Cross-references: GB:M36271; NID:g163747; PIDN:AAA30778.1; PID:g163748
R:Ogawa, Y.; Schmidt, D.K.; Dasch, J.R.; Chang, R.J.; Glaser, C.B.
J. Biol. Chem. 267, 2325-2328, 1992
A:Title: Purification and characterization of transforming growth factor-beta2.3 and
A:Reference number: A42320; MUID:92129307
A:Accession: A42320
A:Molecule type: protein
A:Residues: 204-209,'X',211-217 <OGA>
R:Roberts, A.B.; Anzano, M.A.; Meyers, C.A.; Wideman, J.; Blacher, R.; Pan, Y.C.E.; S
Biochemistry 22, 5692-5698, 1983
A:Title: Purification and properties of a type beta transforming growth factor from b
A:Reference number: A05284; MUID:84104793
A:Accession: A05284
A:Molecule type: protein
A:Residues: 204-218 <ROB>
R:Seyedin, S.M.; Thompson, A.Y.; Bentz, H.; Rosen, D.M.; McPherson, J.M.; Conti, A.;
J. Biol. Chem. 261, 5693-5695, 1986
A:Title: Cartilage-inducing factor-A. Apparent identity to transforming growth factor
A:Reference number: A24322; MUID:86195954
A:Accession: A24322
A:Molecule type: protein
A:Residues: 204-233 <SEY>
R:Jin, Y.; Cox, D.A.; Knecht, R.; Raschdorf, F.; Cerletti, N.
J. Protein Chem. 10, 565-575, 1991
A:Title: Separation, purification, and sequence identification of TGF-beta1 and TGF-b
A:Reference number: A61439; MUID:92189724
A:Accession: B61439
A:Molecule type: protein
A:Residues: 204-209,'X',211-217,'XX',220-232 <JIN>
C:Comment: This polypeptide is composed of two polypeptide chains cross-linked by dis
C:Comment: Type II TGF does not bind to the EGF receptor and lacks intrinsic mitogeni
ion. Cells grown in monolayer do not respond in a similar manner to these growth fact
```

C;Keywords: glycoprotein; growth factor; homodimer; mitogen; transforming
F;1-18/Domain: signal sequence #status predicted <PRO>
F;19-278/Domain: propeptide #status predicted <PRO>
F;244-246/Region: cell attachment (R-C-D) motif
F;279-390/Product: transforming growth factor beta-1 #status experimental <MAT>
F;82,136,176/Binding site: carboxydrate (Asn) (covalent) #status predicted

Query Match 78.9%; Score 500; DB 1; Length 390;
Best Local Similarity 76.8%; Pred. No. 2.3e-43;
Matches 86; Conservative 11; Mismatches 15; Indels 0; Gaps 0;

Qy 1 ALDTNYCFRNLNENCCVRPLYYIDFRQDLGKWKWHEPKGYANFCSGPCPYLRSADTTHTST 60
| | | | | : | | | | | | | | | | | | | | | | | | | | | | : | | : |
Db 279 ALDTNYCFSSFTKKCCVRQLYYIDFRKDLGKWKWHEPKGYHANFCLGPCPYIWSLDTQYSK 338
| | | | | : | | | | | | | | | | | | | | | | | | | | | | : | | : |

Qy 61 VLGLYNTLNPEASAPCCVPQDLEPLTLTYVVGRTPKVEQLSNMIVRSCKCS 112
| | | | | : | | | | | | | | | | | | | | | | | | | | | | : | | | | |
Db 339 VLALYNHNPASAPCCVQALPEPLVYVYVGRPKVEQLSNMIVRSCKCS 390
| | | | | : | | | | | | | | | | | | | | | | | | | | | | : | | | | |

RESULT 17

JC4023
transforming growth factor beta-1 - dog
C;Species: Canis lupus familiaris (dog)
C;Date: 13-Jun-1995 #sequence_revision 14-Jul-1995 #text_change 24-Nov-1999
C;Accession: JC4023
R;Manning, A.M.; Auchampach, J.A.; Drong, R.F.; Slightom, J.L.
Gene 155, 307-308, 1995
A;Title: Cloning of a canine cDNA homologous to the human transforming growth factor-
A;Reference number: JC4023; MUID:95237630
A;Accession: JC4023
A;Molecule type: mRNA
A;Residues: 1-390 <MAN>
A;Cross-references: GB:L34956; NID:g516071; PIDN:AAA51458.1; PID:g516072
C;Comment: This factor plays a multifunctional role as a regulator of mammalian cell
C;Genetics:
A;Gene: tgf-beta1
C;Superfamily: inhibin
C;Keywords: growth factor; transforming protein
F;288-390/Product: transforming growth factor beta 1 #status predicted <MAT>

Query Match 78.9%; Score 500; DB 2; Length 390;
Best Local Similarity 76.8%; Pred. No. 2.3e-43;
Matches 86; Conservative 11; Mismatches 15; Indels 0; Gaps 0;

Qy 1 ALDTNYCFRNLNENCCVRPLYYIDFRQDLGKWKWHEPKGYANFCSGPCPYLRSADTTHTST 60
| | | | | : | | | | | | | | | | | | | | | | | | | | | | : | | : |
Db 279 ALDTNYCFSSFTKKCCVRQLYYIDFRKDLGKWKWHEPKGYHANFCLGPCPYIWSLDTQYSK 338
| | | | | : | | | | | | | | | | | | | | | | | | | | | | : | | : |

Qy 61 VLGLYNTLNPEASAPCCVPQDLEPLTLTYVVGRTPKVEQLSNMIVRSCKCS 112
| | | | | : | | | | | | | | | | | | | | | | | | | | | | : | | | | |
Db 339 VLALYNHNPASAPCCVQALPEPLVYVYVGRPKVEQLSNMIVRSCKCS 390
| | | | | : | | | | | | | | | | | | | | | | | | | | | | : | | | | |

RESULT 18

A26960
transforming growth factor beta-1 precursor - green monkey
C;Species: Cercopithecus aethiops (green monkey, grivet)
C;Date: 05-Oct-1988 #sequence_revision 05-Oct-1988 #text_change 24-Nov-1999
C;Accession: A26960
R;Sharpley, K.; Plogman, G.D.; Rose, T.M.; Twardzik, D.R.; Purchio, A.F.
DNA 6, 239-244, 1987
A;Title: Cloning and sequence analysis of simian transforming growth factor-beta cDNA
A;Reference number: A26960; MUID:87246074
A;Accession: A26960
A;Molecule type: mRNA
A;Residues: 1-390 <SHA>
A;Cross-references: GB:M16658; NID:g176552; PIDN:AAA35369.1; PID:g176553
C;Superfamily: inhibin
C;Keywords: growth factor
F;1-16/Domain: signal sequence #status predicted <SIG>

F:17-390/Product: transforming growth factor beta #status predicted <MAT>

```

Query Match      78.94; Score 500; DB 2; Length 390;
Best Local Similarity 76.89; Pred. No. 2.3e-43;
Matches 86; Conservative 11; Mismatches 15; Indels 0; Gaps 0;

QY      1  ALDINYCFRNLEENCCVRPLIIDFRQDLGKWKWHEPKGYANFCGSGPCPYLRSAATTHST 60
          ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
Db      279  ALDINYCFSTSEKNCVRLYIDFRKDLGKWKWIHEPKGYHANFCLGPCPYIWSLDTQYSK 338

QY      61  VLGLYNTLNPAASAPCCVPQDLEPLTLTYVYGRTPKVEQLSNVWVKSCKS 112
          ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
Db      339  VLALYNQHNPGASAPCCVQALEPLTYVYVGRKPKVEQLSNMIVTRSCKS 390

```

```

RESULT 19
A27512
transforming growth factor beta-1 precursor - pig
N:Alternate names: TGF-beta
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 05-Jun-1988 #sequence_revision 05-Jun-1988 #text_change 16-Jul-1999
C:Accession: A27512; A26356; I46657

```

Nucleic Acids Res. 15, 3187, 1987
A:Title: Sequence of the porcine transforming growth factor-beta precursor.
A:Reference number: A27512; MUID:87174844
A:Accession: A27512
A:Molecule type: mRNA
A:Residues: 1-390 <DER>
R:Cheifetz, S.; Weatherbee, J.A.; Tsang, M.L.S.; Anderson, J.K.; Mole, J.E.; Lucas, R.; Cell 48, 409-415, 1987
A:Title: The transforming growth factor-beta system, a complex pattern of cross-reactive
A:Reference number: A90890; MUID:87102890
A:Accession: A26356
A:Molecule type: protein
A:Residues: 279-322 <CH>
R:Kondaiah, P.; Van Obberghen-Schilling, E.; Ludwig, R.L.; Dhar, R.; Sporn, M.B.; Robert
J. Biol. Chem. 263, 18313-18317, 1988
A:Title: cDNA cloning of porcine transforming growth factor-beta 1 mRNAs. Evidence for a
A:Reference number: I46657; MUID:89054010
A:Accession: I46657

A;Accession: [119007](#)
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-390 <KON>
A;Cross-references: GB:M23703; NID:g755044; PID:g755045
C;Genetics:
A;Gene: TGF β -1
C;Superfamily: inhibin
C;Keywords: growth factor

```

Query Match      78.9%; Score 500; DB 2; Length 390;
Best Local Similarity 76.8%; pred. No. 2.3e-43;
Matches 86; Conservative 11; Mismatches 15; Indels 0; Gaps 0;

Qy 1 ALDNYNCFRNL EENCVRPL YIDFRQDLGKWVHEPKGYAFNFCGPGCPYLRSDATHTST 60
      ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
Db 279 ALDNYNCFST EKNCCVRQL YIDFRKDLGKWVHEPKGYAHNFCILGPGCPYIWSLDQYISK 338

Qy 61 VLGLYNTLNPRASAPCCVPDPLEPLTLYYVGRTPKVEQLSNMVKCKCKS 112
      ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
Db 339 VLALYNHNP GASAAPCCVPQALPEPLTYTYVXVGRPKPKVEQLSNMIVRCKCKS 390

```

RESULT 20
I46463
transforming growth factor beta-1 - sheep
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C:Date: 19-Dec-1997 #sequence_revision 19-Dec-1997 #text_change 24-Nov-1999
C:Accession: I46463; S45115
R:Woodall, C.J.; McLaren, L.J.; Watt, N.J.
Gene 150, 371-373. 1994

A>Title: Sequence and chromosomal localisation of the gene encoding ovine latent transformant 1
A:Reference number: I46463; MUID:95121932
A:Accession: I46463
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-390 <WOO>
A:Cross-references: EMBL:X76916; NID:g496648; PIDN:CAA54242.1; PID:g496649
A>Note: submitted to the EMBL Data Library, December 1993
C:Superfamily: inhibin

Query Match 78.9%; Score 500; DB 2; Length 390;
Best Local Similarity 76.8%; Pred. No. 2.3e-43;
Matches 86; Conservative 11; Mismatches 15; Indels 0; Gaps 0;

```
QY      1 ALDNYCFRNLEENCCVRPLYIDFRQDLGWKWHPEKGYANFCSGPCPYLRSADTHST 60
         ||||| : | |||| | ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
Db     279 ALDNYCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCIGPCPYIWSLDTOYSK 338
```

QY 61 VLGLYNTLNPEASAPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVKSCKS 112
|| || | ||| : |||| |||| | : |||| | |||| | : ||||
Dd 339 VLALYNQHNPGASAAPCCVPALEPLPIVYYVGRPKPKEQLSNIVRSCKS 390

RESULT 21
S01413
transforming growth factor beta-1 precursor - chicken
C:Species: Gallus gallus (chicken)
C:Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 24-Nov-1999
C:Accession: S01413
R:Jakowlew, S.B.; Dillard, P.J.; Sporn, M.B.; Roberts, A.B.
Nucleic Acids Res. 16, 8730, 1988
A:Title: Nucleotide sequence of chicken transforming growth factor-beta 1 (
A:Reference number: S01413; MUID:88335639

A; Residues: 1-391 (GAK)
 A; Cross-references: EMBL:X12373; NID:g63808; PIDN:CAA30933.1; PID:g63809
 C; Superfamily: Inhibin
 C; Keywords: growth factor

Query Match	78.9%;	Score 500;	DB 2;	Length 391;
Best Local Similarity	76.8%;	Pred. No. 2.3e-43;		
Matches	86;	Conservative 11;	Mismatches 15;	Indels 0;
				Gaps 0;

```

QY      1  ALDINYCFRNLSENCVVRPLYDFRQDLGWKWHVEPKGYVYANFCSGPCPYLRSADTTHST 60
        | | | | | : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      280 ALDINYCFSSPEKNCVVRPLYDFRQDLGWKWHVEPKGYVYANFCSGPCPYLRSADTTHST 339

```

Qy	61	VLGLYNTLNPEASASPCCVPQDLEPLTILYVVGRTPKVEQLSNMVVKSCKS	112
		: :	
D _b	340	VLALYNQHNPGASAPCCVPQALEPLPIVYVVGKPKVEQLSNIVRSCKKS	391

RESULT 22
I48196
transforming growth factor beta-1 precursor - golden hamster (fragment)
C.Species: Mesocricetus auratus (golden hamster)
C.Date: 02-Jul-1996 #sequence_revision 04-Oct-1996 #text_change 24-Nov-1999
C.Accession: I48196
C.Wong, D.T.: Donoff, R.B.: Yang, J.: Song, B.Z.: Matossian, K.: Nagura, N.: Elovic, A.
Am. J. Pathol. 143, 130-142, 1993
A.Title: Sequential expression of transforming growth factors alpha and beta 1 by esophageal squamous cell carcinoma
A.Reference number: I48196; MUID:93304479

A; Residues: 1-130 <RES>
A; Cross-references: EMBL:X60296; NID:g396177; PIDN:CAA42838.1; PID:g396178
C; Superfamily: inhibin

R:Sauermann, U.; Meyermann, R.; Schluesener, H.J.
J. Neurosci. Res. 33, 142-147, 1992
A:Title: Cloning of a novel TGF-beta related cytokine, the vgr, from rat brain: cloning
A:Reference number: S37618; MUID:93085758
A:Accession: S37618
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-207 <SAU>
A:Cross-references: EMBL:X58830; NID:g57475; PIDN:CAAA1634.1; PID:g57476
A:Note: the sequence from Fig. 4 is inconsistent with that from Fig. 1 in having 88-Ser
C:Superfamily: inhibin

Query Match 32.5%; Score 206; DB 2; Length 207;
Best Local Similarity 37.2%; Pred. No. 9.5e-14;
Matches 42; Conservative 22; Mismatches 43; Indels 6; Gaps 4;

Qy 4 TNYCFRNLENCVRLPYIDFRDLGK-WVHEPKGYANFCGPGPYLRSD---TTHS 59
Db 95 SDYNSSELKTACKKHELYVSF-QDLGWQDWIIAPGYAANYCDGECSPPLNAHNMATNHA 153
Qy 60 TVLGLYNTLNPEASPCVQDLEPLTILYVGRTPKV-EQLSNMVKSKC 111
Db 154 IVQTLVHLNPEYVPKCCAPTCLNAISLVLYDDNSNVILKKYRNMVVRACGC 206

RESULT 27
BMH06
bone morphogenetic protein 6 precursor - human
C:Species: Homo sapiens (man)
C:Date: 18-Oct-1991 #sequence_revision 03-Aug-1995 #text_change 18-Jun-1999
C:Accession: B39263
R:Celeste, A.J.; Iannuzzi, J.A.; Taylor, R.C.; Hewick, R.M.; Rosen, V.; Wang, E.A.; Wozniak, P.; et al. Proc. Natl. Acad. Sci. U.S.A. 87, 9843-9847, 1990
A:Title: Identification of transforming growth factor beta family members present in bone
A:Reference number: A39263; MUID:91088608
A:Accession: B39263
A:Molecule type: mRNA
A:Residues: 1-513 <CEL>
A:Cross-references: GB:M60315; GB:M38694; NID:g339561; PIDN:AAA36737.1; PID:g339562
C:Genetics:
A:Gene: GDB:BMP6
A:Cross-references: GDB:127596; OMIM:112266
A:Map position: 6pter-6qter
C:Superfamily: inhibin
C:Keywords: bone; glycoprotein
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-374/Domain: propeptide #status predicted <PRO>
F:375-513/Product: bone morphogenetic protein 6 #status predicted <MAT>
F:241,269,386,404,454/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 32.5%; Score 206; DB 1; Length 513;
Best Local Similarity 37.2%; Pred. No. 2.5e-13;
Matches 42; Conservative 22; Mismatches 43; Indels 6; Gaps 4;

Qy 4 TNYCFRNLENCVRLPYIDFRDLGK-WVHEPKGYANFCGPGPYLRSD---TTHS 59
Db 401 SDYNSSELKTACKKHELYVSF-QDLGWQDWIIAPGYAANYCDGECSPPLNAHNMATNHA 459

Qy 60 TVLGLYNTLNPEASPCVQDLEPLTILYVGRTPKV-EQLSNMVKSKC 111
Db 460 IVQTLVHLNPEYVPKCCAPTCLNAISLVLYDDNSNVILKKYRNMVVRACGC 512

RESULT 28
A54798
Vg-1-related protein precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 16-Jul-1999
C:Accession: A54798; A33925; S47442
R:Gitelman, S.E.; Koblin, M.S.; Ye, J.Q.; Lopez, A.R.; Lee, A.; Derynck, R.
J. Cell Biol. 126, 1595-1609, 1994

A:Title: Recombinant vgr-1/BMP-6-expressing tumors induce fibrosis and endochondral b
A:Reference number: A54798; MUID:94375533
A:Accession: A54798
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-510 <GIT>
A:Cross-references: EMBL:X80992; NID:g530729; PIDN:CAA56917.1; PID:g530730
R:Lyons, K.; Graycar, J.L.; Lee, A.; Hashmi, S.; Lindquist, P.B.; Chen, E.Y.; Hogan, Proc. Natl. Acad. Sci. U.S.A. 86, 4554-4558, 1989
A:Title: Vgr-1, a mammalian gene related to Xenopus Vg-1, is a member of the transfer
A:Reference number: A33925; MUID:89282810
A:Accession: A33925
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 'M', 74, 'K', 76-85, 'P', 87-510 <LYO>
A:Cross-references: GB:J04566; NID:g202352; PIDN:AAA40548.1; PID:g202353
C:Superfamily: inhibin

Query Match 32.3%; Score 205; DB 2; Length 510;
Best Local Similarity 37.2%; Pred. No. 3.1e-13;
Matches 42; Conservative 22; Mismatches 43; Indels 6; Gaps 4;

Qy 4 TNYCFRNLENCVRLPYIDFRDLGK-WVHEPKGYANFCGPGPYLRSD---TTHS 59
Db 398 SDYNSSELKTACKKHELYVSF-QDLGWQDWIIAPGYAANYCDGECSPPLNAHNMATNHA 456

Qy 60 TVLGLYNTLNPEASPCVQDLEPLTILYVGRTPKV-EQLSNMVKSKC 111
Db 457 IVQTLVHLNPEYVPKCCAPTCLNAISLVLYDDNSNVILKKYRNMVVRACGC 509

RESULT 29
I47072
inhibin beta-A chain precursor - sheep
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C:Date: 15-Oct-1996 #sequence_revision 15-Oct-1996 #text_change 16-Jul-1999
C:Accession: I47072; B60856
R:Fleming, J.S.; Galloway, S.M.; Crawford, R.J.; Tisdall, D.J.; Greenwood, P.J. Mol. Reprod. Dev. 40, 1-8, 1995
A:Title: Tissue-specific variation in the length of the 5' untranslated region of the
A:Reference number: I47072; MUID:95217464
A:Accession: I47072
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-425 <FL>
A:Cross-references: GB:LJ9218; NID:g310379; PIDN:AA041621.1; PID:g310380
R:Leversha, L.J.; Robertson, D.M.; de Vos, F.L.; Morgan, F.J.; Hearn, M.T.W.; Wettenh J. Endocrinol. 113, 213-221, 1987
A:Title: Isolation of inhibin from ovine follicular fluid.
A:Reference number: A60856; MUID:87224684
A:Accession: B60856
A:Molecule type: protein
A:Residues: 310-312, 'X', 314-319, 'XX', 322 <LEV>
C:Comment: Inhibin suppresses follicle-stimulating hormone secretion.
C:Superfamily: inhibin
C:Keywords: disulfide bond; glycoprotein; gonad; heterodimer; hormone

Query Match 32.2%; Score 204; DB 2; Length 425;
Best Local Similarity 38.3%; Pred. No. 3.3e-13;
Matches 41; Conservative 20; Mismatches 36; Indels 10; Gaps 5;

Qy 15 CCVRPLYIDFRDLGK-WVHEPKGYANFCGPGPC-----YLRADTTHSTVLGYNTL 68
Db 320 CCKKQFYVSFK-DIGWQDWIIAPSGYHANYCEGPCSHIAGTSGSLSFSHTVINHYMR 378

Qy 69 --NPEASASPCVQDLEPLTILYVGRTPKV-EQLSNMVKSKC 112
Db 379 GHSPPANLKKCCVPTKLRMSLYDDGQNIKKDQNIQNMIVCEGCS 425

RESULT 30

[illegible]

C:Accession: S30488; B23556; B24246; A30884; S33351; P00010
R:Tanimoto, K.; Handa, S.I.; Ueno, N.; Murakami, K.; Fukamizu, A.
DNA Seq. 2, 103-110, 1991
A:Title: Structure and sequence analysis of the human activin beta(A) subunit gene.
A:Reference number: S30488; MUID:92135888
A:Accession: S30488
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-426 <TAN>
A:Cross-references: EMBL:X57578; NID:928351; PIDN:CAA40805.1; PID:g825621
A:Note: the authors translated the codon GAG for residue 53 as Gly and GAG for residue 5
R:Stewart, A.G.; Milborrow, H.M.; Ring, J.M.; Crowther, C.E.; Forage, R.G.
FEBS Lett. 206, 329-334, 1986
A:Title: Human inhibin genes. Genomic characterisation and sequencing.
A:Reference number: A91366; MUID:87005283
A:Accession: B23556
A:Molecule type: DNA
A:Residues: 311-426 <STE>
A:Cross-references: GB:X04447; NID:g33928; PIDN:CAA28041.1; PID:g33929
R:Mason, A.J.; Niall, H.D.; Seeburg, P.H.
Biochem. Biophys. Res. Commun. 135, 957-964, 1986
A:Title: Structure of two human ovarian inhibins.
A:Reference number: A90123; MUID:86186863
A:Accession: B24248
A:Molecule type: mRNA
A:Residues: 1-426 <MAS>
A:Cross-references: GB:M13436; NID:gl86414; PIDN:AAA59168.1; PID:g307069
R:Murata, M.; Eto, Y.; Shibai, H.; Sakai, M.; Muramatsu, M.
Proc. Natl. Acad. Sci. U.S.A. 85, 2434-2438, 1988
A:Title: Erythroid differentiation factor is encoded by the same mRNA as that of the inh
A:Reference number: A30884; MUID:88190086
A:Accession: A30884
A:Molecule type: mRNA
A:Residues: 1-426 <MUR>
A:Cross-references: GB:J03634; NID:g181946; PIDN:AAA35787.1; PID:g181947
R:Berg, H.; Walter, M.; Northemann, W.
submitted to the EMBL Data Library, April 1993
A:Description: Nucleotide sequence coding for the mature subunit beta(A) of human inhibi
A:Reference number: S33351
A:Accession: S33351
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 311-376, 'AC', 380-426 <BER>
A:Cross-references: EMBL:X72498; NID:g297786; PIDN:CAA51163.1; PID:g755740
R:Fujimoto, K.; Kawakita, M.; Kato, K.; Yonemura, Y.; Masuda, T.; Matsuzaki, H.; Hirose,
Biochem. Biophys. Res. Commun. 174, 1163-1168, 1991
A:Title: Purification of megakaryocyte differentiation activity from a human fibrous his
A:Reference number: P00010; MUID:91144591
A:Accession: P00010
A:Molecule type: protein
A:Residues: 311-313, 'X', 315-320, 'XX', 323-328, 'X', 330-334 <FUJ>
A:Comment: Activins A and B are homodimers of inhibin beta-A or inhibin beta-B, respecti
bin beta-A and beta-B, respectively.
C:Genetics:
A:Gene: GDB:INHBA
A:Cross-references: GDB:119346; OMIM:147290
A:Map position: 7p15-7p13
A:Introns: 129/3
C:Superfamily: inhibin
C:Keywords: glycoprotein; gonad; heterodimer; homodimer; hormone
F:1-28/Domain: signal sequence #status predicted <SIG>
F:29-310/Domain: propeptide #status predicted <PRO>
F:311-426/Product: inhibin beta A chain #status experimental <MAT>
F:165/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 31.5%; Score 200; DB 1; Length 426;
Best Local Similarity 37.4%; Pred. No. 8.3e-13;
Matches 40; Conservative 21; Mismatches 36; Indels 10; Gaps 5;

Qy 15 CCVRPLXYIDFRODLGWK-WVHEPKGYANFCGPGCPYLR-----YLRSDATHTHSTVLGLYNTL 68
Db 321 CCKQOFFVSKF-DIGWNDWIITAPSGYHANYCGECPSHIAGTSGSLSLFSHSTVINHYRMR 379

QY 69 --NPEASAPCCVPQDLEPLTILYY-VGRTPKVEQLSNMVMVSKCKS 112
Db 380 GHSFPFANLSCCVPTKLRPMNMLYDDGQNIKKDIQNMIIVERCGCS 426
RESULT 34
JC4151
activin beta D chain precursor - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C:Date: 27-Aug-1995 #sequence_revision 19-Oct-1995 #text_change 21-Jul-2000
C:Accession: JC4151
R:Oda, S.; Nishimatsu, S.; Murakami, K.; Ueno, N.
Biochem. Biophys. Res. Commun. 210, 581-588, 1995
A:Title: Molecular cloning and functional analysis of a new activin beta subunit: a d
A:Reference number: JC4151; MUID:95275314
A:Accession: JC4151
A:Molecule type: mRNA
A:Residues: 1-367 <ODA>
A:Cross-references: DBJ:D49543; NID:g961512; PIDN:BAA08494.1; PID:g961513
A:Experimental source: embryo
C:Superfamily: inhibin
C:Keywords: glycoprotein; mesoderm
F:1-253/Domain: signal sequence #status predicted <SIG>
F:254-367/Product: activin beta D chain #status predicted <MAT>
F:64,155,161,208,230/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 31.2%; Score 197.5; DB 2; Length 367;
Best Local Similarity 36.0%; Pred. No. 1.3e-12;
Matches 41; Conservative 25; Mismatches 35; Indels 13; Gaps 6;

QY 10 NLEEN---CCVRPLXYIDFRODLGWK-WVHEPKGYANFCGPGCPYLR-----ADTHTST 60
Db 256 NCDQSNLCRCRDYVDFK-DIGWNDWIITKPEGYQINCYMGLCPMHIIAGAPGMAASFHTT 314
QY 61 VLGLYNTLNPEASAPCCVPQDLEPLTILYYVGRTPK--EQLSNMVMVSKCKS 112
Db 315 VLNLKANNIQTAVNSCCVPTKRRPLSMLYF-DRNNNVLTDTADIMIVEACGCS 367
RESULT 35
A43918
TGFB-beta-related protein 60A precursor - fruit fly (Drosophila melanogaster)
N:Alternate names: bone morphogenetic protein homolog precursor
C:Species: Drosophila melanogaster
C:Date: 10-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 17-Nov-2000
C:Accession: A43918; A41233
R:Doctor, J.S.; Jackson, P.D.; Rashka, K.E.; Visalli, M.; Hoffmann, F.M.
Dev. Biol. 151, 491-505, 1992
A:Title: Sequence, biochemical characterization, and developmental expression of a ne
A:Reference number: A43918; MUID:92290120
A:Accession: A43918
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-455 <DOC>
A:Cross-references: GB:M84795; NID:gl56729; PIDN:AAA28307.1; PID:gl56730
A:Note: sequence extracted from NCBI backbone (NCBI:106399, NCBIP:106400)
R:Wharton, K.A.; Thomsen, G.H.; Gelbart, W.M.
Proc. Natl. Acad. Sci. U.S.A. 88, 9214-9218, 1991
A:Title: Drosophila 60A gene, another transforming growth factor beta family member,
A:Reference number: A41233; MUID:92021021
A:Accession: A41233
A:Molecule type: mRNA
A:Residues: 1-455 <GWA>
A:Cross-references: GB:M77012; NID:gl56727; PIDN:AAA28306.1; PID:gl56728
C:Comment: This protein is a member of the transforming growth factor beta family.
C:Genetics:
A:Gene: 60A
A:Cross-references: FlyBase:FBgn0024234
C:Superfamily: inhibin
C:Keywords: homodimer

	Query Match	30.1%	Score 191;	DB 1;	Length 424;
	Best Local Similarity	36.4%;	Pred. No. 6.8e-12;		
	Matches 39;	Conservative 21;	Mismatches 37;	Indels 10;	Gaps 5;
Qy	15	CCVRLPYIDFRODLGWK-VWHEPKGYANFCSGPCP-----YLRADTHTSTVLGLYNPL	68		
		: : : : : : : : : :			
Db	319	CCKKQFFVSFK-DIGNWDWIAPSGVHANYCEGCPCSHIAGTSGSLFSSTVINHYRMR	377		
Qy	69	--NPASASPCCVPQDLEPLTLIYY-VGRTPKEQLSNMWVKSKCS	112		
		: :			
Db	378	GHSPEANLKSCCVPTKLRRWSMLIYYDDGNIIKKDIQNMIIVEEGCS	424		

RESULT 39
I51284
bone morphogenetic protein-7 - chicken (fragment)
C:Species: Gallus gallus (Chicken)
C:Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 16-Jul-1999
C:Accession: I51284
R:Houston, B.; Thorp, B.H.; Burt, D.W.
J. Mol. Endocrinol. 13, 289-301, 1994
A:Title: Molecular cloning and expression of bone morphogenetic protein-7 in the chick
A:Reference number: I51284; MUID:95200473
A:Accession: I51284
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-313 <HOU>
A:Cross-references: GB:S77477; NID:g957233; PIDN:AAB33846.1; PID:g957234
C:Superfamily: Inhibin

QY 10 NLEEN-----CCVRPLYIDRQDLGWK-WVHEPKGYANFCGCPYLRSA---DTT 57
Matches 40; Conservative 42; Mismatches 39; Indels 14; Gaps 3;
Db 199 NIAENSSDQACKKHEIYVSR-DIGWQDIIAPEGYARYICEGAFPLNNYNAFN 257

C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Jul-1999
C/Accession: JH0590
R:Nishimatsu, S.; Suzuki, A.; Shoda, A.; Murakami, K.; Ueno, N.
Biochem. Biophys. Res. Commun. 186, 1487-1495, 1992
A>Title: Genes for bone morphogenetic proteins are differentially transcribed in early a
A:Reference number: JH0687; MUID:92378616
A/Acession: JH0590
A/Molecule type: mRNA
A/Residues: 1-426 <NIS>
A/Cross-references: GB:X03267; NID:g64591; PIDN:CAA45021.1; PID:g64592
A:Experimental source: oocyte
C:Superfamily: inhibin
C/Keywords: glycoprotein
F:283-426/Product: Bone morphogenetic protein 7 #status predicted <MAT>
F:177,307,367/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 29.5%; Score 187; DB 2; Length 426;
Best Local Similarity 35.4%; Pred. No. 1.8e-11;
Matches 38; Conservative 23; Mismatches 41; Indels 6; Gaps 4;

QY 9 RNLENCVRLPYIDFRDGLGWK-WWHEPKGYANFCSGPCPYLRS--DTTHTSTVLGL 64
 |::| :|| ||||| ::|::| |::| |::| |::| |::| |:
Db 319 RLQAQAKKHFLVSFR-DLGWDWIITAPGAYRAYCDGECAFFLSFMATNTNAIVQT 377
 |::| |::| |::| |::| |::| |::| |::| |::| |::| |:

QY 65 YNTLNPEASPPCCVPDPDLPLTLILYYVGRTPKV-EQLSNMVVKSCKC 111
 :||| |::| |::| |::| |::| |::| |::| |:
Db 378 VHFINTPVRKPCCAPTQLNGISLVLYFDSDSANVLKKYKNMVMVQCACGC 425

RESULT 45
WFPGBB
Inhibin beta-B chain precursor - pig (fragment)
C/Species: Sus scrofa domestica (domestic pig)
C/Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 01-Dec-2000
C/Acession: A01394
R:Mason, A.J.; Hayflick, J.S.; Ling, N.; Esch, F.; Ueno, N.; Ying, S.Y.; Guillemin, R.;
Nature 318, 659-663, 1985
A>Title: Complementary DNA sequences of ovarian follicular fluid inhibin show precursor
A/Reference number: A93371; MUID:86092207
A/Acession: A01394
A/Molecule type: mRNA
A/Residues: 1-349 <NAS>
A/Cross-references: GB:X03267; NID:g2005; PIDN:CAG27021.1; PID:g2006
C/Comment: The source of this protein is ovarian follicular fluid.
C/Comment: The mature protein is the carboxyl-terminal segment of a precursor polypeptide
different forms of inhibin have been isolated (A and B) that differ in the amino-terminals
C/Comment: Inhibin is secreted by ovaries or testes and inhibits the secretion of follitropin
C/Superfamily: inhibin
C/Keywords: contraceptive; follitropin inhibitor; glycoprotein; gonadotropin; propeptide (fragment) #status predicted <PRO>
F:1-234/Domain: intracellular part of the mature protein
F:235-349/Product: inhibin beta-B chain #status predicted <MAT>
F:35/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 29.4%; Score 186.5; DB 1; Length 349;
Best Local Similarity 37.4%; Pred. No. 1.6e-11;
Matches 40; Conservative 21; Mismatches 35; Indels 11; Gaps 7;

QY 15 CCVRPLYIDPRDGLGWK-WWHEPKGYANFCSGPCPYLR-----SADTTHTSTVLGLYNT- 67
 |::| :|||| |::| |::| |::| |::| |::| |::| |:
Db 245 CCRQQFTDFRL-IIGSWDIITPTGGYGNYCEGSCPALAGVPGCSASSFHATAVVNQYRM 303

QY 68 -LAPEASASPCCVPDPDLPLTLILYYVGRTPKVEQ-LSNMVVKSKCKS 112
 |::| ::||: |::| |::| |::| |::| |::| |:
Db 304 GLNP-GTVNSCCIPTKLSTWSMLFYDDENINIKRVDPNMIVECGCA 349

RESULT 46
A0150
Inhibin beta-B chain precursor - human
N/Alternate names: activin AB chain B
C/Species: Homo sapiens (man)

A:Molecule type: mRNA
A:Residues: 1-461 <PON>
A:Cross-references: EMBL:Z48313; NID:g673496; PID:g673497
C:Superfamily: inhibin

Query Match 28.5%; Score 181; DB 2; Length 461;
Best Local Similarity 34.6%; Pred. No. 7.8e-11;
Matches 37; Conservative 22; Mismatches 42; Indels 6; Gaps 4;

Qy 10 NLEENCVRPLYIDFRQDLGW-KWHEPKGYANFCSGPCPYLRSAD---TTHSTVVLGLY 65
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 355 NSDWCKRKNLFVNF-EDLDWQEWIIQPIGYVAFYCGQBCAFLNGHANATNHAIVQTLV 413
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |

Qy 66 NTLNPEASAPCCVPQDLEPLTILYY-VGRTPKVEQLSNMVKSKCK 111
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 414 HMMSPSHVPQCCAPTKLSPITVLYDDSRNVVLKKYKNMVRAGGC 460
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |

RESULT 64
JC2466
inhibin beta-C chain precursor - human
N:Alternate names: activin beta C chain
C:Species: Homo sapiens (man)
C:Date: 29-Mar-1995 #sequence_revision 26-May-1995 #text_change 29-Oct-1999
C:Accession: JC2466
R:Hoetten, G.; Neidhardt, H.; Schneider, C.; Pohl, J.
Biochem. Biophys. Res. Commun. 206, 608-613, 1995
A:Title: Cloning of a new member of the TGF-beta family: A putative new activin betaC chain
A:Reference number: JC2466; MUID:95126961
A:Accession: JC2466
A:Molecule type: mRNA
A:Residues: 1-352 <HO>
A:Cross-references: GB:X82540; NID:g669154; PIDN:CAA57890.1; PID:g669155
A:Experimental source: liver
C:Genetics:
A:Gene: GDB: INHBC
A:Cross-references: GDB:632884
A:Map position: 2cen-2q13
C:Superfamily: inhibin
C:Keywords: glycoprotein
F:1-18/Domain: signal sequence #status predicted <SIG>
F:19-236/Domain: propeptide #status predicted <PRO>
F:237-352/Product: activin beta C #status predicted <MAT>
F:110,143,161/Binding site: carboxydrate (Asn) (covalent) #status predicted

Query Match 28.4%; Score 180; DB 2; Length 352;
Best Local Similarity 37.4%; Pred. No. 7.4e-11;
Matches 40; Conservative 19; Mismatches 38; Indels 10; Gaps 5;

Qy 15 CCVRPLYIDFRQDLGW-KWHEPKGYANFCSGPCPYLRS-----ADTTHSTVVLGLY--N 66
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 247 CCRQEFFVDFR-EIGWHDWIIQPEGYAMNFCGQCP-LHVAGMPGISASFTAVLNLKAN 305
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |

Qy 67 TLNPEASAPCCVPQDLEPLTILYYVGRTPKVE-QLSNMVKSKCKS 112
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 306 TAAGTTGGGSCCVPTARRPLSLLYYDRDSNIVKTDIPDMVVEACGCS 352
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |

RESULT 65
JC5366
activin beta C - mouse
C:Species: Mus musculus (house mouse)
C:Date: 28-May-1997 #sequence_revision 18-Jul-1997 #text_change 26-Aug-1999
C:Accession: JC5366
R:Fang, J.; Wang, S.; Smiley, E.; Bonadio, J.
Biochem. Biophys. Res. Commun. 231, 655-661, 1997
A:Title: Genes coding for mouse activin beta C and beta E are closely linked and exhibit
A:Reference number: JC5366; MUID:97224404
A:Accession: JC5366
A:Molecule type: DNA
A:Residues: 1-352 <FAN>

A:Cross-references: GB:U95962
C:Comment: Activin beta C and beta E form a distinct subset of related activins.
C:Genetics:
A:Introns: 105/3
C:Superfamily: inhibin

Query Match 28.4%; Score 180; DB 2; Length 352;
Best Local Similarity 37.8%; Pred. No. 7.4e-11;
Matches 42; Conservative 20; Mismatches 31; Indels 18; Gaps 7;

Qy 15 CCVRPLYIDFRQDLGW-KWHEPKGYANFCSGPCPYLRSAD-----TTHSTVVLGLYNT 67
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 247 CCRQEFFVDFR-EIGWHDWIIQPEGYAMNFCGQCP-LHVAGMPGISASFTAVL---NL 301
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |

Qy 68 LNPEASA-----SPCCVPQDLEPLTILYYVGRTPKVE-QLSNMVKSKCKS 112
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 302 LKANAAGTGTGSCCVPTSRRLSLLYYDRDSNIVKTDIPDMVVEACGCS 352
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |

RESULT 66
S70580
activin beta C precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 26-Aug-1999
C:Accession: S70580
R:Lau, A.L.; Nishimori, K.; Matzuk, M.M.
Biochim. Biophys. Acta 1307, 145-148, 1996
A:Title: Structural analysis of the mouse activin beta-C gene.
A:Reference number: S70580; MUID:96283807
A:Accession: S70580
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-352 <LAU>
A:Cross-references: EMBL:U40772
C:Genetics:
A:Introns: 106/1
C:Superfamily: inhibin

Query Match 28.4%; Score 180; DB 2; Length 352;
Best Local Similarity 37.8%; Pred. No. 7.4e-11;
Matches 42; Conservative 20; Mismatches 31; Indels 18; Gaps 7;

Qy 15 CCVRPLYIDFRQDLGW-KWHEPKGYANFCSGPCPYLRSAD-----TTHSTVVLGLYNT 67
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 247 CCRQEFFVDFR-EIGWHDWIIQPEGYAMNFCGQCP-LHVAGMPGISASFTAVL---NL 301
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |

Qy 68 LNPEASA-----SPCCVPQDLEPLTILYYVGRTPKVE-QLSNMVKSKCKS 112
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 302 LKANAAGTGTGSCCVPTSRRLSLLYYDRDSNIVKTDIPDMVVEACGCS 352
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |

RESULT 67
S43295
bone morphogenetic protein homolog GDF6 precursor - mouse (fragment)
N:Alternate names: growth and differentiation factor 6
C:Species: Mus musculus (house mouse)
C:Date: 20-Oct-1994 #sequence_revision 07-Feb-1997 #text_change 26-May-2000
C:Accession: S43295
R:Storm, E.E.; Huynh, T.V.; Copeland, N.G.; Jenkins, N.A.; Kingsley, D.M.; Lee, S.J.
Nature 368, 639-643, 1994
A:Title: Limb alterations in brachypodism mice due to mutations in a new member of the
A:Reference number: S43294; MUID:94195427
A:Accession: S43295
A:Molecule type: DNA
A:Residues: 1-125 <STO>
A:Cross-references: EMBL:U08338; NID:g488463; PIDN:AAAL8779.1; PID:g488464
C:Genetics:
A:Gene: Gdf6
C:Superfamily: inhibin
F:1-5/Domain: polypeptide protease recognition site #status predicted <PPR>
F:6-125/Product: bone morphogenetic protein homolog GDF6 (fragment) #status predicted

Db 394 GSTPPSCCVPTKLTIPISILYIDAGNNVYVVEEYEMVVEGCGC 435

RESULT 72

C39364

GDF-1 embryonic growth factor - human

C:Species: Homo sapiens (man)

C:Date: 06-Mar-1992 #sequence_revision 06-Mar-1992 #text_change 24-Nov-1999

C:Accession: C39364

R:Lee, S.J.

Proc. Natl. Acad. Sci. U.S.A. 88, 4250-4254, 1991

A:Title: Expression of growth/differentiation factor 1 in the nervous system: conservation

A:Reference number: A39364; MUID:91239545

A:Accession: C39364

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-372 <LEE>

A:Cross-references: GB:M62302; NID:g183050; PID:g183052

C:Superfamily: inhibin

Query Match 27.4%; Score 174; DB 2; Length 372;

Best Local Similarity 35.8%; Pred. No. 3.2e-10;

Matches 38; Conservative 17; Mismatches 41; Indels 10; Gaps 5;

QY 15 CCVRPLYIDFRQDLGW-KWVHEPKGYANFCGPGC-PYLRSAD-----TTHSTVGLGYN 66

Db 267 CRARLYYSFR-EVGHWRVIAVPRGFLANYCQGCALPVALS GSGGPPALNAVLRLMH 325

QY 67 TLNPEASASPCVPCVODLEPLTILYVGRTPKV-EQLSNMVKSKC 111

Db 326 AAFGAADLPCCVPARTSPISVLFFDSDNVVLROYEDMVDCEGC 371

RESULT 73

A26158

decapentaplegic protein precursor - fruit fly (Drosophila melanogaster)

C:Species: Drosophila melanogaster

C:Date: 24-Jun-1987 #sequence_revision 24-Jun-1987 #text_change 16-Apr-1999

C:Accession: A26158

R:Padgett, R.W.; St. Johnston, R.D.; Gelbart, W.M.

Nature 325, 81-84, 1987

A:Title: A transcript from a Drosophila pattern gene predicts a protein homologous to th

A:Reference number: A26158; MUID:87090408

A:Accession: A26158

A:Molecule type: mRNA

A:Residues: 1-588 <PAD>

A:Cross-references: GB:M30116; NID:g157291; PID:g157292

C:Genetics:

A:Gene: FlyBase:dpp

A:Cross-references: FlyBase:FBgn0000490

C:Keywords: glycoprotein

F:1-15/Domain: signal sequence #status predicted <SIG>

F:120,342,377,529/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 27.1%; Score 172; DB 2; Length 588;

Best Local Similarity 35.8%; Pred. No. 8.3e-10;

Matches 39; Conservative 16; Mismatches 46; Indels 8; Gaps 5;

QY 9 RNLENCVVRPLYIDFRQDLGW-KWVHEPKGYANFCGPGCPYLRSAD---TTHSTVILG 63

Db 481 KNHDDTCRRHSILYDF-SDVGWDDWIVAPLGDAYCYCHGKCFP-PLADHFNSTNNAVVT 538

QY 64 LNTLNPASASPCVPCVODLEPLTILYVGR-TPKVEQLSNMVKSKC 111

Db 539 LVNNNPGKVGKACVPTQLDSVAMLYLNDQSTVVLKNYQEMTVVGGCG 587

RESULT 74

A36192

inhibin beta-A chain - African clawed frog (fragment)

C:Species: Xenopus laevis (African clawed frog)

C:Date: 11-Jan-1991 #sequence_revision 11-Jan-1991 #text_change 15-Jun-1996

C:Accession: A36192

R:Thomsen, G.; Woolf, T.; Whitman, M.; Sokol, S.; Vaughan, J.; Vale, W.; Melton, D.A.

Cell 63, 485-493, 1990

A:Title: Activins are expressed early in Xenopus embryogenesis and can induce axial m

A:Reference number: A36192; MUID:91029481

A:Accession: A36192

A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual

A:Molecule type: DNA

A:Residues: 1-102 <THO>

C:Superfamily: inhibin

Query Match 27.1%; Score 171.5; DB 2; Length 102;

Best Local Similarity 40.7%; Pred. No. 1.4e-10;

Matches 35; Conservative 12; Mismatches 28; Indels 11; Gaps 5;

QY 15 CCVRPLYIDFRQDLGW-KWVHEPKGYANFCGPGCPYLRSADTT-----HSTVGLGYN 67

Db 5 CCKKHVYSFK-DIGWSDWIIAPPYHANYCEGDCP-SHIAGTTGSSLSFSHTVINQYRL 62

QY 68 --LNPEASASPCVPCVODLEPLTILY 91

Db 63 RQSPPTSISKCCVPSKLRAMSLY 88

RESULT 75

I50607

bone morphogenetic protein 2 - chicken (fragment)

C:Species: Gallus gallus (chicken)

C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 16-Jul-1999

C:Accession: I50607

R:Francis, P.H.; Richardson, M.K.; Brickell, P.M.; Tickle, C.

Development 120, 209-218, 1994

A:Title: Bone morphogenetic proteins and a signalling pathway that controls patternin

A:Reference number: I50607; MUID:94163974

A:Accession: I50607

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-353 <FRA>

A:Cross-references: EMBL:X75914; NID:g472927; PID:CAA53513.1; PID:g472928

C:Genetics:

A:Gene: Bmp-2

C:Superfamily: inhibin

Query Match 27.1%; Score 171.5; DB 2; Length 353;

Best Local Similarity 38.5%; Pred. No. 5.4e-10;

Matches 42; Conservative 18; Mismatches 30; Indels 19; Gaps 8;

QY 14 NCCVRPLYIDFRQDLGW-KWVHEPKGYANFCGPGCPY-----LRSADTTHSTVGLGYN 67

Db 252 SKRHPLYYDF-NDVGWDDWIVAPPGYSFYCHGECFPPLADHLNS--TNHAIVQTLVNS 308

QY 68 LN---PEASASPCVPCVODLEPLTILYVGRTPKV--EQLSNMVKSKC 111

Db 309 VNSKPKA-----CCVPTLSAISML-YLDENEKVLKYNQDMVVEGCGC 352

RESULT 76

C42320

transforming growth factor beta-3 - bovine (fragment)

C:Species: Bos primigenius taurus (cattle)

C:Date: 03-Mar-1994 #sequence_revision 03-Mar-1994 #text_change 17-Mar-1999

C:Accession: C42320

R:Ogawa, Y.; Schmidt, D.K.; Dasch, J.R.; Chang, R.J.; Glaser, C.B.

J. Biol. Chem. 267, 2325-2328, 1992

A:Title: Purification and characterization of transforming growth factor-beta.2.3 and

A:Reference number: A42320; MUID:92129307

A:Accession: C42320

A:Molecule type: protein

A:Residues: 1-34 <OGA>

C:Superfamily: inhibin

RESULT 81
I49541
bone morphogenetic protein 4 - mouse
C:Species: Mus musculus (house mouse)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 16-Jul-1999
C:Accession: I49541; S29523; B34201
R:Feng, J.Q.; Chen, D.; Cooney, A.J.; Tsai, M.; Harris, M.A.; Tsai, S.Y.; Feng, M.; Mund
J. Biol. Chem. 270, 28364-28373, 1995
A:Title: The mouse bone morphogenetic protein-4(BMP4) gene: Analysis of promoter utiliza
A:Reference number: I49541; MUID:96081880
A:Accession: I49541
A>Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-420 <RES>
A:Cross-references: GB:I47480; NID:g994733; PIDN:AC37698.1; PID:g994734
R:Dickinson, M.E.; van der Meer-de Jong, R.; Hogan, B.L.M.
submitted to the EMBL Data Library, December 1990
A:Description: Nucleotide sequence of the mouse Bone Morphogenetic Protein-4 (BMP-4) cDN
A:Reference number: S29523
A:Accession: S29523
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 13-420 <DIC>
A:Cross-references: EMBL:X56848; NID:g50180; PIDN:CAA40179.1; PID:g50181
R:Dickinson, M.E.; Kobrin, M.S.; Silan, C.M.; Kingsley, D.M.; Justice, M.J.; Miller, D.A
Peland, N.G.; Jenkins, N.A.
Genomics 6, 505-520, 1990
A:Title: Chromosomal localization of seven members of the murine TGF-beta superfamily su
A:Reference number: A34201; MUID:90228966
A:Accession: B34201
A>Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A:Molecule type: mRNA
A:Residues: 253-420 <DI2>
C:Genetics:
A:Gene: BMP-4
A:Introns: 11/1; 137/1
C:Superfamily: inhibin

Query Match 26.9%; Score 170.5; DB 2; Length 420;
Best Local Similarity 37.7%; Pred. No. 8.2e-10;
Matches 43; Conservative 17; Mismatches 35; Indels 19; Gaps 8;

QY 9 RNLENCVRLYIDFRODLGK-WVHEPKGYANFCGCPY-----LRSADTTHSTVL 62
Db 314 RKNKNCRRHSLYVDF-SDVGNWDWIVAPPGYQAFYCHGDCFPFLADHLNS--TNHAIQV 370

QY 63 GLYNTLN---PEASAPCCVPQDLEPLTILYVGRTPKV--EQLSNMVVKSKC 111
Db 371 TLVNSVSSIPKA----CCVPTLSAISML-YLDEYDKVLKNTQEMVVEGCGC 419

RESULT 82
B36192
inhibin beta-B1 chain - African clawed frog (fragment)
C:Species: Xenopus laevis (African clawed frog)
C>Date: 11-Jan-1991 #sequence_revision 11-Jan-1991 #text_change 15-Jun-1996
C:Accession: B36192
R:Thomsen, G.; Woolf, T.; Whitman, M.; Sokol, S.; Vaughan, J.; Vale, W.; Melton, D.A.
Cell 63, 485-493, 1990
A:Title: Activins are expressed early in Xenopus embryogenesis and can induce axial meso
A:Reference number: A36192; MUID:91029481
A:Accession: B36192
A>Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A:Molecule type: DNA
A:Residues: 1-101 <THO>
C:Superfamily: inhibin

Query Match 26.8%; Score 170; DB 2; Length 101;
Best Local Similarity 41.2%; Pred. No. 2e-10;
Matches 35; Conservative 14; Mismatches 26; Indels 10; Gaps 6;

QY 15 CCVRPLYIDFRODLGK-WVHEPKGYANFCGCPY-YLR-----SADTTHSTVLGLYNT- 67
Db 5 CCRQFYIDFRL-IGNDWIIAPAGYIGNYCEGSCPAYLAGVPGSASSFHTAVVNOYRMR 63

QY 68 -LNPEASAPCCVPQDLEPLTILY 91
Db 64 GLNP-GTVNSCCIPTKLSTMSMLYF 87

RESULT 83
C36192
inhibin beta-B2 chain - African clawed frog (fragment)
C:Species: Xenopus laevis (African clawed frog)
C>Date: 11-Jan-1991 #sequence_revision 11-Jan-1991 #text_change 15-Jun-1996
C:Accession: C36192
R:Thomsen, G.; Woolf, T.; Whitman, M.; Sokol, S.; Vaughan, J.; Vale, W.; Melton, D.A.
Cell 63, 485-493, 1990
A:Title: Activins are expressed early in Xenopus embryogenesis and can induce axial m
A:Reference number: A36192; MUID:91029481
A:Accession: C36192
A>Status: preliminary; nucleic acid sequence not shown; not compared with conceptual
A:Molecule type: DNA
A:Residues: 1-101 <THO>
C:Superfamily: inhibin

Query Match 26.7%; Score 169; DB 2; Length 101;
Best Local Similarity 40.0%; Pred. No. 2.6e-10;
Matches 34; Conservative 15; Mismatches 26; Indels 10; Gaps 6;

QY 15 CCVRPLYIDFRODLGK-WVHEPKGYANFCGCPY-YLR-----SADTTHSTVLGLYNT- 67
Db 5 CCRQFYIDFRL-IGNDWIIAPAGYIGNYCEGSCPAYLAGVPGSASSFHTAVVNOYRMR 63

QY 68 -LNPEASAPCCVPQDLEPLTILY 91
Db 64 GLNP-GTVNSCCIPTKLSTMSMLYF 87

RESULT 84
A45056
osteogenic protein 2 precursor - human
N:Alternate names: bone morphogenetic protein 8; OP-2
C:Species: Homo sapiens (man)
C>Date: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 16-Jul-1999
C:Accession: A45056
R:Ozekaynak, E.; Schneegelsberg, P.N.; Jin, D.F.; Clifford, G.M.; Warren, F.D.; Drier,
J. Biol. Chem. 267, 25220-25227, 1992
A:Title: Osteogenic protein-2. A new member of the transforming growth factor-beta su
A:Reference number: A45056; MUID:93094231
A:Accession: A45056
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-402 <OZK>
A:Cross-references: NID:g189389; PIDN:AAB01360.1; PID:g189390
A:Experimental source: hippocampus
A>Note: sequence extracted from NCBI backbone (NCBIP:120189)
C:Genetics:
A:Gene: GDB:BMP8; OP-2
A:Cross-references: GDB:I36392
C:Superfamily: inhibin

Query Match 26.5%; Score 168; DB 2; Length 402;
Best Local Similarity 38.2%; Pred. No. 1.4e-09;
Matches 39; Conservative 13; Mismatches 44; Indels 6; Gaps 5;

QY 15 CCVRPLYIDFRODLGK-WVHEPKGYANFCGCPY-YLR-----DPTHTSTVLGLYNTLP 70
Db 301 CRRHLYVSF-ODLGLDWIAPQGYIAYCEGSCFPDSCMNATNHALQSLVHLMPK 359

QY 71 EASAPCCVPQDLEPLTILYVGRTPKV--EQLSNMVVKSKC 111
Db 71 EASAPCCVPQDLEPLTILYVGRTPKV--EQLSNMVVKSKC 111

Db 360 NAVPKACCAPTKLSATSVLYDSSNNVILRKHRRMMVVKACGC 401

RESULT 85

A49147

bone morphogenetic protein 4 - African clawed frog

N:Alternate names: BMP-4; ventralizing factor

C:Species: Xenopus laevis (African clawed frog)

C:Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 16-Jul-1999

C:Accession: A49147

R:Dale, L.; Howes, G.; Price, B.M.; Smith, J.C.

Development 115, 573-585, 1992

A:Title: Bone morphogenetic protein 4: a ventralizing factor in early xenopus development

A:Reference number: A49147; MUID:93048819

A:Accession: A49147

A>Status: preliminary

A:Molecule type: nucleic acid

A:Residues: 1-400 <DAL>

A:Cross-references: GB:X64538; GB:S46999; NID:g64589; PIDN:CAA45836.1; PID:g64590

A:Experimental source: XTC cells

A:Note: sequence extracted from NCBI backbone (NCBIN:117127, NCBIP:117128)

C:Superfamily: inhibin

Query Match 26.1%; Score 165.5; DB 2; Length 400;

Best Local Similarity 36.8%; Pred. No. 2.5e-09;

Matches 42; Conservative 18; Mismatches 35; Indels 19; Gaps 8;

QY 9 RNLENCVVRPLYIDFRQDLGKW-WVHEPKGYANFCSGPCPY-----LRSDTTHTSTVL 62

Db 294 RKNKHCRRHSLSYVDF-SDVGWNDWIVAPPGYQAFYCHGDCPPPLADHLNS--TNHAIQV 350

QY 63 GLYNTLN---PEASAPCCVPQDLPTILYVYVGRPKV--EQLSNMVKSKC 111

Db 351 TLVNSVNSIPKA---CCVPTLSAISML-YLDEYDKVLKKNYQEMVVEGCG 399

RESULT 86

JH0689

bone morphogenetic protein 4 precursor - African clawed frog

C:Species: Xenopus laevis (African clawed frog)

C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Jul-1999

C:Accession: JH0689

R:Nishimatsu, S.; Suzuki, A.; Shoda, A.; Murakami, K.; Ueno, N.

Biochem. Biophys. Res. Commun. 186, 1487-1495, 1992

A:Title: Genes for bone morphogenetic proteins are differentially transcribed in early a

A:Reference number: JH0687; MUID:92378616

A:Accession: JH0689

A:Molecule type: mRNA

A:Residues: 1-401 <NIS>

A:Cross-references: GB:X63426; NID:g64587; PIDN:CAA45020.1; PID:g64588

A:Experimental source: oocyte

C:Superfamily: inhibin

C:Keywords: glycoprotein

F:288-401/Product: bone morphogenetic protein 4 #status predicted <MAT>

F:141,204,238,343,358/Binding site: carboxydrate (Asn) (covalent) #status predicted

Query Match 26.1%; Score 165.5; DB 2; Length 401;

Best Local Similarity 36.8%; Pred. No. 2.5e-09;

Matches 42; Conservative 18; Mismatches 35; Indels 19; Gaps 8;

QY 9 RNLENCVVRPLYIDFRQDLGKW-WVHEPKGYANFCSGPCPY-----LRSDTTHTSTVL 62

Db 295 RKNKHCRRHSLSYVDF-SDVGWNDWIVAPPGYQAFYCHGDCPPPLADHLNS--TNHAIQV 351

QY 63 GLYNTLN---PEASAPCCVPQDLPTILYVYVGRPKV--EQLSNMVKSKC 111

Db 352 TLVNSVNSIPKA---CCVPTLSAISML-YLDEYDKVLKKNYQEMVVEGCG 400

RESULT 87

A39364

GDF-1 embryonic growth factor - mouse

C:Species: Mus musculus (house mouse)

C:Date: 06-Mar-1992 #sequence_revision 06-Mar-1992 #text_change 24-Nov-1999

C:Accession: A39364; A35683

R:Lee, S.J.

Proc. Natl. Acad. Sci. U.S.A. 88, 4250-4254, 1991

A:Title: Expression of growth/differentiation factor 1 in the nervous system: conserv

A:Reference number: A39364; MUID:91239545

A:Accession: A39364

A:Molecule type: mRNA

A:Residues: 1-357 <LEE>

A:Cross-references: GB:M62301; NID:g193458; PIDN:AAA37676.1; PID:g193460

R:Lee, S.J.

Mol. Endocrinol. 4, 1034-1040, 1990

A:Title: Identification of a novel member (GDF-1) of the transforming growth factor-b

A:Reference number: A35683; MUID:91133438

A:Accession: A35683

A:Molecule type: mRNA

A:Residues: 1-144, C, 146-357 <LE2>

A:Cross-references: GB:M57639; NID:g193456; PIDN:AAA37674.1; PID:g193457

C:Superfamily: inhibin

Query Match 25.9%; Score 164.5; DB 2; Length 357;

Best Local Similarity 35.5%; Pred. No. 2.8e-09;

Matches 38; Conservative 17; Mismatches 41; Indels 11; Gaps 6;

QY 15 CCVPLXYIDFRQDLGKW-WVHEPKGYANFCSGPCPY---LRSD---TTHTSTVLGLYN 66

Db 251 CRTRLRHVSFR-EVGHWRWVIAPRGFLANFCOGTCALPTLRGPGPPALNHAVALRALMH 309

QY 67 TLNPEASA-SPPCCVPQDLPTILYVYVGRPKV-EQLSNMVKSKC 111

Db 310 AAATPGAGSCCPPERLSPISLVFFDSDNVVLRHYEDMVVDECG 356

RESULT 88

JH0801

bone morphogenetic protein 4 - mouse

C:Species: Mus musculus (house mouse)

C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 21-Jul-2000

C:Accession: JH0801

R:Kurihara, T.; Kitamura, K.; Takaoka, K.; Nakazato, H.

Biochem. Biophys. Res. Commun. 192, 1049-1056, 1993

A:Title: Murine bone morphogenetic protein-4 gene: existence of multiple promoters an

A:Reference number: JH0801; MUID:93282803

A:Accession: JH0801

A:Molecule type: DNA

A:Residues: 1-408 <KUR>

A:Cross-references: GB:D14814; NID:g286069; PIDN:BAA03555.1; PID:g303650

C:Genetics: 125/1

A:Introns: 125/1

C:Superfamily: inhibin

C:Keywords: bone

Query Match 25.8%; Score 163.5; DB 2; Length 408;

Best Local Similarity 37.5%; Pred. No. 4.1e-09;

Matches 42; Conservative 17; Mismatches 34; Indels 19; Gaps 8;

QY 9 RNLENCVVRPLYIDFRQDLGKW-WVHEPKGYANFCSGPCPY---LRSDTTHTSTVL 62

Db 302 RKNKHCRRHSLSYVDF-SDVGWNDWIVAPPGYQAFYCHGDCPPPLADHLNS--TNHAIQV 358

QY 63 GLYNTLN---PEASAPCCVPQDLPTILYVYVGRPKV--EQLSNMVKSKC 109

Db 359 TLVNSVNSIPKA---CCVPTLSAISML-YLDEYDKVLKKNYQEMVVEGC 405

RESULT 89

A46607

growth/differentiation factor GDF-3 precursor - mouse

C:Species: Mus musculus (house mouse)

C; Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 24-Nov-1999
C; Accession: A46607
R; McPherron, A.C.; Lee, S.J.
J. Biol. Chem. 268, 3444-3449, 1993
A; Title: GDF-3 and GDF-9: two new members of the transforming growth factor
A; Reference number: A46607; MUID:93155193
A; Accession: A46607
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-366 <MCP>
A; Cross-references: GB:L064443; NID:g293346; PIDN:AAA53034.1; PID:g567205
C; Superfamily: inhibin

```

Query Match      25.6%; Score 162.5; DB 2; Length 366;
Best Local Similarity 35.1%; Pred. No. 4.6e-09;
Matches 40; Conservative 21; Mismatches 34; Indels 19; Gaps 7;

QY 5 NYCERNLEENCVRPLYIDFRQDLGW-KWVHEPKGYANFCSGGCP-----YLRSDATTH 58
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 264 NFCRH-----QLFINF-QDLGHWKIWAPKGFMANYGCHGCPFSMTTYLNSSN--Y 312

QY 59 STVLGLYNTLNPEASAPCCVPQDLEPLTILY-VGRTPKVEQLSNMVKSKC 111
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 313 AFMOALMHMAADPKVPKA-VCCVPTKLSPTSMILYQDSKNVILRHVEDMVDRCGC 365

```

RESULT 90
A45402 transforming growth factor beta homolog Vgr-2 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 24-Nov-1999
C:Accession: A45402
R:Jones, C.M.; Simon-Chazottes, D.; Guenet, J.L.; Hogan, B.L.
Mol. Endocrinol. 6, 1961-1968, 1992
A:Title: Isolation of Vgr-2, a novel member of the transforming growth factor-beta-related family
A:Reference number: A45402; MUID:93125570
A:Accession: A45402
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-366 <JON>
A:Cross-references: GB:S52658; NID:g263309; PIDN:AAB24876.1; PID:g263310
A:Experimental source: embryo
A:Note: sequence extracted from NCBI backbone (NCBIP:122197)
C:Superfamily: inhibin

[illegible]

RESULT 91
PW0042
activin - fruit fly (*Drosophila* sp.) (fragment)
C:Species: *Drosophila* sp.
C:Date: 18-Jun-1998 #sequence_revision 10-Jul-1998 #text_change 17-Nov-2000
C:Accession: PW0042
R:Kutty, G.; Kutty, R.K.; Samuel, W.; Duncan, T.; Jaworski, C.; Wiggert, B.
Biochem. Biophys. Res. Commun. 246, 644-649, 1998
A:Title: Identification of a new member of transforming growth factor-beta superfamily
A:Reference number: PW0042; MUID:98289585
A:Accession: PW0042
A:Molecule type: mRNA
A:Residues: 1-373 <KUT>

A;Cross-references: GB:AF054822
C;Genetics:
A;Cross-references: FlyBase:FBg
A;Start codon: GGT
A;Introns: 86/3
C;Superfamily: inhibin

```
Query Match      25.1%; Score 159; DB 2; Length 373;  
Best Local Similarity   31.8%; Pred. No. 1.le-08;  
Matches    35; Conservative 14; Mismatches 55; Indels     6; Gaps       4;
```

Qy		7 CERNLENCVRLPYIDFRDQLGW-KWHEPKGYIANFCSGPCP-YLRSD---TTHSTV 61 : : : : : Db CGGALNGOCCSEFYVSFKA-LGMDDWIAPRGYFANYCRGDCTGSFTPDTFQTFAHF 322
Qy		52 LGLNTLNPEASADSCCVQDLEPTILYYVGRTPKVQLSNMVKSKC 111 : : : : Db IEEYKMGIMNMRCPCAPIRFSMSLIYYDGDIKKRDLPKWVVDEGC 372

RESULT 92

BMHU3

bone morphogenetic protein 3 precursor - human

N:Alternate names: osteogenin

C:Species: Homo sapiens (man)

C:Date: 16-Sep-1992 #sequence_revision 03-Aug-1992

C:Accession: D37278

R:Wozney, J.M.; Rosen, V.; Celeste, A.J.; Mittleman, B.; Lawley, R.J.; Wharton, R.; Kessler, J.L.; Melnick, M.L.; Lian, J.B. Science 242, 1528-1534, 1988

A:Title: Novel regulators of bone formation: molecular cloning and characterization of complementary DNAs for osteogenin and osteonectin. PMID:89072730

A:Reference number: A37278; MUID:89072730

A:Accession: D37278

A:Molecule type: mRNA

A:Residues: 1-472 <W04>

A:Cross-references: GB:M22491; NID:g179505; P179505

C:Genetics:

A:Gene: GDB:BMP3

A:Cross-references: GDB:125206; OMIM:112263

A:Map position: 4p14-q421

C:Superfamily: inhibin

C:Keywords: bone; glycoprotein

F:1-22/domain; signal sequence #status predicted

F:23-345/domain; propeptide #status predicted

F:346-472/Product; bone morphogenetic protein

F:117,141,175,220,463/Binding site; carbohydrate binding site

```

Query Match      25.0%; Score 158.5; DB 1; Length 472;
Best Local Similarity 34.3%; pred. No. 1.5e-08;
Matches 37; Conservative 21; Mismatches 35; Indels 15; Gaps 7;

Qy 14 NCCVRLPYIDFRQDLGW-KWVHEPKGYVANCSGPC--PYLRSL-ADTTHSTVLGLYNTLN 69
   || || || || || || || || || || || || || || || || || || || || || ||
Db 369 NCARRYLAVDF-ADIGWSEWIIISPKSPDAYYCSGACQCFMPKSLKPSNHATIQISVRAVG 427
   || || || || || || || || || || || || || || || || || || || || || ||

Qy 70 -----PEASAPCCVPQDLEPLTILY-VGRTPKVEQLSNMVMVSKCK 111
   || || || || || || || || || || || || || || || || || || || || || ||
Db 428 VYPGTPY-----PCCVPKMSLSILIFFEENKNVLLKVPYNMTVESCA 471
   || || || || || || || || || || || || || || || || || || || || || ||

```

RESULT 93
I53032
bone morphogenetic protein 3 - rat (fragment)
C:Species: Rattus sp. (rat)
C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 16-Jul-1999
C:Accession: I53032
R:Chen, D.; Feng, J.Q.; Feng, M.; Harris, M.A.; Mahy, P.; Mundy, G.R.; Harris, S.E.
DNA Cell Biol. 14, 235-239, 1995
A:Title: Sequence and expression of bone morphogenetic protein 3 mRNA in prolonged cu
A:Reference number: I53032; MUID:95186061
A:Accession: I53032
A:Status: preliminary; translated from GB/EMBL/DBJ

```

A:Molecule type: mRNA
A:Residues: 1-360 <RES>
A:Cross-references: GB:S77492; NID:g957225; PIDN:AAB33725.1; PID:g957226
C:Superfamily: inhibin

Query Match          24.78; Score 156.5; DB 2; Length 360;
Best Local Similarity 34.3%; Pred. No. 1.9e-08;
Matches 37; Conservative 20; Mismatches 36; Indels 15; Gaps 7;

Qy 14 NCVVRLPYIDFRDQLGW-KWVHEPKGYANFCSGPC--PYLRS-ADTTHSTVLGLYNTLN 69
      || | || | :||| |: || | :||| | | | :||| : | :
Db 257 NCARYLKVDPF-ADIGSEWIISPKSFDAYCYSGACQFMPKSLKPSNHAIQSIVRAVG 315
      || | || | :||| |: || | :||| | | | :||| : | :

Qy 70 -----PEASAPCCVPQDLEPLTIILY-VGRTPKVEQLSNMVVKSCKC 111
      || ||||| : |:||| : : : || || ||
Db 316 VVSIGPE----PCCVPEKMSSLSILFFDENKNVYLKVYPNNMTVDSCAC 359
      || ||||| : |:||| : : : || || ||

RESULT 94
T25451
transforming growth factor beta homolog - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 17-Mar-2000
C:Accession: T25451
R:Bentley, D.
submitted to the EMBL Data Library, December 1996
A:Description: The sequence of C. elegans, cosmid B0412.
A:Reference number: Z20037
A:Accession: T25451
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-350 <BEN>
A:Cross-references: EMBL:U80953; PIDN:AAB52554.1; GSPDB:GNO0021
A:Experimental source: strain Bristol N2; clone B0412,
C:Genetics:
A:Gene: daf-7
A:Map position: 3
A:Introns: 43/3; 123/3; 184/2; 288/3
C:Superfamily: inhibin

Query Match          23.6%; Score 149.5; DB 2; Length 350;
Best Local Similarity 31.8%; Pred. No. 9.3e-08;
Matches 34; Conservative 19; Mismatches 43; Indels 11; Gaps 6;

Qy 13 ENCCVRPLYIDFRDLGNKWVHEPKGYANFCSGPCPY---LRSADTTHSTVL-GLYNT 67
      ||||| :||| :||| | | | | | | | | | | | | | :
Db 248 KGCCLYLEIEF-EKIGMDWTAVPAINAYMCRGDCHYNHAFNLAEATGGHKIMRAAHKV 306
      ||||| :||| :||| | | | | | | | | | | | | | :

Qy 68 LNPEASAPCCVPQDLEPLTIILYVGRTPKVE--QLSNMVVKSCKCS 112
      |||| | | | : : : | | | | | | | | | | | | |
Db 307 SNPEIGY--CCHPEYDIKLI-IYNRDGRVSIANVNGMIAKKGCS 350
      |||| | | | : : : | | | | | | | | | | | | |

RESULT 95
T03907
TCGF-beta-related protein homolog F39G3.8 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 17-Mar-2000
C:Accession: T03907
R:Du, Z.; Le, T.T.; Holmes, A.
submitted to the EMBL Data Library, July 1997
A:Description: The sequence of C. elegans cosmid F39G3.
A:Reference number: Z15131
A:Accession: T03907
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-366 <DUZ>
A:Cross-references: EMBL:AF016424; NID:g2291203; PIDN:AAB55333.1; PID:g2291211
C:Genetics:
A:Map position: V
A:Introns: 38/2; 86/2; 110/1; 161/2; 205/1; 229/2; 259/1

```

A;Note: F39G3.8
C;Superfamily: inhibin

Query Match 23.3%; Score 148; DB 2; Length 366;
Best Local Similarity 32.7%; Pred.No. 1.4e-07;
Matches 35; Conservative 21; Mismatches 45; Indels 6; Gaps 5;

QY 10 NLEENCCVRPLIDFRDQLGWK-WVHEPKGYANFCSGPC--PYLRSAD-TTHSTVLGLY 65
| | : |||| |||| || |||| || |||| | : : |||| |
Db 260 NENERCQRKLGVDF-DILGWKWVIAPGSFAYCYSCDSACPSFKEMNATSHAIVQSFL 318
| | : |||| |||| || |||| || |||| | : : |||| |

QY 66 NTNLNPASAPCCVPQDLPLETLIYY-VGRTPKVQEQLSNMVVKCKC 111
: | :: | | | | || | : : :::: |||| |

Db 319 HVRVNSTTAKCAPSSLSYGKITLFVDQNKKOVQIKRYRDMVVDEGC 365
| : : |||| |||| || |||| || |||| | : : |||| |

RESULT 96
A40735
TGF beta homolog dsl-1 - chicken
C;Species: Gallus gallus (chicken)
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jul-2000
C;Accession: A40735
R;Basler, K.; Edlund, T.; Jessell, T.M.; Yamada, T.
Cell 73, 687-702, 1993
A;Title: Control of cell pattern in the neural tube: regulation of cell differentiation
A;Reference number: A40735; PMID:93272310
A;Accession: A40735
A>Status: preliminary
A:Molecule type: nucleic acid
A;Residues: 1-427 <BAS>
A;Cross-references: GB:LJ2032; NID:g304379; PIDN:AAA48752.1; PID:g304380
A;Experimental source: spinal cord
A;Note: sequence extracted from NCBI backbone (NCBIN:l32680, NCPIP:l32681)
C;Superfamily: inhibin

Query Match 22.1%; Score 140; DB 2; Length 427;
Best Local Similarity 31.8%; Pred. No. 1.1e-06;
Matches 35; Conservative 21; Mismatches 46; Indels 8; Gaps 5;

QY 9 RNLENCCVR-PLYIDFDROLDW-KWVEHPKGYYANFCGPCPPLYLRSDTT---HSTVLG 63
| : | |||| :|||| : |||| | |||| | |||| | : | : | : | : | : | : |
Db 318 RSIAGHCRRITSLHNFK-EIGWDSWIIIAKPXEAFECGGCFPPLTDNVTPTKHAI VQT 376
| : ||| : : |||| | : |||| | : |||| | : |||| | : |||| |

QY 64 LYNTLNPEASAPCCVPQDLPLETLIYY--VGRTPKVQEQLSNMVVKCKC 111
| : ||: : : |||| | : |||| | : |||| | : |||| | : |||| |

Db 377 LVHLONPRKASKACCPTKDAISLIYDKDGAVPTLLINYEGMKVAECCG 426
| : ||: : : |||| | : |||| | : |||| | : |||| | : |||| |

RESULT 97
JC5697
Placental transforming growth factor-beta homolog - human
C;Species: Homo sapiens (man)
C;Date: 20-Nov-1997 #sequence_revision 20-Nov-1997 #text_change 17-Mar-1999
C;Accession: JC5697
R; Yokoyama-Kobayashi, M.; Saeki, M.; Sekine, S.; Kato, S.
J. Biochem. 122, 622-626, 1997
A;Title: Human cDNA encoding a novel TGF-beta superfamily protein highly expressed in
A;Reference number: JC5697; PMID:98006316
A;Accession: JC5697
A:Molecule type: mRNA
A;Residues: 1-309 <YOK>
A;Cross-references: DDBJ:AB000584
A;Experimental source: fibrosarcoma
C;Comment: This protein plays a role in reproduction.

Query Match 21.4%; Score 135.5; DB 2; Length 309;
Best Local Similarity 27.6%; Pred.No. 2.2e-06;
Matches 24; Conservative 15; Mismatches 47; Indels 1; Gaps 1;

QY 26 QDLGW-KWVEHPKYANFCSGPCPPLYLRSDTTHTSHTVLGTYNTLNPEASAPCCVPQDLLE 84

[illegible]

Db 222 EDLGNADWLSPREVQVTMCIGACSFQFPAANNHQAIKTSLHRLKPDTPAPACVCPVPSYN 281
Qy 85 PLTILYYVGRTPKVEQLSNMVKSCKC 111
Db 282 PMVLQKTDGTGSLQTYDDLLAKDCHC 308
RESULT 98
JC4646
bone morphogenetic protein-3b precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 10-May-1996 #sequence_revision 19-Jul-1996 #text_change 01-Dec-2000
C:Accession: JC4646
R:Takao, M.; Hino, J.; Takeshita, N.; Konno, Y.; Nishizawa, T.; Matsuo, H.; Kangawa, K.
Biochem. Biophys. Res. Commun. 219, 656-662, 1996
A:Title: Identification of rat bone morphogenetic protein-3b (BMP-3b), a new member of E
A:Reference number: JC4646; MUID:96193707
A:Accession: JC4646
A:Molecule type: mRNA
A:Residues: 1-476 <TAK>
A:Cross-references: DDBJ:D49494; NID:g699625; PIDN:BAA08454.1; PID:g699626
A:Experimental source: femur
C:Comment: This protein plays a role in the central nervous system as well as in new bon
acellular matrix.
C:Superfamily: inhibin
C:Keywords: bone; glycoprotein
F:1-29/Domain: signal sequence #status predicted <SIG>
F:30-366/Domain: propeptide #status predicted <PRO>
F:367-476/Product: bone morphogenetic protein-3b #status predicted <MAT>
F:114,152,277,467/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match 21.4%; Score 135.5; DB 2; Length 476;
Best Local Similarity 30.3%; Pred. No. 3.4e-06;
Matches 33; Conservative 22; Mismatches 35; Indels 19; Gaps 7;
Qy 15 CCVRPLYIDFRODLGW-KWVHEPKGYANFCSGPCPY-----LRSADTTHSTVLGLYNL 68
Db 374 CSRRYLKVDV-ADIGWNEWIISPKSFDAYCAGACEFPMKIVRPSN--HATIQSIVRAV 430
Qy 69 N-----PEASAPCCVPQDLEPLTILYY-VGRTPKVEQLSNMVKSCKC 111
Db 431 GIVPGIPE----PCCVPKMNSLGLVFLDENRNVLKVPNNMSVETC 475
RESULT 99
S29718
gene nodal protein - mouse
C:Species: Mus musculus (house mouse)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jul-2000
C:Accession: S29718
R:Zhou, X.; Sasaki, H.; Lowe, L.; Hogan, B.L.M.; Kuehn, M.R.
Nature 361, 543-547, 1993
A:Title: Nodal is a novel TGF-beta-like gene expressed in the mouse node during gastrula
A:Reference number: S29718; MUID:93156841
A:Accession: S29718
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-354 <ZHO>
A:Cross-references: EMBL:X70514; NID:g2632074; PIDN:CAA49914.1; PID:g296605
C:Superfamily: inhibin
Query Match 21.1%; Score 133.5; DB 2; Length 354;
Best Local Similarity 31.9%; Pred. No. 4e-06;
Matches 30; Conservative 13; Mismatches 46; Indels 5; Gaps 3;
Qy 22 IDFRODLGW-KWVHEPKGYANFCSGPCPYLRSAD---TTHSTVLGLYNLNPASASPC 77
Db 261 VDFNL-IGWGSWIIYPKQYNAYRCEGCPNPVGEFFHPTNHAYIQSLKRYQPHRVPSTC 319
Qy 78 CVPQDLEPLTILYYVGRTPKVEQLSNMVKSCKC 111

Db 320 CAPVKTKPLUSMLYVDNGRVLLEHHKDMIVEECG 353
RESULT 100
JC4838
bone morphogenetic protein-3b precursor [similarity] - human
N:Alternate names: BMP-3b; GDF-10
C:Species: Homo sapiens (man)
C:Date: 15-Aug-1996 #sequence_revision 15-Oct-1996 #text_change 01-Dec-2000
C:Accession: JC4838
R:Hino, J.; Takao, M.; Takeshita, N.; Konno, Y.; Nishizawa, T.; Matsuo, H.; Kangawa, K.
Biochem. Biophys. Res. Commun. 223, 304-310, 1996
A:Title: cDNA cloning and genomic structure of human bone morphogenetic protein-3b (B
A:Reference number: JC4838; MUID:96264636
A:Contents: femur
A:Accession: JC4838
A:Molecule type: mRNA
A:Residues: 1-478 <HIN>
A:Cross-references: DDBJ:D49492; NID:g699603; PIDN:BAA08452.1; PID:g699604
C:Comment: This protein induces endochondral bone formation, chemotaxis of monocytes,
C:Genetics:
A:Gene: bmp-3b
C:Superfamily: inhibin
C:Keywords: bone
F:1-33/Domain: signal sequence #status predicted <SIG>
F:34-368/Domain: propeptide #status predicted <PRO>
F:369-478/Product: bone morphogenetic protein-3b #status predicted <MAT>
Query Match 21.1%; Score 133.5; DB 2; Length 478;
Best Local Similarity 30.3%; Pred. No. 5.5e-06;
Matches 33; Conservative 21; Mismatches 36; Indels 19; Gaps 7;
Qy 15 CCVRPLYIDFRODLGW-KWVHEPKGYANFCSGPCPY-----LRSADTTHSTVLGLYNL 68
Db 376 CSRRYLKVDV-ADIGWNEWIISPKSFDAYCAGACEFPMKIVRPSN--HATIQSIVRAV 432
Qy 69 N-----PEASAPCCVPQDLEPLTILYY-VGRTPKVEQLSNMVKSCKC 111
Db 433 GIIPGIPE----PCCVPDKMNSLGLVFLDENRNVLKVPNNMSVDTCAC 477
Search completed: October 30, 2001, 08:52:56
Job time: 180 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 30, 2001, 08:52:36 ; Search time 10.16 Seconds
(without alignments)
380.991 Million cell updates/sec

Title: TGFb3p
Perfect score: 634
Sequence: 1 ALDNTYCFRNLENCVRPL.....RTPKVEQLSNMVKSCSKSX 113

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	633	99.8	410	1	TGF3_MOUSE
2	633	99.8	412	1	TGF3_HUMAN
3	630	99.4	412	1	TGF3_RAT
4	629	99.2	412	1	TGF3_CHICK
5	621	97.9	409	1	TGF3_PIG
6	539	85.0	412	1	TGF2_CHICK
7	535	84.4	412	1	TGF2_BOVIN
8	535	84.4	414	1	TGF2_HUMAN
9	535	84.4	435	1	TGF2_PIG
10	530	83.6	414	1	TGF2_MOUSE
11	516	81.4	413	1	TGF2_XENLA
12	503	79.3	390	1	TGF1_MOUSE
13	503	79.3	390	1	TGF1_RAT
14	500	78.9	315	1	TGF1_BOVIN
15	500	78.9	390	1	TGF1_CANFA
16	500	78.9	390	1	TGF1_CERAE
17	500	78.9	390	1	TGF1_HUMAN
18	500	78.9	390	1	TGF1_SHEEP
19	500	78.9	390	1	TGF1_PIG
20	499	78.7	390	1	TGF1_HORSE
21	488	77.0	390	1	TGF1_CAVPO
22	461	72.7	373	1	TGF1_CHICK
23	439	69.2	382	1	TGF1_XENLA
24	217	34.2	374	1	GDF8_BRARE
25	208.5	32.9	375	1	GDF8_PAPHA
26	208	32.8	350	1	IHBE_MOUSE
27	208	32.8	350	1	IHBE_RAT
28	207.5	32.7	375	1	GDF8_SHEEP
29	206	32.5	207	1	BMP6_RAT
30	206	32.5	426	1	IHBA_HORSE
31	206	32.5	513	1	IHBA_HUMAN
32	205	32.3	510	1	BMP6_MOUSE
33	204.5	32.3	375	1	GDF8_CHICK

34	204.5	32.3	375	1	GDF8_HUMAN
35	204.5	32.3	375	1	GDF8_MELGA
36	204.5	32.3	375	1	GDF8_PIG
37	204.5	32.3	376	1	GDF8_MOUSE
38	204.5	32.3	376	1	GDF8_RAT
39	204	32.2	355	1	DVRI_BRARE
40	204	32.2	405	1	IHBA_SHEEP
41	203	32.0	425	1	GDFB_MOUSE
42	203	32.0	407	1	GDFB_HUMAN
43	201.5	31.8	375	1	GDF8_BOVIN
44	200	31.5	424	1	IHBA_MOUSE
45	200	31.5	424	1	IHBA_PIG
46	200	31.5	424	1	IHBA_RAT
47	200	31.5	425	1	IHBA_BOVIN
48	200	31.5	426	1	IHBA_HUMAN
49	195.5	30.8	436	1	60A_DROVI
50	195	30.8	455	1	60A_DROME
51	191.5	30.2	391	1	IHBB_CHICK
52	191	30.1	424	1	IHBA_CHICK
53	190	30.0	360	1	DVRI_XENLA
54	189	29.8	431	1	BMP7_HUMAN
55	187	29.5	426	1	BMP7_XENLA
56	186.5	29.4	349	1	IHBB_PIG
57	186.5	29.4	407	1	IHBB_HUMAN
58	186.5	29.4	408	1	IHBB_BOVIN
59	184.5	29.1	255	1	IHBB_MOUSE
60	184.5	29.1	345	1	GDFB_RAT
61	183	28.9	430	1	BMP7_MOUSE
62	182.5	28.8	393	1	BMP2_RAT
63	182.5	28.8	394	1	BMP2_MOUSE
64	182.5	28.8	395	1	BMP2_RABIT
65	182.5	28.8	396	1	BMP2_DAMDA
66	182.5	28.8	396	1	BMP2_HUMAN
67	182.5	28.8	398	1	BMPA_XENLA
68	182.5	28.8	398	1	BMPB_XENLA
69	182	28.7	495	1	GDF5_MOUSE
70	182	28.7	501	1	GDF5_HUMAN
71	181	28.5	461	1	DVRI_STRPU
72	180	28.4	352	1	IHBC_HUMAN
73	180	28.4	352	1	IHBC_MOUSE
74	180	28.4	621	1	DECA_DROPS
75	179	28.2	125	1	GDF6_MOUSE
76	179	28.2	452	1	BMP5_MOUSE
77	179	28.2	454	1	BMP5_HUMAN
78	176	27.8	151	1	GDF7_MOUSE
79	175	27.6	436	1	GDF6_BOVIN
80	174.5	27.5	424	1	BM10_HUMAN
81	174	27.4	372	1	DECA_TRICA
82	174	27.4	372	1	GDF1_HUMAN
83	172	27.1	588	1	DECA_DROME
84	172	27.1	593	1	DECA_DROSI
85	171.5	27.1	353	1	BMP2_CHICK
86	171	27.0	399	1	BM8B_MOUSE
87	170.5	26.9	405	1	BMP4_CHICK
88	170.5	26.9	408	1	BMP4_DAMDA
89	170.5	26.9	408	1	BMP4_HUMAN
90	170.5	26.9	408	1	BMP4_MOUSE
91	170.5	26.9	408	1	BMP4_RAT
92	169.5	26.7	409	1	BMP4_RABIT
93	169	26.7	383	1	UNIV_STRPU
94	168.5	26.6	420	1	BM10_MOUSE
95	168	26.5	399	1	BM8A_MOUSE
96	168	26.5	402	1	BMP8_HUMAN
97	165.5	26.1	401	1	BMP4_XENLA
98	164.5	25.9	357	1	GDF1_MOUSE
99	162.5	25.6	366	1	GDF3_MOUSE
100	160	25.2	364	1	GDF3_HUMAN

ALIGNMENTS

299 ALDINYCERNLEENCVRPLIYDFRQDLGWKWHIEPKGYIANFCSGPCPYLRSDATTHST 350

61 VGLGYNTLNPEASAPCCVPQDLPLTILYVYVGRTPKVEQLSNMVKSCKS 112
 |||||||

359 VGLGYNTLNPEASAPCCVPQDLPLTILYVYVGRTPKVEQLSNMVKSCKS 410

RESULT 2

TF3_HUMAN	STANDARD;	PRT;	412 AA.
ID	AC	P10600;	
DT	01-JUL-1989	(Rel. 11, Created)	
DT	01-JUL-1989	(Rel. 11, Last sequence update)	
DE	15-JUL-1999	(Rel. 38, Last annotation update)	
DE	TRANSFORMING GROWTH FACTOR BETA 3 PRECURSOR (TGF-BETA 3).		
GN	TGFβ3.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxId=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=88263019;	PubMed=3164476;	
RA	ten Dijke P., Hansen P., Iwata K., Pieler C., Foulkes J.G.;		
RT	"Identification of another member of the transforming growth factor		
RL	type beta gene family."		
RL	Proc. Natl. Acad. Sci. U.S.A. 85:4715-4719(1988).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Placenta;		
RX	MEDLINE=89091120;	PubMed=3208746;	
RA	Derynck R., Lindquist P.B., Lee A., Wen D., Tamm J., Graycar J.L.,		
RA	Rhee L., Mason A.J., Miller D.A., Coffey R.J., Moses H.L., Chen E.Y.;		
RT	"A new type of transforming growth factor-beta, TGF-beta 3."		
RL	EMBO J. 7:3737-3743(1988).		
RN	[3]		
RP	X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 301-412.		
RX	MEDLINE=96416253;	PubMed=8819159;	
RA	Mittl P.R., Priestle J.P., Cox D.A., McMaster G., Cerletti N.,		
RA	Grueter M.G.;		
RT	"The crystal structure of TGF-beta 3 and comparison to TGF-beta 2:		
RT	Implications for receptor binding."		
RL	Protein Sci. 5:1261-1271(1996).		
CC	-1- SUBUNIT: HOMODIMER, DISULFIDE-LINKED.		
CC	-1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.		
CC	-----		
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration		
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CC	or send an email to license@isb-sib.ch).		
CC	-----		
DR	EMBL;	J03241; AAA61161.1;	-.
DR	EMBL;	X14149; CAA32362.1;	-.
DR	EMBL;	X14885; CAA33024.1;	ALT INIT.
DR	EMBL;	X14886; CAA33024.1;	JOINED.
DR	EMBL;	X14887; CAA33024.1;	JOINED.
DR	EMBL;	X14888; CAA33024.1;	JOINED.
DR	EMBL;	X14889; CAA33024.1;	JOINED.
DR	EMBL;	X14890; CAA33024.1;	JOINED.
DR	EMBL;	X14891; CAA33024.1;	JOINED.
DR	PIR;	S01824;	
DR	PIR;	A36169;	A36169.
DR	PDB;	1TGG;	11-JAN-97.
DR	PDB;	1TGG;	12-MAR-97.
DR	MM;	190230;	-.
DR	InterPro;	IPR001111;	-.
DR	InterPro;	IPR001839;	-.
DR	InterPro;	IPR002400;	-.
DR	Pfam;	PF00019;	TGF-beta; 1.
DR	Pfam;	PF00688;	TGFβ_propeptide; 1.

RT Identification and characterization of the chicken transforming

RL growth factor-beta 3 promoter.";
 CC Mol. Endocrinol. 6:1285-1298(1992).
 CC -1- SUBUNIT: HOMODIMER, DISULFIDE-LINKED.
 CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
 CC
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 CC
 CC -----
 CC EMBL; M31154; AAA49089.1; -;
 CC EMBL; X58127; CAA41128.1; -;
 CC EMBL; X60055; CAA42653.1; -;
 CC EMBL; S46000; AAB23575.1; -;
 CC PIR; A34939; A34939.
 CC HSSP; P10600; ITGK.
 CC InterPro; IPR001111; -;
 CC InterPro; IPR001839; -;
 CC InterPro; IPR002400; -;
 CC Pfam; PF00019; TGF-beta; 1.
 CC Pfam; PF00688; TGF-beta-propeptide; 1.
 CC PRINTS; PR00438; GFCYSKNOT.
 CC PROSITE; PS00250; TGF_BETA_1; 1.
 CC Growth factor; Mitogen; Glycoprotein; Signal.
 CC KW
 CC SIGNAL 1 23
 CC PROPEP 24 300
 CC CHAIN 301 412 TRANSFORMING GROWTH FACTOR BETA 3.
 CC FT DISULFID 307 316 BY SIMILARITY.
 CC FT DISULFID 315 378 BY SIMILARITY.
 CC FT DISULFID 344 409 BY SIMILARITY.
 CC FT DISULFID 348 411 BY SIMILARITY.
 CC FT DISULFID 377 377 INTERCHAIN (BY SIMILARITY).
 CC FT CARBOHYD 74 74 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 135 135 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 142 142 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT SITE 261 263 CELL ATTACHMENT SITE (POTENTIAL).
 CC SEQUENCE 412 AA; 47184 MW; E15266B79D3F30F7 CRC64;

Query Match 99.2%; Score 629; DB 1; Length 412;
 Best Local Similarity 99.1%; Pred. No. 4.2e-60;
 Matches 111; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALDNTYCFRNLENCVVRPLYIDFRQDLGKWKVWHEPKGYANFCGPGCPYLRSDTTHST 60
 |||||

Db 301 ALDNTYCFRNLENCVVRPLYIDFRQDLGKWKVWHEPKGYANFCGPGCPYLRSDTTHST 360
 |||||

Qy 61 VLGLYNTLNPEASAPCCVPQDLEPLTILYVGRTPKVEQLSNMVKSKCS 112
 |||||

Db 361 VLGLYNTLNPEASAPCCVPQDLEPLTILYVGRTPKVEQLSNMVKSKCS 412
 |||||

RESULT 5

TGF3_PIG 5
 ID TGF3_PIG STANDARD; PRT; 409 AA.

AC P15203;
 DT 01-APR-1990 (Rel. 14, Created)

DT 01-APR-1990 (Rel. 14, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE TRANSFORMING GROWTH FACTOR BETA 3 PRECURSOR (TGF-BETA 3).
 TGF3.

GN Sus scrofa (Pig).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

OX NCBI_TaxID=9823;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Ovary;

RX MEDLINE=89091120; PubMed=3208746;

RA Derynck R., Lindquist B., Lee A., Wen D., Tamm J., Graycar J.L.,

RA Rhee L., Mason A.J., Miller D.A., Coffey R.J., Moses H.L.,

RA Chen E.Y.;
 RT "A new type of transforming growth factor-beta, TGF-beta 3.";

RL EMBO J. 7:3737-3743(1988).

CC -1- SUBUNIT: HOMODIMER, DISULFIDE-LINKED.

CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.

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 CC
 CC -----
 CC EMBL; X14150; CAA32363.1; -;
 CC PIR; S01825; S01825.
 CC HSSP; P10600; ITGK.
 CC InterPro; IPR001111; -;
 CC InterPro; IPR001839; -;
 CC InterPro; IPR002400; -;
 CC Pfam; PF00019; TGF-beta; 1.
 CC Pfam; PF00688; TGF-beta-propeptide; 1.
 CC PRINTS; PR00438; GFCYSKNOT.
 CC PROSITE; PS00250; TGF_BETA_1; 1.
 CC Growth factor; Mitogen; Glycoprotein; Signal.
 CC KW
 CC SIGNAL 1 18
 CC PROPEP 19 297
 CC CHAIN 298 409 TRANSFORMING GROWTH FACTOR BETA 3.
 CC FT DISULFID 304 313 BY SIMILARITY.
 CC FT DISULFID 312 375 BY SIMILARITY.
 CC FT DISULFID 341 406 BY SIMILARITY.
 CC FT DISULFID 345 408 BY SIMILARITY.
 CC FT DISULFID 374 374 INTERCHAIN (BY SIMILARITY).
 CC FT CARBOHYD 72 72 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 133 133 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 140 140 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT SITE 259 261 CELL ATTACHMENT SITE (POTENTIAL).
 CC SEQUENCE 409 AA; 46814 MW; B4900235B5CC955E CRC64;

Query Match 97.9%; Score 621; DB 1; Length 409;
 Best Local Similarity 98.2%; Pred. No. 3e-59;
 Matches 110; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ALDNTYCFRNLENCVVRPLYIDFRQDLGKWKVWHEPKGYANFCGPGCPYLRSDTTHST 60
 |||||

Db 298 ALDNTYCFRNLENCVVRPLYIDFRQDLGKWKVWHEPKGYANFCGPGCPYLRSDTTHSS 357
 |||||

Qy 61 VLGLYNTLNPEASAPCCVPQDLEPLTILYVGRTPKVEQLSNMVKSKCS 112
 |||||

Db 358 VLGLYNTLNPEASAPCCVPQDLEPLTILYVGRTPKVEQLSNMVKSKCS 409
 |||||

RESULT 6

TGF2_CHICK 6
 ID TGF2_CHICK STANDARD; PRT; 412 AA.

AC P30371;
 DT 01-APR-1993 (Rel. 25, Created)

DT 01-APR-1993 (Rel. 25, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE TRANSFORMING GROWTH FACTOR BETA 2 PRECURSOR (TGF-BETA 2).
 TGF2.

GN Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

OC Gallus.

OX NCBI_TaxID=9031;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-WHITE LEGHORN; TISSUE=Blood;

RX MEDLINE=92075163; PubMed=1683775;

RA Burt D.W., Paton I.R.;
RT "Molecular cloning and primary structure of the chicken transforming
RT growth factor-beta 2 gene";
RL DNA Cell Biol. 10:723-734(1991).
CC -!- FUNCTION: TGF-BETA 2 HAS SUPPRESSIVE EFFECTS ON INTERLEUKIN-2
CC DEPENDENT T-CELL GROWTH.
CC -!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED.
CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
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CC
CC -----
DR EMBL: X58071; CAA41101.1;
DR EMBL: X59082; CAA41101.1; JOINED.
DR EMBL: X59081; CAA41101.1; JOINED.
DR EMBL: X59080; CAA41101.1; JOINED.
DR PIR: A39489; A39489.
DR HSP: P08112; 1TFG.
DR InterPro: IPR001111;
DR InterPro: IPR001839;
DR Pfam: PF00019; TGF-beta; 1.
DR Pfam: PF00688; TGF-beta; 1.
DR PRINTS: PR00438; GFCYSKNOT.
DR PROSITE: PS00250; TGF-BETA_1; 1.
KW Growth factor; Mitogen; Glycoprotein; Signal.
FT SIGNAL 1 20
FT PROPEP 21 300
FT CHAIN 301 412
FT DISULFID 307 316
FT DISULFID 315 378
FT DISULFID 344 409
FT DISULFID 348 411
FT DISULFID 377 377
FT CARBOHYD 72 72
FT CARBOHYD 139 139
FT CARBOHYD 240 240
SQ SEQUENCE 412 AA; 47606 MW; 93E759BF1BD958DC CRC64;

Query Match 85.0%; Score 539; DB 1; Length 412;
Best Local Similarity 79.5%; Pred. No. 1.9e-50;
Matches 89; Conservative 15; Mismatches 8; Indels 0; Gaps 0;

QY 1 ALDTNYCFRNLENCVVRPLYIDFRDLGKWKVHEPKGYANFCGCPYLRSADTTHST 60
DB 301 ALDAAACYFRNVQDNCCLRPYIDFRDLGKWKVHEPKGYANFCAGACPYLWSSTQHSR 360

QY 61 VLGLYNTLNPEASPCCVQDLEPLTILYVGRTPKVEQLSNMVKSKCS 112
DB 361 VLSLNTINPEASPCCVSQDLEPLTILYVGRTPKVEQLSNMVKSKCS 412

RESULT 7
TGFB2_BOVIN
ID TGFB2_BOVIN STANDARD; PRT: 112 AA.
AC P21214;
DT 01-MAY-1991 (Rel. 18, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE TRANSFORMING GROWTH FACTOR BETA 2 (TGF-BETA 2) (MILK GROWTH FACTOR)
DE (MGF).
GN TGFB2.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;

RN
RP SEQUENCE.
RC TISSUE=Milk;
RX MEDLINE=92189724; PubMed=1799413;
RA Jin Y., Cox D.A., Knecht R., Raschdorf F., Cerletti N.;
RT "Separation, purification, and sequence identification of TGF-beta 1
RT and TGF-beta 2 from bovine milk";
RL J. Protein Chem. 10:565-575(1991).
[2]
RN SEQUENCE OF 1-30.
RP
RC TISSUE=Bone;
RX MEDLINE=87137406; PubMed=3469199;
RA Seyedin S.M., Segarini P.R., Rosen D.M., Thompson A.Y., Bentz H.,
RA Graycar J.;
RT "Cartilage-inducing factor-B is a unique protein structurally and
RT functionally related to transforming growth factor-beta";
RL J. Biol. Chem. 262:1946-1949(1987).
[3]
RN SEQUENCE OF 1-19.
RP
RC TISSUE=Milk;
RX MEDLINE=91224126; PubMed=2026157;
RA Cox D.A., David A., Buerk R.R.;
RT "Isolation and characterization of milk growth factor, a
RT transforming-growth-factor-beta 2-related polypeptide, from bovine
RT milk";
RL Eur. J. Biochem. 197:353-358(1991).
[4]
RN SUBUNITS.
RP
RC TISSUE=Bone;
RX MEDLINE=92129307; PubMed=1733936;
RA Ogawa Y., Schmidt D.K., Dasch J.R., Chang R.J., Glaser C.B.;
RT "Purification and characterization of transforming growth factor-beta
RT 2.3 and -beta 1.2 heterodimers from bovine bone";
RL J. Biol. Chem. 267:2325-2328(1992).
CC -!- FUNCTION: TGF-BETA 2 HAS SUPPRESSIVE EFFECTS ON INTERLEUKIN-2
CC -!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED. HETERODIMERS OF TGF-BETA 1/2
CC AND OF TGF-BETA 2/3 HAVE BEEN FOUND IN BONE.
CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR PIR: S15389; S15389.
DR HSP: P08112; 1TFG.
DR InterPro: IPR001839;
DR InterPro: IPR002400;
DR Pfam: PF00019; TGF-beta; 1.
DR PRINTS: PR00438; GFCYSKNOT.
DR PROSITE: PS00250; TGF-BETA_1; 1.
KW Growth factor; Mitogen; Milk.
FT DISULFID 7 16 BY SIMILARITY.
FT DISULFID 15 78 BY SIMILARITY.
FT DISULFID 44 109 BY SIMILARITY.
FT DISULFID 48 111 BY SIMILARITY.
FT DISULFID 77 77 INTERCHAIN (BY SIMILARITY).
SQ SEQUENCE 112 AA; 12719 MW; 5142C7432C4EBC1C CRC64;

Query Match 84.4%; Score 535; DB 1; Length 112;
Best Local Similarity 79.5%; Pred. No. 1.3e-50;
Matches 89; Conservative 14; Mismatches 9; Indels 0; Gaps 0;

QY 1 ALDTNYCFRNLENCVVRPLYIDFRDLGKWKVHEPKGYANFCGCPYLRSADTTHST 60
DB 1 ALDAAACYFRNVQDNCCLRPYIDFRDLGKWKVHEPKGYANFCAGACPYLWSSTQHSR 60

QY 61 VLGLYNTLNPEASPCCVQDLEPLTILYVGRTPKVEQLSNMVKSKCS 112
DB 61 VLSLNTINPEASPCCVSQDLEPLTILYVGRTPKVEQLSNMVKSKCS 112

RESULT 8
TGFB2_HUMAN
ID TGFB2_HUMAN STANDARD; PRT: 414 AA.
AC P08112; Q15581;
DT 01-AUG-1988 (Rel. 08, Created)


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QY 61 VLGLYNTLNPEASPCVQDLEPLTILYVGRTPKVEQLSNMVKSKCS 112
DB 363 VLSLYNTINPEASPCVQDLEPLTILYVGRTPKVEQLSNMVKSKCS 414

RESULT 9
TGF2_PIG
ID TGF2_PIG STANDARD; PRT; 435 AA.
AC P09858;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE TRANSFORMING GROWTH FACTOR BETA 2 PRECURSOR (TGF-BETA 2).
GN TGF2.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE OF 2-435 FROM N.A.
RC TISSUE=Lung;
RA Zhou Y.;
RL Submitted (DEC-1992) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 303-345.
RX MEDLINE=87102890; PubMed=2879635;
RA Cheifetz S., Weatherbee J.A., Tsang M.L.S., Anderson J.K., Mole J.E.,
RA Lucas R., Massague J.;
RT "The transforming growth factor-beta system, a complex pattern of
RT cross-reactive ligands and receptors.";
RL Cell 48:409-415(1987).
CC -!- FUNCTION: TGF-BETA 2 HAS SUPPRESSIVE EFFECTS ON INTERLEUKIN-2
CC DEPENDENT T-CELL GROWTH.
CC -!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED.
CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
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CC
CC EMBL: L08375; AAB03850.1; -
CC PIR: B26356; B26356.
CC HSP: P08112; ITFG.
CC InterPro: IPR001111; -
CC InterPro: IPR001839; -
CC InterPro: IPR002400; -
CC Pfam: PF00019; TGF-beta; 1.
CC Pfam: PF00688; TGF-beta; 1.
CC PRINTS: PR00438; GFCYSKNOT.
CC PROSITE: PS00250; TGF_BETA_1; 1.
CC Growth factor; Mitogen; Glycoprotein; Signal.
CC SIGNAL 1 19
CC PROPEP 20 302
CC CHAIN 303 435
CC TRANSFORMING GROWTH FACTOR BETA 2.
CC BY SIMILARITY.
CC DISULFID 309 318
CC BY SIMILARITY.
CC DISULFID 317 380
CC BY SIMILARITY.
CC DISULFID 346 411
CC BY SIMILARITY.
CC DISULFID 350 413
CC BY SIMILARITY.
CC DISULFID 379 379
CC INTERCHAIN (BY SIMILARITY).
CC CARBOHYD 72 72
CC N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 140 140
CC N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 241 241
CC N-LINKED (GLCNAC. . .) (POTENTIAL).
CC SEQUENCE 435 AA; 49922 MW; 438282E288B32322 CRC64;
SQ

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Query Match 84.4%; Score 535; DB 1; Length 435;
 Best Local Similarity 79.5%; Pred. No. 5.3e-50;
 Matches 89; Conservative 14; Mismatches 9; Indels 0; Gaps 0;

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QY 1 ALDNYCFRNLEENCVRPLYIDFQDLGKWKVHEPKGYANFCSPCPYLSADTTHST 60
DB 303 ALDNYCFRNVDNCLRLYIDFQDLGKWKVHEPKGYANFCACACYPYLSADTTHST 362

QY 61 VLGLYNTLNPEASPCVQDLEPLTILYVGRTPKVEQLSNMVKSKCS 112
DB 363 VLSLYNTINPEASPCVQDLEPLTILYVGRTPKVEQLSNMVKSKCS 414

RESULT 10
TGF2_MOUSE
ID TGF2_MOUSE STANDARD; PRT; 414 AA.
AC P27090;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE TRANSFORMING GROWTH FACTOR BETA 2 PRECURSOR (TGF-BETA 2).
GN TGF2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90014832; PubMed=2797004;
RA Miller D.A., Lee A., Pelton R.W., Chen E.Y., Moses H.L.,
RA Derynck R.;
RT "Murine transforming growth factor-beta 2 cDNA sequence and
RT expression in adult tissues and embryos.";
RL Mol. Endocrinol. 3:1108-1114(1989).
CC -!- FUNCTION: TGF-BETA 2 HAS SUPPRESSIVE EFFECTS ON INTERLEUKIN-2
CC DEPENDENT T-CELL GROWTH.
CC -!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED.
CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
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CC
CC EMBL: X57413; CAA04672.1; -
CC PIR: A0148; WMSB2.
CC HSP: P08112; ITFG.
CC MGD: MGI:98726; Tgfb2.
CC InterPro: IPR001111; -
CC InterPro: IPR001839; -
CC InterPro: IPR002400; -
CC Pfam: PF00019; TGF-beta; 1.
CC Pfam: PF00688; TGF-beta; 1.
CC PRINTS: PR00438; GFCYSKNOT.
CC PROSITE: PS00250; TGF_BETA_1; 1.
CC Growth factor; Mitogen; Glycoprotein; Signal.
CC SIGNAL 1 19
CC PROPEP 20 302
CC CHAIN 303 414
CC TRANSFORMING GROWTH FACTOR BETA 2.
CC BY SIMILARITY.
CC DISULFID 309 318
CC BY SIMILARITY.
CC DISULFID 317 380
CC BY SIMILARITY.
CC DISULFID 346 411
CC BY SIMILARITY.
CC DISULFID 350 413
CC BY SIMILARITY.
CC DISULFID 379 379
CC INTERCHAIN (BY SIMILARITY).
CC CARBOHYD 72 72
CC N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 140 140
CC N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 241 241
CC N-LINKED (GLCNAC. . .) (POTENTIAL).
CC SEQUENCE 414 AA; 47601 MW; 449BC6FA22087FB6 CRC64;
SQ

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Query Match 83.6%; Score 530; DB 1; Length 414;
 Best Local Similarity 78.6%; Pred. No. 1.7e-49;
 Matches 88; Conservative 14; Mismatches 10; Indels 0; Gaps 0;

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Qy 1 ALDITNCFRNLENCVVRPLYIDFRDLGKWKVHEPKGYANFCGPGCPYLRSADTTHST 60
    ||| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 303 ALDAAFCFRNVQDNCCLRLPLIDFKDLGKWKIHEPKGYANFCAGACPYLWSSDTHSR 362
    ||| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 61 VLGLYNTLNPEASAPCCVPQDLEPLTILYVGRTPKVEQLSNMVKSKCS 112
    || |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 363 VLSLYNTINPEASAPCCVQDLDLSLTILYIGNPKPKIEQLSNMVKSKCS 414
    ||| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 11
TGFB2_XENLA STANDARD; PRT; 413 AA.
AC P17247;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE TRANSFORMING GROWTH FACTOR BETA 2 PRECURSOR (TGF-BETA 2).
GN TGF2.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90245678; PubMed=2336403;
RA Rebert M.L., Bhatia-Dey N., Dawid I.B.;
RT "The sequence of TGF-beta 2 from Xenopus laevis.";
RL Nucleic Acids Res. 18:2185-2185(1990).
CC -!- FUNCTION: TGF-BETA 2 HAS SUPPRESSIVE EFFECTS ON INTERLEUKIN-2
CC DEPENDENT T-CELL GROWTH.
CC -!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED.
CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
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CC -----
DR EMBL; X51817; CAA36116.1; -
DR EMBL; X51817; CAA36117.1; ALT_INIT.
DR PR; S09510; S09510.
DR HSP; P08112; 1TFG.
DR InterPro; IPR001111; -
DR InterPro; IPR001839; -
DR InterPro; IPR002400; -
DR Pfam; PF00688; TGF-beta; 1.
DR PRINTS; PR00438; GFCYSKNOT.
DR PROSITE; PS00250; TGF_BETA_1; 1.
KW Signal; Mitogen; Glycoprotein; Growth factor.
FT SIGNAL 1 19
FT PROPEP 20 301
FT CHAIN 302 413
FT DISULFID 308 317
FT DISULFID 316 379
FT DISULFID 345 410
FT DISULFID 349 412
FT DISULFID 378 378
FT CARBOHYD 72 72
FT CARBOHYD 140 140
FT CARBOHYD 241 241
SQ SEQUENCE 413 AA; 47639 MW; 6127715B38734010 CRC64;

Query Match 81.4%; Score 516; DB 1; Length 413;
Best Local Similarity 76.8%; Pred. No. 5.4e-48;
Matches 86; Conservative 14; Mismatches 12; Indels 0; Gaps 0;

Qy 1 ALDITNCFRNLENCVVRPLYIDFRDLGKWKVHEPKGYANFCGPGCPYLRSADTTHST 60

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Db 302 ALDAAFCFRNVQDNCCLRLPLIDFKDLGKWKIHEPKGYANFCAGACPYLWSSDTHSR 361
    ||| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 61 VLGLYNTLNPEASAPCCVPQDLEPLTILYVGRTPKVEQLSNMVKSKCS 112
    || |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 362 VLSLYNTINPEASAPCCVQDLDLSLTILYIGNPKPKIEQLSNMVKSKCS 413
    ||| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 12
TGFB1_MOUSE STANDARD; PRT; 390 AA.
AC P04202;
DT 20-MAR-1987 (Rel. 04, Created)
DT 20-MAR-1987 (Rel. 04, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE TRANSFORMING GROWTH FACTOR BETA 1 PRECURSOR (TGF-BETA 1).
GN TGF1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86168129; PubMed=3007454;
RA Derynck R., Jarrett J.A., Chen E.Y., Goeddel D.V.;
RT "The murine transforming growth factor-beta precursor.";
RL J. Biol. Chem. 261:4377-4379(1986).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=BALB/C;
RC MEDLINE=96096545; PubMed=8522200;
RA Guron C., Sudarshan C., Raghow R.;
RT "Molecular organization of the gene encoding murine transforming
RT growth factor beta 1.";
RL Gene 165:325-326(1995).
RN [3]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6, AND NOD/LIT; TISSUE=Spleen;
RC Poirot L., Benoist C., Mathis D.;
RA "Transforming growth factor-beta 1 sequence and expression: no
RT difference between NOD/Lt and C57BL/6 mouse strains.";
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: TGF-BETA IS A MULTIFUNCTIONAL PEPTIDE THAT CONTROL
CC PROLIFERATION, DIFFERENTIATION, AND OTHER FUNCTIONS IN MANY CELL
CC TYPES. MANY CELLS SYNTHESIZE TGF-BETA AND ESSENTIALLY ALL OF THEM
CC HAVE SPECIFIC RECEPTORS FOR THIS PEPTIDE. TGF-BETA REGULATES THE
CC ACTIONS OF MANY OTHER PEPTIDE GROWTH FACTORS AND DETERMINES
CC A POSITIVE OR NEGATIVE DIRECTION OF THEIR EFFECTS.
CC -!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED.
CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M13177; AAA40423.1; -
DR EMBL; L42462; AAB00138.1; -
DR EMBL; L42456; AAB00138.1; JOINED.
DR EMBL; L42457; AAB00138.1; JOINED.
DR EMBL; L42458; AAB00138.1; JOINED.
DR EMBL; L42459; AAB00138.1; JOINED.
DR EMBL; L42460; AAB00138.1; JOINED.
DR EMBL; L42461; AAB00138.1; JOINED.
DR EMBL; L42461; AAB00138.1; JOINED.
DR PIR; A01396; WFM52.
DR HSSP; P01137; 1KLC.
DR MGD; MGI:98725; Tgfb1.
DR InterPro; IPR001111; -
DR InterPro; IPR001839; -

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R HSP; P01137; 1KLC.
R InterPro: IPR001111; -.
R InterPro: IPR001839; -.
R InterPro: IPR002400; -.
R Pfam: PF00019; TGF-beta; 1.
R Pfam: PF00688; TGF-beta-propeptide; 1.
R PRINTS: PR00438; GFCYSKNOT.
R PROSITE: PS00250; TGF_BETA_1; 1.
W Growth factor; Mitogen; Glycoprotein; Signal.
T SIGNAL 1 23
T 23 POTENTIAL.
T PROPEP 24 278
T CHAIN 279 390 TRANSFORMING GROWTH FACTOR BETA 1.
T DISULFID 285 294 BY SIMILARITY.
T DISULFID 293 356 BY SIMILARITY.
T DISULFID 322 387 BY SIMILARITY.
T DISULFID 326 389 BY SIMILARITY.
T DISULFID 355 355 INTERCHAIN (BY SIMILARITY).
T CARBOHYD 82 82 N-LINKED (GLCNAC. .) (POTENTIAL).
T CARBOHYD 136 136 N-LINKED (GLCNAC. .) (POTENTIAL).
T CARBOHYD 176 176 N-LINKED (GLCNAC. .) (POTENTIAL).
T SITE 244 246 CELL ATTACHMENT SITE (POTENTIAL).
T SEQUENCE 390 AA; 44329 MW; 5E21108ED50D853C CRC64;
Query Match 79.3%; Score 503; DB 1; Length 390;
Best Local Similarity 77.7%; Pred. No. 1.3e-46;
Matches 87; Conservative 10; Mismatches 15; Indels 0; Gaps 0;
y 1 ALDTNYCFRNLEENCVRPLYIDIFRDGLGKWKVHEPKGYGNFCGPGCPYLRSADTHTST 60
||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
b 279 ALDTNYCFSTENKCCVRQYIDFRKDLGKWKIHEPKGYHANFCLGPGCPYIWSLDYQYSK 338
y 61 VLGTNYFLNPEASPCVPPQDLLEPLILYVVGRTPKVEQLSNMVKSCKS 112
||| || ||||| ||||| ||||| ||||| ||||| ||||| |||||
b 339 VLALYNOHNPFCASPCVPPQALEPLIVYVVGRTPKVEQLSNMIVRSCKS 390
||| || ||||| ||||| ||||| ||||| ||||| ||||| |||||
RESULT 14
GFL_BOVIN STANDARD; PRT; 315 AA.
C P18341;
T 01-NOV-1990 (Rel. 16, Created)
T 01-NOV-1990 (Rel. 16, Last sequence update)
T 15-JUL-1999 (Rel. 38, Last annotation update)
E TRANSFORMING GROWTH FACTOR BETA 1 PRECURSOR (TGF-BETA 1) (FRAGMENT).
T TGFBI.
S Bos taurus (Bovine).
C Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
C Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
C Bovidae; Bovinae; Bos.
X NCBI_TaxID=9913;
N [1]
N SEQUENCE FROM N.A.
P MEDLINE=91042552; PubMed=3153459;
X van Obberghen-Schilling E., Kondaiah P., Ludwig R.L., Sporn M.B.,
A Baker C.C.;
A "Complementary deoxyribonucleic acid cloning of bovine transforming
T growth factor-beta 1";
T Mol. Endocrinol. 1:693-698(1987).
L [2]
N SUBUNITS.
P TISSUE=Bone;
X MEDLINE=92129307; PubMed=1733936;
A Ogawa Y., Schmidt D.K., Dasch J.R., Chang R.J., Glaser C.B.;
T "Purification and characterization of transforming growth factor-beta
T 2.3 and -beta 1.2 heterodimers from bovine bone.";
L J. Biol. Chem. 267:2325-2328(1992).
C -1- FUNCTION: TGF-BETA IS A MULTIFUNCTIONAL PEPTIDE THAT CONTROL
C PROLIFERATION, DIFFERENTIATION, AND OTHER FUNCTIONS IN MANY CELL
C TYPES. MANY CELLS SYNTHESIZE TGF-BETA AND ESSENTIALLY ALL OF THEM
C HAVE SPECIFIC RECEPTORS FOR THIS PEPTIDE. TGF-BETA REGULATES THE
C ACTIONS OF MANY OTHER PEPTIDE GROWTH FACTORS AND DETERMINES
C A POSITIVE OR NEGATIVE DIRECTION OF THEIR EFFECTS.

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 DR EMBL; X99438; CAA67801.1; -;
 DR HSP; P01137; IKLC.
 DR InterPro; IPR001111; -;
 DR InterPro; IPR001839; -;
 DR InterPro; IPR002400; -;
 DR Pfam; PF00019; TGF-beta; 1.
 DR Pfam; PF00688; TGFB_propeptide; 1.
 DR PRINTS; PR00438; GFCYSKNOT.
 DR PROSITE; PS00250; TGF_BETA_1; 1.
 KW Growth factor; Mitogen; Glycoprotein; Signal.
 FT SIGNAL 1 23
 FT PROPEP 24 278
 FT CHAIN 279 390
 FT DISULFID 285 294
 FT DISULFID 293 356
 FT DISULFID 322 387
 FT DISULFID 326 389
 FT DISULFID 355 355
 FT CARBOHYD 82 82
 FT CARBOHYD 136 136
 FT CARBOHYD 176 176
 SQ SEQUENCE 390 AA; 43974 MW; A86D715F44549691 CRC64;

Query Match 78.7%; Score 499; DB 1; Length 390;
 Best Local Similarity 76.8%; Pred. No. 3.4e-46;
 Matches 86; Conservative 11; Mismatches 15; Indels 0; Gaps 0;

QY 1 ALDNYCFRNLENCVRLPYIDFRDLGWKWHPEKGYANFCGPGPYLRSDTTHST 60
 ||||| : ||||| |||||:||||:||||:||||:||||:||||: ||| : ||| :
 Db 279 ALDNYCFESSTKCCVRLQYIDFRDLGWKWHPEKGYHANFCLGPGPYLWSDTQYSK 338

QY 61 VLGYNLTNPASPCVCPDLEPLTILYVYVGRTPKVEQLSNMVKSCKS 112
 || ||| || |||:|||| ||||| |||||:|||| |||||:|||| |||||
 Db 339 VLALYQHNPGASAPCCVQVLEPLPIVYVYVGRKPKVEQLSNMIVRSCKS 390

RESULT 21
 TGFB1_CAVPO
 ID TGFB1_CAVPO STANDARD; PRT; 390 AA.
 AC Q9Z1Y6; Q9OZB3; Q9R148;
 DT 01-OCT-2000 (Rel. 40, Created)
 DT 01-OCT-2000 (Rel. 40, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE TRANSFORMING GROWTH FACTOR BETA 1 PRECURSOR (TGF-BETA 1).
 GN TGFB1.
 OS Cavia porcellus (Guinea pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
 OX NCBI_TaxID=10141;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=HARTLEY;
 RA Jeevan A., McMurray D.N., Yoshimura T.;
 RT "Guinea pig transforming growth factor-beta in peritoneal exudates after BCG vaccination."
 RT Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE OF 265-382 FROM N.A.
 RX MEDLINE=99144670; PubMed=10025978;
 RA Scarozza A.M., Ramsingh A.I., Wicher V., Wicher K.;
 RT "Spontaneous cytokine gene expression in normal guinea pig blood and tissues."
 RT Cytokine 10:851-859(1998).
 RL [3]
 RP SEQUENCE OF 279-371 FROM N.A.
 RC STRAIN=HARTLEY; TISSUE=Trachea;
 RA Morishima Y., Uchida Y., Nomura A., Ishii Y., Sakamoto T.,

RA Sekizawa K.;
 RT "Guinea-pig transforming growth factor-beta expression in injured tracheal epithelium";
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 CC !- FUNCTION: MULTIFUNCTIONAL PEPTIDE THAT CONTROLS PROLIFERATION,
 CC DIFFERENTIATION, AND OTHER FUNCTIONS IN MANY CELL TYPES. MANY
 CC CELLS SYNTHESIZE TGF-BETA 1 AND ESSENTIALLY ALL OF THEM HAVE
 CC SPECIFIC RECEPTORS FOR THIS PEPTIDE. TGF-BETA 1 REGULATES THE
 CC ACTIONS OF MANY OTHER PEPTIDE GROWTH FACTORS AND DETERMINES A
 CC POSITIVE OR NEGATIVE DIRECTION OF THEIR EFFECTS.
 CC !- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
 CC !- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
 CC
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 DR EMBL; AF191297; AAF02780.1; -;
 DR EMBL; AF097509; AAC83807.1; -;
 DR EMBL; AF169347; AAD49347.1; -;
 DR HSP; P01137; IKLA.
 DR InterPro; IPR001839; -;
 DR Pfam; PF00019; TGF-beta; 1.
 DR PROSITE; PS00250; TGF_BETA_1;
 KW Growth factor; Mitogen; Glycoprotein; Signal.
 FT SIGNAL 1 24
 FT PROPEP 25 278
 FT CHAIN 279 390
 FT DISULFID 285 294
 FT DISULFID 293 356
 FT DISULFID 322 387
 FT DISULFID 326 389
 FT DISULFID 355 355
 FT CARBOHYD 82 82
 FT CARBOHYD 136 136
 FT CARBOHYD 176 176
 FT SITE 244 246
 FT CONFLICT 279 279
 FT CONFLICT 286 286
 FT CONFLICT 309 309
 FT CONFLICT 322 322
 FT CONFLICT 350 350
 SQ SEQUENCE 390 AA; 44328 MW; 1539F849BA0C0FF1 CRC64;

Query Match 77.0%; Score 488; DB 1; Length 390;
 Best Local Similarity 75.7%; Pred. No. 5.1e-45;
 Matches 84; Conservative 11; Mismatches 16; Indels 0; Gaps 0;

QY 2 LDTNYCFRNLENCVRLPYIDFRDLGWKWHPEKGYANFCGPGPYLRSDTTHSTV 61
 ||||| : ||||| |||||:||||:||||:||||:||||:||||: ||| : ||| :
 Db 280 LDTNYCFESSTKCCVRLQYIDFRDLGWKWHPEKGYHANFCLGPGPYLWSDTQYSK 339

QY 62 LGLYNTLNPASPCVCPDLEPLTILYVYVGRTPKVEQLSNMVKSCKS 112
 || ||| || |||:|||| ||||| |||||:|||| |||||:|||| |||||
 Db 340 LALYQHNPGASAPCCVQVLEPLPIVYVYVGRKPKVEQLSNMIVRSCKS 390

RESULT 22
 TGFB1_CHICK
 ID TGFB1_CHICK STANDARD; PRT; 373 AA.
 AC P09531;
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE TRANSFORMING GROWTH FACTOR BETA 1 PRECURSOR (TGF-BETA 1) (TGF-BETA 4)
 DE (FRAGMENT).
 GN TGFB1.
 OS Gallus gallus (Chicken).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-WHITE LEIGHORN;
RX MEDLINE=89112198; PubMed=2464131;
RA Jakowlew S.B., Dillard P.J., Sporn M.B., Roberts A.B.;
RT "Complementary deoxyribonucleic acid cloning of a messenger
RT ribonucleic acid encoding transforming growth factor beta 4 from
RT chicken embryo chondrocytes";
RL Mol. Endocrinol. 2:1186-1195(1988).
RN [2]
RP REVISIONS.
RX MEDLINE=92357039; Pubmed=1353860;
RA Burt D.W., Jakowlew S.B.:
RT "Correction: a new interpretation of a chicken transforming growth
RT factor-beta 4 complementary DNA.";
RL Mol. Endocrinol. 6:989-992(1992).
CC -I- FUNCTION: TGF-BETA IS A MULTIFUNCTIONAL PEPTIDE THAT CONTROL
CC PROLIFERATION, DIFFERENTIATION, AND OTHER FUNCTIONS IN MANY CELL
CC TYPES. MANY CELLS SYNTHESIZE TGF-BETA AND ESSENTIALLY ALL OF THEM
CC HAVE SPECIFIC RECEPTORS FOR THIS PEPTIDE. TGF-BETA REGULATES THE
CC ACTIONS OF MANY OTHER PEPTIDE GROWTH FACTORS AND DETERMINES
CC A POSITIVE OR NEGATIVE DIRECTION OF THEIR EFFECTS.
CC -I- SUBUNIT: HOMODIMER, DISULFIDE-LINKED.
CC -I- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.

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EMBL; M31160; AAC05637.1; -.
DR PIR; A34941; A34941.
DR PIR; S03110; S03110.
DR HSP; P01137; IKLC.
DR InterPro; IPR001111; -.
DR InterPro; IPRO01839; -.
DR Pfam; PF000019; TGF-beta; 1.
DR Pfam; PF00688; TGFB_propeptide; 1.
DR ProSITE; PS00250; TGF_BETA_1; 1.
KW Growth factor; Mitogen; Glycoprotein; Signal.
FT NON_TER 1 1
FT SIGNAL <1 1 POTENTIAL.
FT CHAIN 2 259 POTENTIAL.
FT FTCH 260 373 TRANSFORMING GROWTH FACTOR BETA 1.
FT DISULFID 266 277 BY SIMILARITY.
FT DISULFID 276 339 BY SIMILARITY.
FT DISULFID 305 370 BY SIMILARITY.
FT DISULFID 309 372 BY SIMILARITY.
FT DISULFID 338 338 INTERCHAIN (BY SIMILARITY).
FT CARBOHYD 54 54 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 109 109 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 153 153 N-LINKED (GLCNAC...) (POTENTIAL).
FT SITE 224 226 CELL ATTACHMENT SITE (POTENTIAL).
SQ SEQUENCE 373 AA; 42634 MW; 9903f3479c852E5 CRC64;

[illegible]

7

72 ASASPCCVPQDL¹EPLTILY²VGRTPKV-EQLSNM³VVK⁴SKCS 112

RESULT	30
IHBA_HORSE	

QY 72 ASAPCCVPQDLEPLTILYYVGRTPKV-EQLSNMVMVKSCKCS 112

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AC P55102;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DE 01-OCT-2000 (Rel. 40, Last annotation update)
DE INHIBIN BETA A CHAIN PRECURSOR (ACTIVIN BETA-A CHAIN).
GN INHBA.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Ovary;
RX MEDLINE=96031670; PubMed=7548399;
RA Yoshida S., Famanouchi K., Hasegawa T., Ikeda A., Suzuki M.,
RA Chang K., Matsuyama S., Nishihara M., Takahashi M.;
RT "Molecular cloning of cDNA for equine ovarian inhibin/activin beta A
RT subunit.";
RL J. Vet. Med. Sci. 57:469-473(1995).
CC -!- FUNCTION: INHIBIN IS A GONADAL GLYCOPROTEIN THAT INHIBITS THE
CC SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND. ON THE OTHER HAND
CC ACTIVIN ACTIVATES THE SECRETION OF FOLLITROPIN. ACTIVIN IS ALSO
CC IMPORTANT IN EMBRYONIC AXIAL DEVELOPMENT.
CC -!- SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE BONDS.
CC INHIBIN A IS A DIMER OF ALPHA AND BETA-A.
CC INHIBIN B IS A DIMER OF ALPHA AND BETA-B.
CC ACTIVIN A IS A DIMER OF BETA-A.
CC ACTIVIN AB IS A DIMER OF BETA-A AND BETA-B.
CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC -----
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CC -----
DR EMBL; D50326; BRA08862.1; -.
DR HSSP; P18075; IBMP.
DR InterPro; IPR000491; -.
DR InterPro; IPR001111; -.
DR InterPro; IPR001839; -.
DR InterPro; IPR002400; -.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGF-beta-propeptide; 1.
DR PRINTS; PR00438; GFCYSKNOT.
DR PRINTS; PR00670; INHIBINBA.
DR PROSITE; PS00250; TGF_BETA_1; 1.
KW Follitropin inhibitor; Contrapeptive; Hormone; Glycoprotein; Signal.
FT SIGNAL 1 20
FT PROPEP 21 310 INHIBIN BETA A CHAIN.
FT CHAIN 311 426 BY SIMILARITY.
FT DISULFID 314 322 BY SIMILARITY.
FT DISULFID 321 391 BY SIMILARITY.
FT DISULFID 350 423 BY SIMILARITY.
FT DISULFID 354 425 BY SIMILARITY.
FT DISULFID 390 390 INTERCHAIN (BY SIMILARITY).
FT CARBOHYD 165 165 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 426 AA; 47709 MW; E481060B8368A77D CRC64;

Query Match 32.5%; Score 206; DB 1; Length 426;
Best Local Similarity 38.3%; Pred. No. 9e-15;
Matches 41; Conservative 20; Mismatches 36; Indels 10; Gaps 5;

Qy 15 CCVRLYIDFRODLGWK-VWHEPKGYANFCGSPCP-----YLRSDTTHSTVLGLYNLT 68
Db 321 CKKQFFVFSK-DIGWNOWIITAPSHYANCCEGSPHTAGTSGSLSPHSTVINQYRLR 379

Qy 69 --NPASAPCCVPQDLPTLTLY-YGRTPKVEQLSNMVKSKCS 112
Db 380 GNPFPANLKSCCVPTKLRPMSMLYDDGONTIKDKIQNVIVECGCS 426

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RESULT 31
BMP6_HUMAN STANDARD; PRT; 513 AA.
ID BMP6_HUMAN
AC P22004;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DE 01-OCT-2000 (Rel. 40, Last annotation update)
DE BONE MORPHOGENETIC PROTEIN 6 PRECURSOR (BMP-6).
GN BMP6.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Bone;
RX MEDLINE=91088608; PubMed=2263636;
RA Celeste A.J., Iannazzi J.A., Taylor R.C., Hewick R.M., Rosen V.,
RA Wang E.A., Wozney J.M.;
RT "Identification of transforming growth factor beta family members
RT present in bone-inductive protein purified from bovine bone.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:9843-9847(1990).
CC -!- FUNCTION: INDUCES CARTILAGE AND BONE FORMATION.
CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M60315; AAA36737.1; -.
DR PIR; B39263; B39263.
DR HSSP; P18075; IBMP.
DR MIM; 112266; -.
DR InterPro; IPR001111; -.
DR InterPro; IPR001839; -.
DR InterPro; IPR002400; -.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGF-beta-propeptide; 1.
DR PRINTS; PR00438; GFCYSKNOT.
DR PRINTS; PS00250; TGF_BETA_1; 1.
KW Signal; Growth factor; Cytokine; Bone; Cartilage; Glycoprotein.
FT SIGNAL 1 20 POTENTIAL.
FT PROPEP 21 381 POTENTIAL.
FT CHAIN 382 513 BONE MORPHOGENETIC PROTEIN 6.
FT DISULFID 412 478 BY SIMILARITY.
FT DISULFID 441 510 BY SIMILARITY.
FT DISULFID 445 512 BY SIMILARITY.
FT DISULFID 477 477 INTERCHAIN (BY SIMILARITY).
FT CARBOHYD 241 241 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 269 269 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 386 386 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 404 404 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 454 454 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 513 AA; 57225 MW; 3F19155B36049278 CRC64;

Query Match 32.5%; Score 206; DB 1; Length 513;
Best Local Similarity 37.2%; Pred. No. 1.e-14;
Matches 42; Conservative 22; Mismatches 43; Indels 6; Gaps 4;

Qy 4 TNYCFERNLENCVVRPLYIDFRODLGWK-VWHEPKGYANFCGSPCYLRSD--TTHS 59
Db 401 SDINSELKTACKRHHELYVSF-QDLGWQDWIITAPKGYAANYDCGECFPLNAHNATNHA 459

Qy 60 TVLGLYNLTNPESASPCCVQDLPTLTLYYVGRTPKV-EQLSNMVKSKC 111
Db 460 IVOTLVHLMNPVEYVPCCAPTKLNAISVLYFDNSNVILKKYRNMVVRGCC 512

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RESULT 32
BMP6_MOUSE
ID BMP6_MOUSE STANDARD; PRT; 510 AA.
AC P20722;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE BONE MORPHOGENETIC PROTEIN 6 PRECURSOR (BMP-6) (VG-1-RELATED PROTEIN)
DE (VGR-1).
DE BMP6 OR BMP-6 OR VGR1.
GN Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RN SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=94375533; PubMed=8089189;
RA Gitelman S.E., Kobrin M.S., Ye J.Q., Lopez A.R., Lee A., Derynck R.;
RT "Recombinant Vgr-1/BMP-6-expressing tumors induce fibrosis and
RT endochondral bone formation in vivo.";
RL J. Cell Biol. 126:1595-1609(1994).
RN [2]
RN SEQUENCE FROM N.A.
RX MEDLINE=9722480; PubMed=9069123;
RA Gitelman S.E., Kobrin M., Lee A., Fet V., Lyons K., Hogan B.L.M.,
RA Derynck R.;
RT "Structure and sequence of the mouse Bmp6 gene.";
RL Mamm. Genome 8:212-214(1997).
RN [3]
RN SEQUENCE OF 73-510 FROM N.A.
RX MEDLINE=89282810; PubMed=2734307;
RA Lyons K., Graycar J.L., Lee A., Hashmi S., Lindquist P.B., Chen E.Y.,
RA Hogan B.L.M., Derynck R.;
RT "Vgr-1, a mammalian gene related to Xenopus Vg-1, is a member of the
RT transforming growth factor beta gene superfamily.";
RL Proc. Natl. Acad. Sci. U.S.A. 86:4554-4558(1989).
CC -!- FUNCTION: INDUCES CARTILAGE AND BONE FORMATION (BY SIMILARITY).
CC -!- TISSUE SPECIFICITY: EXPRESSED IN THE LUNGS. LOW LEVELS SEEN IN
CC THE KIDNEY.
CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; X80992; CAA56917.1;
CC EMBL; U73520; AAB18235.1;
CC EMBL; U73515; AAB18235.1; JOINED.
CC EMBL; U73516; AAB18235.1; JOINED.
CC EMBL; U73517; AAB18235.1; JOINED.
CC EMBL; U73518; AAB18235.1; JOINED.
CC EMBL; U73519; AAB18235.1; JOINED.
CC EMBL; J04566; AAA40548.1;
CC PIR; A33925; A33925.
CC HSSP; P18075; IBMP.
CC MGD; MGI:88182; Bmp6.
CC InterPro; IPR001111;
CC InterPro; IPR001839;
CC InterPro; IPR002400;
CC Pfam; PF00019; TGF-beta; 1.
CC Pfam; PF00688; TGF-beta; 1.
CC PRINTS; PR00438; GFCYSKNOT.
CC PROSITE; PS00250; TGF-BETA_1; 1.
KW Signal; Growth factor; Cytokine; Bone; Cartilage; Glycoprotein.
FT SIGNAL 1 20 POTENTIAL.
FT PROPEP 21 378 POTENTIAL.

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FT CHAIN 379 510 BONE MORPHOGENETIC PROTEIN 6.
FT DISULFID 409 475 BY SIMILARITY.
FT DISULFID 438 507 BY SIMILARITY.
FT DISULFID 442 509 BY SIMILARITY.
FT CARBOHYD 474 474 INTERCHAIN (BY SIMILARITY).
FT CARBOHYD 238 238 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 286 286 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 383 383 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 401 401 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 451 451 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 73 73 K -> M (IN REF. 3).
FT CONFLICT 75 75 E -> K (IN REF. 3).
FT CONFLICT 86 86 L -> P (IN REF. 3).
SQ SEQUENCE 510 AA; 56431 MW; 910B68531289FCD2 CRC64;

Query Match 32.3%; Score 205; DB 1; Length 510;
Best Local Similarity 37.2%; Pred. No. 1.4e-14;
Matches 42; Conservative 22; Mismatches 43; Indels 6; Gaps 4;

QY 4 TNYCFRNLENCVVRPLYIDFRQDLGWK-WVHEPKGYANFCSGPCPYLRSAD---TTHS 59
Db 398 SDYNGSELKTACKKHELYVSF-QDLGWQWITAPKGYANYCDGECSPFLNAHMHATNHA 456

QY 60 TVLGLYNTLNPEASAPCCVPQDLEPLTILYVGRTPKV-EQLSNMVKSKCK 111
Db 457 IVQTLVHLNPEYVPRCCAPTCLNAISVLVYFDNSNVILKRYNNMVRACGC 509

RESULT 33
ID GDF8_CHICK STANDARD; PRT; 375 AA.
AC O42220;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update).
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE GROWTH/DIFFERENTIATION FACTOR 8 PRECURSOR (GDF-8) (MYOSTATIN).
GN GDF8 OR MSTN.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN-WHITE LEGHORN; TISSUE=Skeletal muscle;
RX MEDLINE=98024153; PubMed=9356471;
RA McPherron A.C., Lee S.-J.;
RT "Double muscling in cattle due to mutations in the myostatin gene.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:12457-12461(1997).
CC -!- FUNCTION: ACTS SPECIFICALLY AS A NEGATIVE REGULATOR OF SKELETAL
CC MUSCLE GROWTH.
CC -!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC
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CC
CC EMBL; AF019621; AAB86688.1;
CC InterPro; IPR001111;
CC InterPro; IPR001839;
CC Pfam; PF00019; TGF-beta; 1.
CC Pfam; PF00688; TGF-beta; 1.
CC PROSITE; PS00250; TGF-BETA_1; 1.
KW Growth factor; Cytokine; Glycoprotein; Signal.
FT SIGNAL 1 23 POTENTIAL.
FT PROPEP 24 266 POTENTIAL.
FT CHAIN 267 375 GROWTH/DIFFERENTIATION FACTOR 8.

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FT DISULFID 281 340 BY SIMILARITY.
FT DISULFID 309 372 BY SIMILARITY.
FT DISULFID 313 374 BY SIMILARITY.
FT DISULFID 339 374 INTERCHAIN (BY SIMILARITY).
FT CARBOHYD 71 71 N-LINKED (GLCNAC... ) (POTENTIAL).
SQ SEQUENCE 375 AA; 42707 MW; DA732DB9426E4D4F CRC64;

Query Match 32.3%; Score 204.5; DB 1; Length 375;
Best Local Similarity 39.4%; Pred. No. 1.1e-14;
Matches 41; Conservative 15; Mismatches 39; Indels 9; Gaps 4;

QY 12 EENCVRPLDYDFRODLGWKWHPEKGYANFCSGPCP--YLRSDTHTSTVLGLYNTLN 69
DB 278 ESRCCRYPLTVDF-EAFGWDWIIAPRYKANYCSGCEFEVLQKYPHTH-----LVHQAN 331
QY 70 PEASAPCCVPQDLPLTILYVGRTPKV-EQLSNMVKSCKCS 112
DB 332 PRGSAGPCTPTKMSPINLDFMGKEQIIYKGIPAMVVDRCGCS 375

RESULT 34
GDF8_HUMAN
ID GDF8_HUMAN STANDARD; PRT; 375 AA.
AC O14793;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE GROWTH/DIFFERENTIATION FACTOR 8 PRECURSOR (GDF-8) (MYOSTATIN).
GN GDF8 OR MSTN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RX MEDLINE=98024153; PubMed=9356471;
RA McPherron A.C., Lee S.-J.;
RT "Double muscling in cattle due to mutations in the myostatin gene.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:12457-12461(1997).
CC -!- FUNCTION: ACTS SPECIFICALLY AS A NEGATIVE REGULATOR OF SKELETAL
CC MUSCLE GROWTH.
CC -!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC -----
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CC -----
DR EMBL; AF019627; AAB86694.1; -.
DR MIM; 601788; -.
DR InterPro; IPR001111; -.
DR InterPro; IPR001839; -.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGF-beta; 1.
DR PROSITE; PS00250; TGF_BETA_1; 1.
DR Growth factor; Cytokine; Glycoprotein; Signal.
FT SIGNAL 1 23
FT PROPEP 24 266
FT CHAIN 267 375
FT DISULFID 281 340
FT DISULFID 309 372
FT DISULFID 313 374
FT DISULFID 339 374
FT CARBOHYD 71 71
FT SEQUENCE 375 AA; 42750 MW; EBF6129725E6AFA CRC64;

Query Match 32.3%; Score 204.5; DB 1; Length 375;
Best Local Similarity 39.4%; Pred. No. 1.1e-14;
Matches 41; Conservative 15; Mismatches 39; Indels 9; Gaps 4;

QY 12 EENCVRPLDYDFRODLGWKWHPEKGYANFCSGPCP--YLRSDTHTSTVLGLYNTLN 69
DB 278 ESRCCRYPLTVDF-EAFGWDWIIAPRYKANYCSGCEFEVLQKYPHTH-----LVHQAN 331
QY 70 PEASAPCCVPQDLPLTILYVGRTPKV-EQLSNMVKSCKCS 112
DB 332 PRGSAGPCTPTKMSPINLDFMGKEQIIYKGIPAMVVDRCGCS 375

RESULT 34
GDF8_HUMAN
ID GDF8_HUMAN STANDARD; PRT; 375 AA.
AC O14793;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE GROWTH/DIFFERENTIATION FACTOR 8 PRECURSOR (GDF-8) (MYOSTATIN).
GN GDF8 OR MSTN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RX MEDLINE=98024153; PubMed=9356471;
RA McPherron A.C., Lee S.-J.;
RT "Double muscling in cattle due to mutations in the myostatin gene.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:12457-12461(1997).
CC -!- FUNCTION: ACTS SPECIFICALLY AS A NEGATIVE REGULATOR OF SKELETAL
CC MUSCLE GROWTH.
CC -!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF019627; AAB86694.1; -.
DR MIM; 601788; -.
DR InterPro; IPR001111; -.
DR InterPro; IPR001839; -.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGF-beta; 1.
DR PROSITE; PS00250; TGF_BETA_1; 1.
DR Growth factor; Cytokine; Glycoprotein; Signal.
FT SIGNAL 1 23
FT PROPEP 24 266
FT CHAIN 267 375
FT DISULFID 281 340
FT DISULFID 309 372
FT DISULFID 313 374
FT DISULFID 339 374
FT CARBOHYD 71 71
FT SEQUENCE 375 AA; 42750 MW; EBF6129725E6AFA CRC64;

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```

Query Match 32.3%; Score 204.5; DB 1; Length 375;
Best Local Similarity 39.4%; Pred. No. 1.1e-14;
Matches 41; Conservative 15; Mismatches 39; Indels 9; Gaps 4;

QY 12 EENCVRPLDYDFRODLGWKWHPEKGYANFCSGPCP--YLRSDTHTSTVLGLYNTLN 69
DB 278 ESRCCRYPLTVDF-EAFGWDWIIAPRYKANYCSGCEFEVLQKYPHTH-----LVHQAN 331
QY 70 PEASAPCCVPQDLPLTILYVGRTPKV-EQLSNMVKSCKCS 112
DB 332 PRGSAGPCTPTKMSPINLDFMGKEQIIYKGIPAMVVDRCGCS 375

RESULT 35
GDF8_MELGA
ID GDF8_MELGA STANDARD; PRT; 375 AA.
AC O42221;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE GROWTH/DIFFERENTIATION FACTOR 8 PRECURSOR (GDF-8) (MYOSTATIN).
GN GDF8 OR MSTN.
OS Meleagris gallopavo (Common turkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Meleagridae; Meleagris.
OX NCBI_TaxID=9103;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RX MEDLINE=98024153; PubMed=9356471;
RA McPherron A.C., Lee S.-J.;
RT "Double muscling in cattle due to mutations in the myostatin gene.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:12457-12461(1997).
CC -!- FUNCTION: ACTS SPECIFICALLY AS A NEGATIVE REGULATOR OF SKELETAL
CC MUSCLE GROWTH.
CC -!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
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CC -----
DR EMBL; AF019625; AAB86692.1; ALT_INIT.
DR InterPro; IPR001111; -.
DR InterPro; IPR001839; -.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGF-beta; 1.
DR PROSITE; PS00250; TGF_BETA_1; 1.
DR Growth factor; Cytokine; Glycoprotein; Signal.
FT SIGNAL 1 23
FT PROPEP 24 266
FT CHAIN 267 375
FT DISULFID 281 340
FT DISULFID 309 372
FT DISULFID 313 374
FT DISULFID 339 339
FT CARBOHYD 71 71
FT SEQUENCE 375 AA; 42784 MW; D2AEAB732AE84E77 CRC64;

Query Match 32.3%; Score 204.5; DB 1; Length 375;
Best Local Similarity 39.4%; Pred. No. 1.1e-14;
Matches 41; Conservative 15; Mismatches 39; Indels 9; Gaps 4;

QY 12 EENCVRPLDYDFRODLGWKWHPEKGYANFCSGPCP--YLRSDTHTSTVLGLYNTLN 69
DB 278 ESRCCRYPLTVDF-EAFGWDWIIAPRYKANYCSGCEFEVLQKYPHTH-----LVHQAN 331
QY 70 PEASAPCCVPQDLPLTILYVGRTPKV-EQLSNMVKSCKCS 112

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	Query Match	32.3%; Score 204.5; DB 1; Length 375;
	Best Local Similarity	39.4%; Pred. No. 1.le-14;
	Matches	41; Conservative 15; Mismatches 39; Indels 9; Gaps 4;
QY	12	BENCCVRLYIDFRDQLGKWHKPYANFCGPGCP--YLSADTHTHVTGLYLTLN 69
DB	278	ESRCCRYPPLTVDF-EAFGWDMIIAPKRYKANYCGECEFVLQKYPHTH-----LVHQAN 331
QY	70	PEASAPCCVPQDLPLTYLYVGRTPKV-EOLSNMVMVKSCKS 112
DB	332	PRSGAGCCTPTKMPSPINMLYFNGKEQLIYGKIPAMVVDRGGCS 375
RESULT 37		
GDF8_MOUSE		
ID	GDF8_MOUSE	STANDARD; PRT; 376 AA.
AC	O08689;	
DT	01-NOV-1997 (Rel. 35, Created)	
DT	01-NOV-1997 (Rel. 35, Last sequence update)	
DT	30-MAY-2000 (Rel. 39, Last annotation update)	
DE	GROWTH/DIFFERENTIATION FACTOR 8 PRECURSOR (GDF-8) (MYOSTATIN).	
GN	GDF8 OR MSTN.	
OS	Mus musculus (Mouse).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
OX	NCBI_TaxID=10090;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=DUCO, HAMPSHIRE, MEISHAN, & YORKSHIRE; TISSUE=Skeletal muscle;	
RX	MEDLINE=97284412; PubMed=9139826;	
RA	McPherron A.C., Lawler A.M., Lee S.-J.;	
RT	"Regulation of skeletal muscle mass in mice by a new TGF-beta superfamily member.";	
RL	Nature 387:83-90(1997).	
CC	-!- FUNCTION: ACTS SPECIFICALLY AS A NEGATIVE REGULATOR OF SKELETAL MUSCLE GROWTH.	
CC	-!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).	
CC	-!- TISSUE SPECIFICITY: EXPRESSED SPECIFICALLY IN DEVELOPING AND ADULT SKELETAL MUSCLE. WEAK EXPRESSION IN ADIPOSE TISSUE.	
CC	-!- DEVELOPMENTAL STAGE: FIRST DETECTED AT DAY 9.5 POST-COITUM IN ONE-THIRD OF DEVELOPING SOMITES. AT LATER STAGES OF DEVELOPMENT, DETECTED IN A WIDE RANGE OF DEVELOPING MUSCLES. EXPRESSION CONTINUES IN ADULTHOOD.	
CC	-!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.	
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CC	EMBL; U04005; AAC53167.1; -	
DR	HSSP; P18075; IBMP.	
DR	MGI; 95691; Mstn.	
DR	InterPro; IPR001111; -	
DR	InterPro; IPR001839; -	
DR	Pfam; PF00019; TGF-beta; 1.	
DR	Pfam; PF00688; TGFB_propeptide; 1.	
DR	PROSITE; PS00250; TGF_BETA_1; 1.	
KW	Growth factor; Cytokine; Glycoprotein; Signal.	
FT	SIGNAL	1 24 POTENTIAL.
FT	PROPEP	25 267 POTENTIAL.
FT	CHAIN	268 376 GROWTH/DIFFERENTIATION FACTOR 8.
FT	DISELFD	282 341 BY SIMILARITY.
FT	DISELFD	310 373 BY SIMILARITY.
FT	DISELFD	314 375 BY SIMILARITY.
FT	DISELFD	340 340 INTERCHAIN (BY SIMILARITY).
FT	CARBOHYD	72 72 N-LINKED (GLCNAC...) (POTENTIAL).
SQ	SEQUENCE	376 AA; 42921 MW; 3E19814DDG2C08BE CRC64;

QY	70	PEASAPCCVPQDLEPLTILYYVGRTPRV-EQLSNMVMVKSCKS	112
Db	333	PRGSAGPCCTPTKMSPINMLYFNGKEQIILYGIKIPAMVVDRCGS	376

RESULT 39
DVR1_BRARE
ID DVR1_BRARE STANDARD; PRT; 355 AA.

01-JUN-1994 (Rel. 29, Created)
DT
01-JUN-1994 (Rel. 29, Last sequence update)
DT
15-JUL-1999 (Rel. 38, Last annotation update)
DT
DVR-1 PROTEIN PRECURSOR.
DE

GN
VGL OR DVR-1.
OS Brachydanio rerio (zebrafish) (zebra danio).
OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Cypriniformes; Cyprinidae; Rasbora; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=94009920; PubMed=8405668;
RA Helde K.A., Grunwald D.J.;
RT "The DVR-1 (Vgl) transcript of zebrafish is maternally supplied and
RT distributed throughout the embryo.";
RL Dev. Biol. 159:418-426(1993).
CC -1- FUNCTION: SERVES TO FACILITATE THE DIFFERENTIATION OF EITHER
CC MESODERM OR ENDODERM EITHER AS A COFACTOR IN AN INSTRUCTIVE
CC SIGNAL OR BY PROVIDING PERMISSIVE ENVIRONMENT.
CC -1- SUBUNIT: HOMODIMER (PROBABLE).
CC -1- TISSUE SPECIFICITY: ABUNDANT IN OVARIES AND EGGS, AND EQUALLY
CC DISTRIBUTED AMONG ALL BLASTOMERES.
CC -1- DEVELOPMENTAL STAGE: CONCENTRATED IN THE STREAMING CYTOPLASM IN
CC JUST-FERTILIZED EGGS. EVENLY PARTITIONED DURING CLEAVAGE AMONG ALL
CC BLASTOMERES. ABSENT IN THE YOLK CELL DURING CLEAVAGE, BLASTULA AND
CC GASTRULA STAGES. DISTRIBUTED HOMOGENEOUSLY AMONG ALL CELLS OF THE
CC GASTRULA.

1. SIMILARITY: BELONGS TO THE IG-BETA FAMILY.

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EMBL; U00931; AAC27347.1; -.
DR HSP; P18075; 1BMP.
DR ZFIN; ZDB-GENE-980526-389; vgl.
DR InterPro; IPR001111; -.
DR InterPro; IPR001839; -.
DR InterPro; IPR002400; -.
DR Pfam; PF000019; TGF-beta; 1.
DR Pfam; PF00688; TGFb_propeptide; 1.
DR PRINTS; PR00438; GFCYSKNOT.
DR PROSITE; PS00250; TGF_BETA_1; 1.
KW Growth factor; Mitogen; Glycoprotein; Signal.
FT SIGNAL 1 15 POTENTIAL.
FT PROPEP 16 240 POTENTIAL.
FT CHAIN 241 355 DVR-1 PROTEIN.
FT DISULFID 254 320 BY SIMILARITY.

1	DISULFID	207	38	DR SIMILARITY	INTERCHAIN (BY SIMILARITY).
T	DISULFID	319	319	N-LINKED (GLCNAC. .)	(POTENT)
T	CARBOHYD	108	108	N-LINKED (GLCNAC. .)	(POTENT)
T	CARBOHYD	179	179	N-LINKED (GLCNAC. .)	(POTENT)
T	CARBOHYD	296	296	N-LINKED (GLCNAC. .)	(POTENT)
T	CARBOHYD	355	AA;	40201 MW;	0ED5B9850EBFB222 CRC64;
Q	SEQUENCE				
Query Match		32.2%;	Score 204;	DB 1;	Length 355;

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FT CARBOHYD 165 165 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 425 AA; 47565 MW; C910F7F64FF82F67 CRC64;

Query Match 32.2%; Score 204; DB 1; Length 425;
Best Local Similarity 38.3%; Pred. No. 1.5e-14;
Matches 41; Conservative 20; Mismatches 36; Indels 10; Gaps 5;

QY 15 CCVRLPIDRQDLGWR-WVHEPKGYANRCSGPCP-----YLRSADTHTSTVLGLNYTL 68
Db 320 CCKKQFTVSFK-DIGNDWIIAPSGYHANCYCEGCPSHIAGTSGGSFSTVINHYRMR 378
QY 69 --NPEASASPCVQDLEPLTILY-VGRTPKVBQLSNMVVKCKCS 112
Db 379 GHSPFANLKSCCVPTKLPRMSMLYDDGQNIKDIQNMIVECCGS 425

RESULT 41
ID GDFB_MOUSE STANDARD; PRT; 405 AA.
AC Q921M4; Q9QX55; Q9R221;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE GROWTH/DIFFERENTIATION FACTOR 11 PRECURSOR (BONE MORPHOGENETIC PROTEIN
GN 11).
GN GDF11 OR BMP11.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99177155; PubMed=10075854;
RA Gamer L.W., Wolfman N.M., Celeste A.J., Hattersley G., Hewick R.,
RT Rosen V.;
RT "A novel BMP expressed in developing mouse limb, spinal cord, and tail
RL bud is a potent mesoderm inducer in Xenopus embryos.";
RN Dev. Biol. 208:222-232(1999).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=129/SVJ;
RN MEDLINE=993118097; PubMed=10391213;
RA McPherron A.C., Lawler A.M., Lee S.-J.;
RT "Regulation of anterior/posterior patterning of the axial skeleton by
RN growth/differentiation factor 11.";
RN Nat. Genet. 22:260-264(1999).
RN [3]
RP SEQUENCE OF 75-405 FROM N.A.
RX MEDLINE=99173787; PubMed=10072786;
RA Nakashima M., Toyono T., Akamine A., Joyner A.;
RT "Expression of growth/differentiation factor 11, a new member of the
RN BMP/TGF-beta superfamily during mouse embryogenesis.";
RN Mech. Dev. 80:185-189(1999).
CC -1- FUNCTION: SECRETED SIGNAL THAT ACTS GLOBALLY TO SPECIFY POSITIONAL
CC IDENTITY ALONG THE ANTERIOR/POSTERIOR AXIS DURING DEVELOPMENT.
CC PLAY CRITICAL ROLES IN PATTERNING BOTH MESODERMAL AND NEURAL
CC TISSUES AND IN ESTABLISHING THE SKELETAL PATTERN.
CC -1- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: SECRETED (PROBABLE).
CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN THE DEVELOPING LIMB BUD.
CC INITIALLY DETECTED IN THE DISTAL MESENCHYME, AND LATER LOCALIZING
CC TO REGIONS AROUND THE DEVELOPING BONES. IS ALSO EXPRESSED IN ADULT
CC DENTAL PULP AND BRAIN.
CC -1- DEVELOPMENTAL STAGE: FIRST STRONGLY EXPRESSED IN RESTRICTED
CC DOMAINS AT 8.5 DAYS POST COITUS (DPC) WHERE IT IS HIGHEST IN THE
CC TAIL BUD. AT 10.5 DPC, EXPRESSED IN THE BRANCHIAL ARCHES, LIMB
CC BUD, TAIL BUD AND POSTERIOR DORSAL NEURAL TUBE. LATER, EXPRESSED
CC IN TERMINALLY-DIFFERENTIATED ODONTOBLASTS, THE NASAL EPITHELIUM,
CC RETINA AND SPECIFIC REGIONS OF THE BRAIN.
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; AF100906; AAC72853.1; --
 DR EMBL; AF100904; AAC72853.1; JOINED.
 DR EMBL; AF100905; AAC72853.1; JOINED.
 DR EMBL; AF028337; AAF21633.1; --
 DR EMBL; AF028335; AAF21633.1; JOINED.
 DR EMBL; AF028336; AAF21633.1; JOINED.
 DR EMBL; AF028334; AAF21633.1; --
 DR MGD; MGI:1338027; Gdf11.
 DR HSP; PI8075; IBMP.
 DR InterPro; IPR001111; --
 DR InterPro; IPR001839; --
 DR Pfam; PF00688; TGF-beta; 1.
 DR Pfam; PF00688; TGF-beta; 1.
 DR PROSITE; PS00250; TGF_BETA; 1.
 KW Growth factor; Cytokine; Glycoprotein; Signal.
 FT SIGNAL 1 20
 FT PROPEP 21 296
 FT CHAIN 297 405
 FT DOMAIN 29 39
 FT DOMAIN 208 213
 FT DISULFID 311 370
 FT DISULFID 339 402
 FT DISULFID 343 404
 FT DISULFID 369 369
 FT CARBOHYD 92 92
 FT CONFLICT 75 75
 FT CONFLICT 171 171
 FT SIGNAL 1 20
 FT PROPEP 25 298
 FT CHAIN 299 407
 FT DOMAIN 29 41
 FT DOMAIN 210 215
 FT DISULFID 313 372
 FT DISULFID 341 404
 FT DISULFID 345 406
 FT DISULFID 371 371
 FT CARBOHYD 94 94
 SQ SEQUENCE 405 AA; 44946 MW; A74E382710A14781 CRC64;
 Query Match 32.0%; Score 203; DB 1; Length 405;
 Best Local Similarity 36.7%; Pred. No. 1.8e-14;
 Matches 44; Conservative 11; Mismatches 39; Indels 26; Gaps 5;
 QY 9 RNL-----EENCVRPLYIDFRDLGKWKVHEPKGYANFCGPGCPYLRSADTTHS 59
 Db 296 RNLGLDCDEHSSRCRCRYPLTVDF-EAFGWDWIAPKRYKANYCGSGCEYMFQKYPHT 354
 QY 60 TVLGLYNTLNPEASPCCPVQDLEPLTILY-----VGRTPKVEQLSNMVKSCKS 112
 Db 355 ---HLVQANPRGSAGPCCTPTKMSPINLNFNDKQOIIYKIP-----GMVYDRCGCS 405
 RESULT 42
 GDFB_HUMAN
 ID GDFB_HUMAN STANDARD; PRT; 407 AA.
 AC O95390; Q9UID1; Q9UID2;
 DT 01-OCT-2000 (Rel. 40, Created)
 DT 01-OCT-2000 (Rel. 40, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE GROWTH/DIFFERENTIATION FACTOR 11 PRECURSOR (BONE MORPHOGENETIC PROTEIN
 DE 11).
 GN GDF11 OR BMP11.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Fetal brain;
 RX MEDLINE=99177155; PubMed=10075854;
 RA Ganser L.W., Wolfman N.M., Celeste A.J., Hattersley G., Hewick R.,
 RA Rosen V.;
 RT "A novel BMP expressed in developing mouse limb, spinal cord, and tail
 RT bud is a potent mesoderm inducer in Xenopus embryos.";
 RL Dev. Biol. 208:222-232(1999).

RN SEQUENCE FROM N.A.
 RP MEDLINE=99318097; PubMed=10391213;
 RX McPherron A.C., Lawler A.M., Lee S.-J.;
 RA "Regulation of anterior/posterior patterning of the axial skeleton by
 RT growth/differentiation factor 11";
 RL Nat. Genet. 22:260-264(1999).
 CC -1- FUNCTION: SECRETED SIGNAL THAT ACTS GLOBALLY TO SPECIFY POSITIONAL
 CC IDENTITY ALONG THE ANTERIOR/POSTERIOR AXIS DURING DEVELOPMENT.
 CC PLAY CRITICAL ROLES IN PATTERNING BOTH MESODERMAL AND NEURAL
 CC TISSUES AND IN ESTABLISHING THE SKELETAL PATTERN.
 CC -1- SUBUNIT: HOMODIMER. DISULFIDE-LINKED (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: SECRETED (PROBABLE).
 CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
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 CC -----
 DR EMBL; AF100907; AAC72852.1; --
 DR EMBL; AF028333; AAF21630.1; --
 DR EMBL; AF028334; AAF21631.1; --
 DR MIM; 603936; --
 DR HSP; PI8075; IBMP.
 DR InterPro; IPR001111; --
 DR InterPro; IPR001839; --
 DR Pfam; PF00019; TGF-beta; 1.
 DR Pfam; PF00688; TGF-beta; 1.
 DR PROSITE; PS00250; TGF_BETA; 1.
 KW Growth factor; Cytokine; Glycoprotein; Signal.
 FT SIGNAL 1 24
 FT PROPEP 25 298
 FT CHAIN 299 407
 FT DOMAIN 29 41
 FT DOMAIN 210 215
 FT DISULFID 313 372
 FT DISULFID 341 404
 FT DISULFID 345 406
 FT DISULFID 371 371
 FT CARBOHYD 94 94
 SQ SEQUENCE 407 AA; 45090 MW; E8FF48E3635BA8 CRC64;
 Query Match 32.0%; Score 203; DB 1; Length 407;
 Best Local Similarity 36.7%; Pred. No. 1.8e-14;
 Matches 44; Conservative 11; Mismatches 39; Indels 26; Gaps 5;
 QY 9 RNL-----EENCVRPLYIDFRDLGKWKVHEPKGYANFCGPGCPYLRSADTTHS 59
 Db 298 RNLGLDCDEHSSRCRCRYPLTVDF-EAFGWDWIAPKRYKANYCGSGCEYMFQKYPHT 356
 QY 60 TVLGLYNTLNPEASPCCPVQDLEPLTILY-----VGRTPKVEQLSNMVKSCKS 112
 Db 357 ---HLVQANPRGSAGPCCTPTKMSPINLNFNDKQOIIYKIP-----GMVYDRCGCS 407
 RESULT 43
 GDF8_BOVIN
 ID GDF8_BOVIN STANDARD; PRT; 375 AA.
 AC O18836; O18829;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE GROWTH/DIFFERENTIATION FACTOR 8 PRECURSOR (GDF-8) (MYOSTATIN).
 GN GDF8 OR MSTN OR MH.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
 OC Bovidae; Bovinae; Bos.

[illegible]

DR	PROSITE; PS00250; TGF_BETA-1; 1.
KW	Follitropin inhibitor; Contraceptive; Hormone; Glycoprotein; Signal.
FT	SIGNAL 1 20
FT	PROPEP 21 308
FT	CHAIN 309 424
FT	INHIBIN BETA A CHAIN.
FT	DISULFID 312 320
FT	BY SIMILARITY.
FT	DISULFID 319 389
FT	BY SIMILARITY.
FT	DISULFID 348 421
FT	BY SIMILARITY.
FT	DISULFID 352 423
FT	BY SIMILARITY.
FT	INTERCHAIN (BY SIMILARITY).
FT	CARBOHYD 165 165
FT	N-LINKED (GLCNAC...) (POTENTIAL).
FT	SEQUENCE 424 AA; 47476 MW; 4368C62226DFAF52 CRC64;
QY	Query Match 31.5%; Score 200; DB 1; Length 424;
DB	Best Local Similarity 37.4%; Pred. No. 3.9e-14;
DB	Matches 40; Conservative 21; Mismatches 36; Indels 10; Gaps 5;
QY	15 CCVRPLVYIDPRQDLGWK-WHEHPKGYANFCGSPCP-----YLSADTHSTVIGLVNTL 68
DB	319 CCKQKFVSPK-DIGWNDWIIAPSHYHANYCEGPCSHAGTSGSSLSFHSVTVINHYRMR 377
QY	69 --NPEASASCCVPDLEPLTILYV-WGRTPKVQLSNMVMKSKCS 112
DB	378 GHSPFANLKSCVPTKLRPMSMLYDDGQNTIKKIDQNMIVEECGS 424
RESULT 46	
INHBA_RAT	
ID	INHBA_RAT STANDARD; PRT; 424 AA.
AC	P18331;
DT	01-NOV-1990 (Rel. 16, Created)
DT	01-NOV-1990 (Rel. 16, Last sequence update)
DT	01-OCT-2000 (Rel. 40, Last annotation update)
DE	INHIBIN BETA A CHAIN PRECURSOR (ACTIVIN BETA-A CHAIN).
GN	INHBA.
OS	Rattus norvegicus (Rat).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX	NCBI_TaxID=10116;
RP	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=91042598; PubMed=3153478;
RA	Woduff T.K., Meunier H., Jones P.B.C., Hsueh A.J.W., Mayo K.E.;
RT	"Rat inhibin: molecular cloning of alpha- and beta-subunit
RT	complementary deoxyribonucleic acids and expression in the ovary.";
RL	Mol. Endocrinol. 1:561-568(1987).
CC	-1- FUNCTION: INHIBIN IS A GONADAL GLYCOPETIDE THAT INHIBITS THE
CC	SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND. ON THE OTHER HAND
CC	ACTIVIN ACTIVATES THE SECRETION OF FOLLITROPIN. ACTIVIN IS ALSO
CC	IMPORTANT IN EMBRYONIC AXIAL DEVELOPMENT.
CC	-1- SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE BONDS.
CC	INHIBIN A IS A DIMER OF ALPHA AND BETA-A.
CC	INHIBIN B IS A DIMER OF ALPHA AND BETA-B.
CC	ACTIVIN A IS A DIMER OF BETA-A.
CC	ACTIVIN AB IS A DIMER OF BETA-A AND BETA-B.
CC	-1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC	-----
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CC	or send an email to license@isb-sib.ch).
CC	-----
DR	EMBL; M37482; AAA41436.1; -.
DR	PIR; B40056; B40056.
DR	HSP; P18075; IBMP.
DR	InterPro; IPR000491; -.
DR	InterPro; IPR001111; -.
DR	InterPro; IPR001839; -.
DR	InterPro; IPR002400; -.

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DR Pfam: PF00019; TGF-beta; 1.
DR Pfam: PF00688; TGF-beta; 1.
DR PRINTS: PR00438; GFCYSKNOT.
DR PRINTS: PR00670; INHIBINB.
DR PROSITE: PS00250; TGF_BETA_1; 1.
KW Follitropin inhibitor; Contrapeptive; Hormone; Glycoprotein; Signal.
FT SIGNAL 1 20
FT CHAIN 21 308
FT PROPEP 309 424
FT CHAIN 309 424
FT DISULFID 312 320
FT DISULFID 319 389
FT DISULFID 348 421
FT DISULFID 352 423
FT DISULFID 388 388
FT CARBOHYD 165 165
SQ SEQUENCE 424 AA; 47406 MW; B2DAF791FA50984 CRC64;

Query Match 31.5%; Score 200; DB 1; Length 424;
Best Local Similarity 37.4%; Pred. No. 3.9e-14;
Matches 40; Conservative 21; Mismatches 36; Indels 10; Gaps 5;

Qy 15 CCVRPLYIDFRODLGK-WVHEPKGYANFCGPGP-----YLRSDTTHSTVLGLYNTL 68
Db 319 CCKKQFFVSEFK-DIGNDWIITAPSGYHANYCEGCPHSHAGTSGSSLSFHSIVINHMR 377
Qy 69 --NPEASAPCCVPQDLEPLTILY-VGRTPKVEQLSNMVKSCKCS 112
Db 378 GHSPFANLKSCCVPTKLRPMSLMYDDGQNIKKDIQNMIIVECGCS 424

RESULT 47
IHBA_BOVIN STANDARD; PRT; 425 AA.
AC P07995;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE INHIBIN BETA A CHAIN PRECURSOR (ACTIVIN BETA-A CHAIN).
GN INHBA.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP TISSUE=Liver.
RC MEDLINE=95112839; PubMed=7813465;
RA Thompson D.A., Cronin C.N., Martin F.;
RT "Genomic cloning and sequence analyses of the bovine alpha-, beta A-
RT and beta B-inhibin/activin genes. Identification of transcription
RT factor AP-2-binding sites in the 5'-flanking regions by DNase I
RT footprinting";
RL Eur. J. Biochem. 226:751-764(1994).
RN [2]
SQ SEQUENCE OF 258-425 FROM N.A.
RC TISSUE=Follicular fluid;
RX MEDLINE=86205842; PubMed=3458167;
RA Forage R.G., Ring J.M., Brown R.W., McInerney B.V., Cobon G.S.,
RA Gregson R.P., Robertson D.M., Morgan F.J., Hearn M.T.W., Findlay J.K.,
RA Wattenhall R.E.H., Burger H.G., de Kretser D.M.;
RT "Cloning and sequence analysis of cDNA species coding for the two
RT subunits of inhibin from bovine follicular fluid.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:3091-3095(1986).
CC -I- FUNCTION: INHIBIN IS A GONADAL GLYCOPROTEIN THAT INHIBITS THE
CC SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND. ON THE OTHER HAND
CC ACTIVIN ACTIVATES THE SECRETION OF FOLLITROPIN. ON THE OTHER HAND
CC IMPORTANT IN EMBRYONIC AXIAL DEVELOPMENT.
CC -I- SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE BONDS.
CC INHIBIN A IS A DIMER OF ALPHA AND BETA-A.
CC INHIBIN B IS A DIMER OF ALPHA AND BETA-B.
CC ACTIVIN A IS A DIMER OF BETA-A.

CC ACTIVIN AB IS A DIMER OF BETA-A AND BETA-B.
CC -I- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
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CC or send an email to license@isb-sib.ch).
CC EMBL: U16239; AAB60627.1;
CC EMBL: U16238; AAB60627.1; JOINED.
CC EMBL: M13274; AAA97415.1;
CC PIR: B25732; B25732.
CC HSSP: P18075; 1BMP.
CC InterPro: IPR000491;
CC InterPro: IPR001111;
CC InterPro: IPR001839;
CC InterPro: IPR002400;
CC Pfam: PF00019; TGF-beta; 1.
CC PRINTS: PR00438; GFCYSKNOT.
CC PRINTS: PR00670; INHIBINB.
CC PROSITE: PS00250; TGF_BETA_1; 1.
KW Follitropin inhibitor; Contrapeptive; Hormone; Glycoprotein;
Signal.
FT SIGNAL 1 20
FT PROPEP 21 309
FT CHAIN 310 425
FT DISULFID 313 321
FT DISULFID 320 390
FT DISULFID 349 422
FT DISULFID 353 424
FT DISULFID 389 389
FT CARBOHYD 165 165
SQ SEQUENCE 425 AA; 47521 MW; 2D8799D7197CDA37 CRC64;

Query Match 31.5%; Score 200; DB 1; Length 425;
Best Local Similarity 37.4%; Pred. No. 4e-14;
Matches 40; Conservative 21; Mismatches 36; Indels 10; Gaps 5;

Qy 15 CCVRPLYIDFRODLGK-WVHEPKGYANFCGPGP-----YLRSDTTHSTVLGLYNTL 68
Db 320 CCKKQFFVSEFK-DIGNDWIITAPSGYHANYCEGCPHSHAGTSGSSLSFHSIVINHMR 378
Qy 69 --NPEASAPCCVPQDLEPLTILY-VGRTPKVEQLSNMVKSCKCS 112
Db 379 GHSPFANLKSCCVPTKLRPMSLMYDDGQNIKKDIQNMIIVECGCS 425

RESULT 48
IHBA_HUMAN STANDARD; PRT; 426 AA.
AC P08476; Q14599;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE INHIBIN BETA A CHAIN PRECURSOR (ACTIVIN BETA-A CHAIN) (ERYTHROID
DE DIFFERENTIATION PROTEIN) (EDF).
GN INHBA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86186863; PubMed=3754442;
RA Mason A.J., Niall H.D., Seeburg P.H.;
RT "Structure of two human ovarian inhibins.";
RL Biochem. Biophys. Res. Commun. 135:957-964(1986).
RN [2]
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RX SEQUENCE FROM N.A.
RX MEDLINE=88190086; PubMed=3267209;
RA Murata M., Eto Y., Shibai H., Sakai M., Muramatsu M.;
RT "Erythroid differentiation factor is encoded by the same mRNA as that
RT of the inhibin beta A chain.";
RN Proc. Natl. Acad. Sci. U.S.A. 85:2434-2438(1988).
[3]
RN SEQUENCE FROM N.A.
RX MEDLINE=92135888; PubMed=1777673;
RA Tanimoto K., Handa S.I., Ueno N., Murakami K., Fukamizu A.;
RT "Structure and sequence analysis of the human activin beta A subunit
RT gene.";
RN DNA Seq. 2:103-110(1991).
[4]
RN SEQUENCE OF 311-426 FROM N.A.
RX MEDLINE=87005283; PubMed=3758355;
RA Stewart A.G., Milbrow H.M., Ring J.M., Crowther C.E., Forage R.G.;
RT "Human inhibin genes. Genomic characterisation and sequencing.";
RN FEBS Lett. 206:329-334(1986).
[5]
RN SEQUENCE OF 311-426 FROM N.A.
RC TISSUE=Testis;
RA Berg H., Walter M., Northmann W.;
RL Submitted (MAY-1993) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: INHIBIN IS A GONADAL GLYCOPROTEIN THAT INHIBITS THE
CC SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND. ON THE OTHER HAND
CC ACTIVIN ACTIVATES THE SECRETION OF FOLLITROPIN. ACTIVIN IS ALSO
CC IMPORTANT IN EMBRYONIC AXIAL DEVELOPMENT.
CC -!- SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE BONDS.
CC INHIBIN A IS A DIMER OF ALPHA AND BETA-A.
CC INHIBIN B IS A DIMER OF ALPHA AND BETA-B.
CC ACTIVIN A IS A DIMER OF BETA-A.
CC ACTIVIN AB IS A DIMER OF BETA-A AND BETA-B.
CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC
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CC -----
DR EMBL; M13436; AAA59168.1; -
DR EMBL; X04447; CAA28041.1; -
DR EMBL; X57578; CAA40805.1; -
DR EMBL; X57579; CAA40805.1; JOINED.
DR EMBL; J03634; AAA35787.1; -
DR EMBL; A14422; CAA01159.1; -
DR EMBL; X72498; CAA51163.1; -
DR PIR; A30884; A30884.
DR PIR; B24248; B24248.
DR PIR; B23556; B23556.
DR PIR; S30488; S30488.
DR HSSP; P18075; LBMP.
DR MIM; 147290; -.
DR InterPro; IPR000491; -.
DR InterPro; IPR001111; -.
DR InterPro; IPR001839; -.
DR InterPro; IPR002400; -.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGF-beta; 1.
DR PRINTS; PR00438; GFCYSKNOT.
DR PRINTS; PR00670; INHIBINBA.
DR PROSITE; PS00250; TGF_BETA_1; 1.
KW Follitropin inhibitor; Contraceptive; Hormone; Glycoprotein; Signal.
FT SIGNAL 1 20
FT PROPEP 21 310
FT CHAIN 311 426
FT DISULFID 314 322
FT DISULFID 321 391
FT DISULFID 350 423

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FT DISULFID 354 425
FT DISULFID 390 390
FT CARBOHYD 165 165
FT CONFLICT 377 379
SQ SEQUENCE 426 AA; 47442 MW; 201CDEDF99CB6919 CRC64;
BY SIMILARITY.
INTERCHAIN (BY SIMILARITY).
N-LINKED (GLCNAC. . .) (POTENTIAL).
RMR -> AC (IN REF. 5).
Query Match 31.5%; Score 200; DB 1; Length 426;
Best Local Similarity 37.4%; Pred. No. 4e-14;
Matches 40; Conservative 21; Mismatches 36; Indels 10; Gaps 5;
QY 15 CCVRPLYIDFQDLGKWK-WVHEPKGYANFCSGPCP-----YLRADTTHSTVGLYNTL 68
Db 321 CKKQKFFVSFK-DIGWNDWIITAPSGYHANYCEGECPSHAGTSGSLSPHSTVINHRMR 379
QY 69 --NPEASASPCVQDLEPLILY-VGRTPKVEOLSNMNVKSCKCS 112
Db 380 GHSPFANLKSCCVTKLRPMMLYDDQNIKKDIQNIWIVECGCS 426
RESULT 49
60A_DROVI
ID 60A_DROVI STANDARD; PRT; 436 AA.
AC Q24735;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE 60A PROTEIN PRECURSOR (GLASS BOTTOM BOAT PROTEIN).
GN GBB OR 60A OR TGF-beta-60A.
OS Drosophila virilis (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7244;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96305349; PubMed=8688461;
RA Du W., Doctor J.S.;
RT "Isolation and sequence of the Drosophila virilis 60 A gene, a
RT transforming growth factor-beta superfamily member related to
RT vertebrate bone morphogenetic proteins.";
RL Biochim. Biophys. Acta 1307:273-279(1996).
CC -!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U48595; AAC47262.1; -.
DR HSSP; P18075; LBMP.
DR FlyBase; FBgn0015681; Dvir\gbb.
DR InterPro; IPR001111; -.
DR InterPro; IPR001839; -.
DR InterPro; IPR002400; -.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGF-beta; 1.
DR PRINTS; PR00438; GFCYSKNOT.
DR PROSITE; PS00250; TGF_BETA_1; 1.
KW Growth factor; Cytokine; Glycoprotein; Signal.
FT SIGNAL 1 27
FT PROPEP 28 317
FT CHAIN 318 436
FT DISULFID 335 401
FT DISULFID 364 433
FT DISULFID 368 435
FT DISULFID 400 400
FT CARBOHYD 102 102
FT CARBOHYD 114 114

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FT CARBOHYD 217 217 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 229 229 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 377 377 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 436 AA; 49999 MW; C744B4AE58796692 CRC64;

Query Match 30.8%; Score 195.5; DB 1; Length 436;
Best Local Similarity 39.18; Pred. No. 1.2e-13;
Matches 45; Conservative 18; Mismatches 43; Indels 9; Gaps 5;

QY 5 NYCERNLEEN---CCVRPLYIDFRODLGW-KWVHEPKGYANFCGPGCYLRSD---TT 57
Db 322 NPFIENSIENTRSCOMQTLIDFK-DLGWDHDIAPAEGYAFYCSGECNFPNNAHMNATN 380
QY 58 HSTVLGLYNTLNPRASAPCCVPQDLEPLTILYYVG-RTPKVEQLSNMVKSCCK 111
Db 381 HAIVQTLVHLLPEKVRPKPCAPTRLGALPVLVHLNDENVNLKKYRNMIKSCGC 435

RESULT 50
60A_DROME STANDARD; PRT; 455 AA.
AC P27091; Q9W114;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE 60A PROTEIN PRECURSOR (GLASS BOTTOM BOAT PROTEIN)
GN GBB OR 60A OR TGFB-60A OR CG5562.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RX SEQUENCE FROM N.A.
RA Wharton K.A., Thomson G.H., Gelbart W.M.;
RT "Drosophila 60A gene, another transforming growth factor beta family member, is closely related to human bone morphogenetic proteins.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:9214-9218(1991).
RN [2]
RX SEQUENCE FROM N.A.
RA MEDLINE=92290120; PubMed=1601181;
RA Doctor J.S., Jackson P.D., Rashka K.E., Visalli M., Hoffmann F.M.;
RT "Sequence, biochemical characterization, and developmental expression of a new member of the TGF-beta superfamily in Drosophila melanogaster.";
RL Dev. Biol. 151:491-505(1992).
RN [3]
RX SEQUENCE FROM N.A.
RA STRAIN=BERKELEY;
RA MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Anantides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Vandal M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler J., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Fosler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
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RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarly C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reineut K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RL "The genome sequence of Drosophila melanogaster.";
Science 287:2185-2195(2000).
CC -!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED.
CC -!- DEVELOPMENTAL STAGE: EXPRESSED THROUGHOUT DEVELOPMENT WITH PEAKS
CC OF TRANSCRIPTION DURING EARLY EMBRYOGENESIS, IN PUPAE, AND IN
CC ADULT MALES.
CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC -----
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CC -----
CC EMBL; M77012; AAA28306.1; -
CC DR EMBL; M84795; AAA28307.1; -
CC DR EMBL; AE003462; AAF47075.1; -
CC DR PIR; A41233; A41233.
CC DR PIR; A43918; A43918.
CC DR HSSP; P18075; IBMP.
CC DR FlyBase; FBgn0024234; gbb.
CC DR InterPro; IPR001111; -
CC DR InterPro; IPR001839; -
CC DR InterPro; IPR002400; -
CC DR Pfam; PF00019; TGF-beta; 1.
CC DR Pfam; PF00688; TGF-beta-propeptide; 1.
CC DR PRINTS; PR00438; GFCYSKNOT.
CC DR PROSITE; PS00250; TGF_BETA_1; 1.
KW Growth factor; Cytokine; Glycoprotein; Signal.
FT SIGNAL 1 36
FT PROPEP 37 335
FT CHAIN 336 455
FT DISULFID 354 420
FT DISULFID 383 452
FT DISULFID 387 454
FT DISULFID 419 419
FT CARBOHYD 238 238
FT CARBOHYD 250 250
FT CARBOHYD 396 396
SQ SEQUENCE 455 AA; 51687 MW; C8FA795556341F94 CRC64;

Query Match 30.8%; Score 195; DB 1; Length 455;
Best Local Similarity 39.8%; Pred. No. 1.5e-13;
Matches 41; Conservative 19; Mismatches 37; Indels 6; Gaps 4;

QY 14 NCVCVRLYIDFRODLGW-KWVHEPKGYANFCGPGCYLRSD---TTHTVGLYNTLN 69
Db 353 SQCMQTLIDFK-DLGWDHDIAPAEGYAFYCSGECNFPNNAHMNATNHAIVQTLVHLL 411
QY 70 PRASAPCCVPQDLEPLTILYYVG-RTPKVEQLSNMVKSCCK 111
Db 412 PKKVPKPCAPTRLGALPVLVHLNDENVNLKKYRNMIKSCGC 454

RESULT 51
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Query Match	30.2%	Score 191.5	DB 1	Length 391
Best Local Similarity	38.3%	Pred. No. 3e-13		
Matches 41	Conservative 20	Mismatches 35	Indels 11	Gaps 7
QY 15	CCVRPLYIDRQDLGKW-VWHEPKGYANECGPCP-YLR----	SADTTHSTVLGLYNT-	67	
Db 287	CCRQFFYIDRFL-IGWNWDIIAPSGYGYNCBSCPAYLAGVPGSASSFHTAVVNYRMR	345		
QY 68	-LNPEASASPCPDLEPLTILYVGRTPKVEQ-LSNMVVKSKCS	112		
Db 346	GLNP-GTVNSCCPTKLTSMYLFDDDEYNIVKRDVPMIVECGCA	391		
RESULT 52				
INHA_CHK				
ID INHA_CHK	STANDARD;	PRT;	424 AA.	
AC P27092;	Q90697;			
DT 01-AUG-1992	(Rel. 23, Created)			
DT 01-NOV-1995	(Rel. 32, Last sequence update)			
DT 01-OCT-2000	(Rel. 40, Last annotation update)			
DE INHIBIN BETA A CHAIN PRECURSOR (ACTIVIN BETA-A CHAIN).				
GN INHBA				
OS Gallus gallus (Chicken).				
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;				
OC Gallus.				
OX NCBI_TaxID=9031;				
RN [1]				
RP SEQUENCE FROM N.A.				
RC STRAIN=WHITE LEGHORN;				
RA MEDLINE=96380183; PubMed=8788196;				
RX Chen C.C., Johnson P.A.;				
RT "Molecular cloning of inhibin/activin beta A-subunit complementary				
RT deoxyribonucleic acid and expression of inhibin/activin alpha- and				
RT beta A-subunits in the domestic hen.;"				
RL Biol. Reprod. 54:429-435(1996).				
RN [3]				
RP SEQUENCE OF 317-349 FROM N.A.				
RC TISSUE=Hypoblast;				
RC MEDLINE=91029482; PubMed=2225063;				
RX Mitrani E., Ziv T., Thomsen G., Shimoni Y., Melton D.A., Brill A.;				
RA "Activin can induce the formation of axial structures and is				
RT expressed in the hypoblast of the chick.;"				
RL Cell 63:495-501(1990).				
CC -! FUNCTION: INHIBIN IS A GONADAL GLYCOPROTEIN THAT INHIBITS THE				
CC SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND. ON THE OTHER HAND				
CC ACTIVIN ACTIVATES THE SECRETION OF FOLLITROPIN. ACTIVIN IS ALSO				
CC IMPORTANT IN EMBRYONIC AXIAL DEVELOPMENT.				
CC -! SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE BONDS.				
CC INHIBIN A IS A DIMER OF ALPHA AND BETA-A.				
CC INHIBIN B IS A DIMER OF ALPHA AND BETA-B.				
CC ACTIVIN A IS A DIMER OF BETA-A.				
CC ACTIVIN AB IS A DIMER OF BETA-A AND BETA-B.				
CC -! SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.				
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CC or send an email to license@isb-sib.ch).				
CC -----				
DR EMBL; U26946; AAA68174.1;				
DR EMBL; U42377; AAC59738.1;				
DR EMBL; M61167; AAA48569.1;				


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SQ SEQUENCE 426 AA; 48965 MW; 6401D5151AC97117 CRC64;

Query Match 29.5%; Score 187; DB 1; Length 426;
Best Local Similarity 35.2%; Pred. No. 9.8e-13;
Matches 38; Conservative 23; Mismatches 41; Indels 6; Gaps 4;

QY 9 RNLENCVRLYIDFRODLGK-WVHEPKGYANFCSPCPYLBSA---DTHTSTVGLGL 64
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 319 RFLQAKCKHLEVSFR-DLGQDWIITAPTYGYNYCEGCPAYLAGVPGSASFHTAVVNOYRMR 377
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |

QY 65 YNTLNPRASAPCCVPQDLEPLTILYVGRTPKV-EQLSNMVVKSCKC 111
: | | | | | | | | | | | : | | | | | : | | | | |

Db 378 VHFNPETVPKPCAPTQLNGISVLFDSDSANVLKKNMVVQKCGC 425
: | | | | | | | | | | | : | | | | | : | | | | |

RESULT 56
ID INBB_PIG STANDARD; PRT; 349 AA.
AC P04088;

DT 01-NOV-1986 (Rel. 03, Created)
DT 01-NOV-1986 (Rel. 03, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE INHIBIN BETA B CHAIN PRECURSOR (ACTIVIN BETA-B CHAIN) (FRAGMENT).
GN INHBB.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Ovarian follicular fluid;
RX MEDLINE=86092207; PubMed=2417121;
RA Mason A.J., Hayflick J.S., Ling N., Esch F., Ueno N., Ying S.-Y.,
RA Guillemin R., Niall H., Seeburg P.H.;
RT "Complementary DNA sequences of ovarian follicular fluid inhibin show
RT precursor structure and homology with transforming growth
RT factor-beta.";
RL Nature 318:659-663(1985).
RN [2]
RP SEQUENCE OF 235-249.
RX MEDLINE=92355604; PubMed=1644823;
RA Nakamura T., Asashima M., Eto Y., Takio K., Uchiyama H., Moriya N.,
RA Arizumi T., Yoshino T., Sugino K., Titani K., Sugino H.;
RT "Isolation and characterization of native activin B.";
RL J. Biol. Chem. 267:16385-16389(1992).
CC -1- FUNCTION: INHIBIN IS A GONADAL GLYCOPROTEIN THAT INHIBITS THE
CC SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND. ON THE OTHER HAND
CC ACTIVIN ACTIVATES THE SECRETION OF FOLLITROPIN. ACTIVIN IS ALSO
CC IMPORTANT IN EMBRYONIC AXIAL DEVELOPMENT.
CC -1- SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE BONDS.
CC INHIBIN A IS A DIMER OF ALPHA AND BETA-A.
CC INHIBIN B IS A DIMER OF ALPHA AND BETA-B.
CC ACTIVIN A IS A DIMER OF BETA-A.
CC ACTIVIN AB IS A DIMER OF BETA-A AND BETA-B.
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC -----
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CC -----
CC EMBL; X03267; CAA27021.1; -
CC PIR; A01394; WFEGBB.
CC HSSP; P18075; 1BMP.
CC InterPro; IPR001111; -
CC InterPro; IPR001839; -
CC Pfam; PF00019; TGF-beta; 1.
CC Pfam; PF00688; TGFB_propeptide; 1.
CC PROSITE; PS00250; TGF_BETA_1; 1.

```

```

KW Follitropin inhibitor; Contraceptive; Hormone; Glycoprotein.
FT NON_TER 1
FT PROPEP <1 234
FT CHAIN 235 349 INHIBIN BETA B CHAIN.
FT DISULFID 238 246 BY SIMILARITY.
FT DISULFID 245 314 BY SIMILARITY.
FT DISULFID 274 346 BY SIMILARITY.
FT DISULFID 278 348 BY SIMILARITY.
FT DISULFID 313 313 INTERCHAIN (BY SIMILARITY).
FT CARBOHYD 35 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 349 AA; 39354 MW; C571EA91ADA5DE77 CRC64;

Query Match 29.4%; Score 186.5; DB 1; Length 349;
Best Local Similarity 37.4%; Pred. No. 9e-13;
Matches 40; Conservative 21; Mismatches 35; Indels 11; Gaps 7;

QY 15 CCVRPLYIDFRODLGK-WVHEPKGYANFCSPCP-YLR-----SADTHSTVGLYNT- 67
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 245 CCRQOFFIDFRL-IGWSDWIIAPTGYGYNYCEGCPAYLAGVPGSASFHTAVVNOYRMR 303
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |

QY 68 -LNPRASAPCCVPQDLEPLTILYVGRTPKVQO-LSNMVVKSCKCS 112
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 304 GLNP-GTVNSCCIPTKLSTMSMLYDFDDEYNIVKRVDPNMIVEECGCA 349

RESULT 57
ID INBB_HUMAN STANDARD; PRT; 407 AA.
AC P09529;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE INHIBIN BETA B CHAIN PRECURSOR (ACTIVIN BETA-B CHAIN).
GN INHBB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90114200; PubMed=2575216;
RA Mason A.J., Berkmeier L.M., Schmelzer C.H., Schwall R.H.;
RT "Activin B; precursor sequences, genomic structure and in vitro
RT activities.";
RL Mol. Endocrinol. 3:1352-1358(1989).
RN [2]
RP SEQUENCE OF 22-407 FROM N.A.
RX MEDLINE=89295443; PubMed=2739657;
RA Feng Z.M., Baird C.W., Chen C.L.;
RT "Characterization and regulation of testicular inhibin beta-subunit
RT mRNA.";
RL Mol. Endocrinol. 3:939-948(1989).
RN [3]
RP SEQUENCE OF 55-407 FROM N.A.
RX MEDLINE=86186863; PubMed=3754442;
RA Mason A.J., Niall H.D., Seeburg P.H.;
RT "Structure of two human ovarian inhibins.";
RL Biochem. Biophys. Res. Commun. 135:957-964(1986).
CC -1- FUNCTION: INHIBIN IS A GONADAL GLYCOPROTEIN THAT INHIBITS THE
CC SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND. ON THE OTHER HAND
CC ACTIVIN ACTIVATES THE SECRETION OF FOLLITROPIN. ACTIVIN IS ALSO
CC IMPORTANT IN EMBRYONIC AXIAL DEVELOPMENT.
CC -1- SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE BONDS.
CC INHIBIN A IS A DIMER OF ALPHA AND BETA-A.
CC INHIBIN B IS A DIMER OF ALPHA AND BETA-B.
CC ACTIVIN A IS A DIMER OF BETA-A.
CC ACTIVIN AB IS A DIMER OF BETA-A AND BETA-B.
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC -----
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GN BMP7 OR BMP-7 OR OP1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91354237; PubMed=1715687;
RT Oezkaynak E., Schneegelsberg P.N.J., Oppermann H.;
RT "Murine osteogenic protein (OP-1): high levels of mRNA in kidney.";
RL Biochem. Biophys. Res. Commun. 179:116-123(1991).
CC -1- FUNCTION: INDUCES CARTILAGE AND BONE FORMATION. MAY BE THE
CC OSTEOINDUCTIVE FACTOR RESPONSIBLE FOR THE PHENOMENON OF
CC EPITHELIAL OSTEOGENESIS. PLAYS A ROLE IN CALCIUM REGULATION
CC AND BONE HOMEOSTASIS.
CC -1- SUBUNIT: HOMODIMER, DISULFIDE-LINKED.
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
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DR EMBL; X56906; CAA40222.1; -.
DR PIR; J01184; J01184.
DR HSP; P18075; IBMP.
DR MGD; MG1:103302; Bmp7.
DR InterPro; IPR001111; -.
DR InterPro; IPR001839; -.
DR InterPro; IPR002400; -.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGF-beta; 1.
DR PRINTS; PR00438; GFCYSKNOT.
DR PROSITE; PS00250; TGF_BETA_1; 1.
KW Signal; Growth factor; Cytokine; Bone; Cartilage; Glycoprotein.
FT SIGNAL 1 29 POTENTIAL.
FT PROPEP 30 231 POTENTIAL.
FT CHAIN 292 430 BONE MORPHOGENETIC PROTEIN 7.
FT DISULFID 329 395 BY SIMILARITY.
FT DISULFID 358 427 BY SIMILARITY.
FT DISULFID 362 429 BY SIMILARITY.
FT DISULFID 394 394 INTERCHAIN (BY SIMILARITY).
FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 301 301 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 320 320 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 371 371 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 430 AA; 49283 MW; 486C36DD97754047 CRC64;

Query Match 28.9%; Score 183; DB 1; Length 430;
Best Local Similarity 35.3%; Pred. No. 2.7e-12;
Matches 36; Conservative 22; Mismatches 38; Indels 6; Gaps 4;

QY 15 CCVRPLIDFRQDLGNK-WVHEPKGYANFCSPGCPYLRSA---DTHSTVGLYNTLNP 70
| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 329 CKKHLYVSFR-DLQWQDIIAPEGAAAYCEGECAPPLNSYMNATNHAIVQTLVHPINP 387
: ||| | | : ||| : : : ||| : | : : ||| : | : : ||| : | : : |||

QY 71 EASASPCVPQDLPTILYVGRTPKV-EQLSNMVVKSCKC 111
: ||| | | : ||| : : : ||| : | : : ||| : | : : |||

Db 388 DTVPKCCAPTQLNAISLVYFDSSNVILKKYRNMVVRACG 429

RESULT 62
BMP2_RAT
ID BMP2_MOUSE STANDARD; PRT; 393 AA.
AC P49001;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE BONE MORPHOGENETIC PROTEIN 2 PRECURSOR (BMP-2) (BMP-2A).

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GN BMP2 OR BMP-2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Bone;
RT Feng J.Q., Chen D., Feng M., Harris M.A., Mundy G.R., Harris S.E.;
RT Submitted (SEP-1993) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: INDUCES CARTILAGE AND BONE FORMATION.
CC -1- SUBUNIT: HOMODIMER, DISULFIDE-LINKED.
CC -1- TISSUE SPECIFICITY: FEMUR, CALVARIA, TRACHEA, LUNG AND OVARY.
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; Z58668; CAA81088.1; -.
DR HSP; P18075; IBMP.
DR InterPro; IPR001111; -.
DR InterPro; IPR001839; -.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGF-beta; 1.
DR PROSITE; PS00250; TGF_BETA_1; 1.
KW Signal; Growth factor; Cytokine; Bone; Cartilage; Glycoprotein.
FT SIGNAL 1 19 POTENTIAL.
FT PROPEP 20 279 BONE MORPHOGENETIC PROTEIN 2.
FT CHAIN 280 393 BY SIMILARITY.
FT DISULFID 293 358 BY SIMILARITY.
FT DISULFID 322 390 BY SIMILARITY.
FT DISULFID 326 392 BY SIMILARITY.
FT DISULFID 357 357 INTERCHAIN (BY SIMILARITY).
FT CARBOHYD 133 133 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 161 161 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 197 197 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 335 335 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 393 AA; 44383 MW; 7D20865852E0F213 CRC64;

Query Match 28.8%; Score 182.5; DB 1; Length 393;
Best Local Similarity 37.7%; Pred. No. 2.7e-12;
Matches 43; Conservative 21; Mismatches 31; Indels 19; Gaps 8;

QY 9 RNLENCVRLPYIDFRQDLGNK-WVHEPKGYANFCSPGCPY-----LRSADTTHSTVL 62
: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 287 KRLSSCKRHPLYVDF-SDVGNDWDIVAPPGYHAFYCHGECPPPLADHLNS--TNHAIVQ 343
: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 63 GLYNTLN---PEASASPCVPQDLPTILYVGRTPKV-EQLSNMVVKSCKC 111
| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 344 TLVSNVSKIPKA---CCVTLSAISML-YLDENEKVLKYNQDMVVEGCGC 392

RESULT 63
BMP2_MOUSE
ID BMP2_MOUSE STANDARD; PRT; 394 AA.
AC P21274;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE BONE MORPHOGENETIC PROTEIN 2 PRECURSOR (BMP-2) (BMP-2A).
GN BMP2 OR BMP-2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.

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```

OS Dama dama (Fallow deer) (Cervus dama).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervidae;
OC Cervidae; Cervinae; Cervus.
OX NCBI_TaxID=30532;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Antler;
RX MEDLINE=97157076; PubMed=9003457;
RA Feng J.Q., Chen D., Ghosh-Choudhury N., Esparza J., Mundy G.R.,
RA Harris S.E.;
RT "Bone morphogenetic protein 2 transcripts in rapidly developing deer
RT antler tissue contain an extended 5' non-coding region arising from a
RT distal promoter.";
RL Biochim. Biophys. Acta 1350:47-52(1997).
CC -!- FUNCTION: INDUCES CARTILAGE AND BONE FORMATION.
CC -!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED.
CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AJ001817; CAA05033.1; -.
DR HSP; P18075; IBMF.
DR InterPro: IPR001111; -.
DR InterPro: IPR001839; -.
DR Pfam: PF00019; TGF-beta; 1.
DR Pfam: PF00688; TGF-beta; 1.
DR PROSITE: PS00250; TGF_BETA_1; 1.
DR Signal; Growth factor; Cytokine; Bone; Cartilage; Glycoprotein.
KW SIGNAL
FT SIGNAL 1 23 POTENTIAL.
FT PROPEP 24 282 BY SIMILARITY.
FT CHAIN 283 396 BONE MORPHOGENETIC PROTEIN 2.
FT DISULFID 296 361 BY SIMILARITY.
FT DISULFID 325 393 BY SIMILARITY.
FT DISULFID 329 395 BY SIMILARITY.
FT DISULFID 360 360 INTERCHAIN (BY SIMILARITY).
FT CARBOHYD 135 135 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 163 163 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 164 164 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 200 200 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 338 338 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT SEQUENCE 396 AA; 44646 MW; 5FE23A0AC7F91572 CRC64;

Query Match 28.8%; Score 182.5; DB 1; Length 396;
Best Local Similarity 37.7%; Pred. No. 2.8e-12;
Matches 43; Conservative 21; Mismatches 31; Indels 19; Gaps 8;

QY 9 RNLENCVVRPLVPRDGLGNK-WVHEPKGYVANCSPGCPY-----LRSDTTHSTVL 62
DB 290 KRLKSCXKRLPLVDP-SDGVNDWIVAPPYHAFYGCPCPLADHLNS--TNHAIQV 346

QY 63 GLYNTLN---PEASAPCCVPQDLEPLTILYVGRTPKV---EQLSNNVKSCKC 111
DB 347 TLVNSVNSKIPKA-----CCVPTLSAISML-YLDENEKVKVKNYQDMVVEGCC 395

RESULT 66
ID BMP2_HUMAN
AC P12643;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE BONE MORPHOGENETIC PROTEIN 2 PRECURSOR (BMP-2) (BMP-2A).
GN BMP2 OR BMP2A.
OS Homo sapiens (Human).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89072730; PubMed=3201241;
RA Wozney J.M., Rosen V., Celeste A.J., Mitsock L.M., Whitters M.J.,
RA Kriz R.W., Hewick R.M., Wang E.A.;
RT "Novel regulators of bone formation: molecular clones and
RT activities.";
RL Science 242:1528-1534(1988).
RN [2]
RP SEQUENCE FROM N.A.
RA Shore E.M., Xu M.-Q., Calvert G., Moriatis J., Kaplan F.S.;
RT "Human bone morphogenetic protein 2 (BMP-2) genomic DNA sequence.";
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Blakey S.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RX X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF 292-396.
RA Scheufler C., Sebald W., Huelsmeyer M.;
RT "Crystal structure of human bone morphogenetic protein-2 at 2.7 A
RT resolution.";
RL J. Mol. Biol. 287:103-115(1999).
CC -!- FUNCTION: INDUCES CARTILAGE AND BONE FORMATION.
CC -!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED.
CC -!- TISSUE SPECIFICITY: PARTICULARLY ABUNDANT IN LUNG, SPLEEN AND
CC COLON AND IN LOW BUT SIGNIFICANT LEVELS IN HEART, BRAIN, PLACENTA,
CC LIVER, SKELETAL MUSCLE, KIDNEY, PANCREAS, PROSTATE, OVARY AND
CC SMALL INTESTINE.
CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC -----
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CC -----
DR EMBL: M22489; AAA51834.1; -.
DR EMBL: AF040249; AAF21646.1; -.
DR EMBL: AL035668; CAB82007.1; -.
DR PIR: B37278; B37278.
DR PDB: 3BMP; 12-MAR-00.
DR TM: 112261; -.
DR InterPro: IPR001111; -.
DR InterPro: IPR001839; -.
DR Pfam: PF00019; TGF-beta; 1.
DR Pfam: PF00688; TGF-beta; 1.
DR PROSITE: PS00250; TGF_BETA_1; 1.
DR Signal; Growth factor; Cytokine; Bone; Cartilage; Glycoprotein;
KW 3D-STRUCTURE.
FT SIGNAL 1 23 POTENTIAL.
FT PROPEP 24 282 BONE MORPHOGENETIC PROTEIN 2.
FT CHAIN 283 396
FT DISULFID 296 361
FT DISULFID 325 393
FT DISULFID 329 395
FT DISULFID 360 360 INTERCHAIN.
FT CARBOHYD 135 135 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 163 163 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 164 164 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 200 200 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT SEQUENCE 396 AA; 44702 MW; 20653A3987B25E60 CRC64;

Query Match 28.8%; Score 182.5; DB 1; Length 396;
Best Local Similarity 37.7%; Pred. No. 2.8e-12;
Matches 43; Conservative 21; Mismatches 31; Indels 19; Gaps 8;

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QY 9 RNLEENCVRPLYIDFRODLGK-WVHEPKGYANFCSGPCPY-----LRSADTTHSTVL 62
Db 290 KRLKSSCRHPLYVDF-SDVGWMDWIVAPPGYHAFYCHGECPPPLADHLNS--TNHAIQV 346
QY 63 GLYNTLN---PEASASPCVPODLEPLTLTYVVGTRPKV--EQLSNMVVKSCKC 111
Db 347 TLVNSVNSKIPKA-----CCVPTLSAISML-YLDENEKVVLYQDMVVEGCGC 395

RESULT 67
BMPA_XENLA
ID BMPA_XENLA STANDARD; PRT; 398 AA.
AC P25703;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 01-JUL-1993 (Rel. 26, Last annotation update)
DE BONE MORPHOGENETIC PROTEIN 2-I PRECURSOR (BMP-2-I).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipiloidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=91274367; PubMed=2054389;
RA Plessow S., Koester M., Knoechel W.;
RT "cDNA sequence of Xenopus laevis bone morphogenetic protein 2
(BMP-2).";
RL Biochim. Biophys. Acta 1089:280-282(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=92378616; PubMed=1510675;
RX Nishimatsu S., Suzuki A., Shoda A., Murakami K., Ueno N.;
RT "Genes for bone morphogenetic proteins are differentially transcribed
in early amphibian embryos.";
RL Biochem. Biophys. Res. Commun. 186:1487-1495(1992).
CC -!- FUNCTION: INDUCES CARTILAGE AND BONE FORMATION.
CC -!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED.
CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.

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CC EMBL; X55031; CAA38850.1; -
DR EMBL; X63424; CAA45018.1; -
DR PIR; S16244; S16244.
DR PIR; JH0687; JH0687.
DR HSSP; P18075; IBMP.
DR InterPro; IPR001839; -
DR Pfam; PF00688; TGF-beta; 1.
DR InterPro; IPR001839; -
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGF-beta; 1.
DR PROSITE; PS00250; TGF-beta; 1.
DR PROSITE; PS00250; TGF-beta; 1.
KW Signal; Growth factor; Cytokine; Bone; Cartilage; Glycoprotein.
FT SIGNAL 1 23 POTENTIAL.
FT PROPEP 24 284 POTENTIAL.
FT CHAIN 285 398 BONE MORPHOGENETIC PROTEIN 2-I.
FT DISULFID 298 363 BY SIMILARITY.
FT DISULFID 327 395 BY SIMILARITY.
FT DISULFID 331 397 BY SIMILARITY.
FT DISULFID 362 362 INTERCHAIN (BY SIMILARITY).
FT CARBOHYD 137 137 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 202 202 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 340 340 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 7 7 S -> P (IN REF. 2).
FT CONFLICT 16 16 V -> L (IN REF. 2).
FT CONFLICT 233 233 N -> T (IN REF. 2).

SQ SEQUENCE 398 AA; 45575 MW; 150AC64A47D2E15F CRC64;
Query Match 28.8%; Score 182.5; DB 1; Length 398;
Best Local Similarity 37.7%; Pred. No. 2.8e-12;
Matches 43; Conservative 21; Mismatches 31; Indels 19; Gaps 8;
QY 9 RNLEENCVRPLYIDFRODLGK-WVHEPKGYANFCSGPCPY-----LRSADTTHSTVL 62
Db 292 KRLKSSCRHPLYVDF-SDVGWMDWIVAPPGYHAFYCHGECPPPLADHLNS--TNHAIQV 348
QY 63 GLYNTLN---PEASASPCVPODLEPLTLTYVVGTRPKV--EQLSNMVVKSCKC 111
Db 349 TLVNSVNTNIPKA-----CCVPTLSAISML-YLDENEKVVLYQDMVVEGCGC 397

RESULT 68
BMPB_XENLA
ID BMPB_XENLA STANDARD; PRT; 398 AA.
AC P30884;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE BONE MORPHOGENETIC PROTEIN 2-II PRECURSOR (BMP-2-II).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipiloidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92378616; PubMed=1510675;
RX Nishimatsu S., Suzuki A., Shoda A., Murakami K., Ueno N.;
RT "Genes for bone morphogenetic proteins are differentially transcribed
in early amphibian embryos.";
RL Biochem. Biophys. Res. Commun. 186:1487-1495(1992).
CC -!- FUNCTION: INDUCES CARTILAGE AND BONE FORMATION.
CC -!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED.
CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.

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CC EMBL; X63425; CAA45019.1; -
DR PIR; JH0688; JH0688.
DR HSSP; P18075; IBMP.
DR InterPro; IPR001839; -
DR InterPro; IPR001839; -
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGF-beta; 1.
DR PROSITE; PS00250; TGF-beta; 1.
DR PROSITE; PS00250; TGF-beta; 1.
KW Signal; Growth factor; Cytokine; Bone; Cartilage; Glycoprotein.
FT SIGNAL 1 23 POTENTIAL.
FT PROPEP 24 284 POTENTIAL.
FT CHAIN 285 398 BONE MORPHOGENETIC PROTEIN 2-II.
FT DISULFID 298 363 BY SIMILARITY.
FT DISULFID 327 395 BY SIMILARITY.
FT DISULFID 331 397 BY SIMILARITY.
FT DISULFID 362 362 INTERCHAIN (BY SIMILARITY).
FT CARBOHYD 137 137 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 202 202 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 237 237 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 340 340 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 398 AA; 45616 MW; 60E41FA2C8E603DC CRC64;
Query Match 28.8%; Score 182.5; DB 1; Length 398;
Best Local Similarity 37.7%; Pred. No. 2.8e-12;


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DR Pfam; PF00688; Tgfb_propeptide; 1.
DR PRINTS; PR00438; GFCYSKNOT.
DR PROSITE; PS00250; TGF_BETA_1; 1.
KW Signal; Growth factor; Cytokine; Glycoprotein.
FT SIGNAL 1 27
FT PROPEP 28 381
FT CHAIN 382 501
FT DISULFID 400 466
FT DISULFID 429 498
FT DISULFID 433 500
FT DISULFID 465 465
FT CARBOHYD 189 189
FT CONFLICT 38 38
FT CONFLICT 254 258
FT CONFLICT 276 276
FT CONFLICT 321 321
FT CONFLICT 384 384
SQ SEQUENCE 501 AA; 55640 MW; EF631EA03417A348 CRC64;

Query Match 28.7%; Score 182; DB 1; Length 501;
Best Local Similarity 37.0%; Pred. No. 4e-12;
Matches 40; Conservative 23; Mismatches 39; Indels 6; Gaps 5;

QY 9 RNLENCVRLPYIDFRODLGW-KWHEPKGYANFCGPGPY-IRS--ADTHSTVLGL 64
Db 394 NKLKARCSKALHVNFK-DMGWDDWIIAPLEYEAPHCGLCEFFPLRSHLEPTNHAIVOTL 452

QY 65 YNTLNPEASAPCCVPQDLEPLTILYYVGRTPKV-EQLSNMVVVKSCCK 111
Db 453 MNSMDPESTPTCCVPTLSPISILFIDSANNVYKQYEDMVVESCVC 500

RESULT 71
DVR1_STRPU STANDARD; PRT; 461 AA.
AC P48969;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE DVR-1 PROTEIN HOMOLOG PRECURSOR.
GN DVR1.
OS Strongylocentrotus purpuratus (Purple sea urchin).
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC Echinoidea; Euechinoidea; Echinacea; Echinoidea; Strongylocentrotidae;
OC Strongylocentrotus.
OX NCBI_TaxID=7668;
RN [1]
RP SEQUENCE FROM N.A.
RA Ponce M.R., Micol J.L., Davidson E.H.;
RL Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.
CC -1- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (PROBABLE).
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; Z48313; CAA88306.1; -
CC HSSP; P18075; LBMP.
CC InterPro; IPR001111; -
CC InterPro; IPR001839; -
CC Pfam; PF00019; TGF-beta; 1.
CC Pfam; PF00688; Tgfb_propeptide; 1.
CC PRINTS; PR00438; GFCYSKNOT.
KW PROSITE; PS00250; TGF_BETA_1; 1.
KW Growth factor; Cytokine; Glycoprotein; signal.
FT SIGNAL 1 30
FT SIGNAL 30

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FT PROPEP 31 338
FT CHAIN 339 461
FT DISULFID 360 426
FT DISULFID 389 458
FT DISULFID 393 460
FT DISULFID 425 425
FT CARBOHYD 149 149
FT CARBOHYD 402 402
SQ SEQUENCE 461 AA; 51881 MW; 2573D54B6625F7EF CRC64;

Query Match 28.5%; Score 181; DB 1; Length 461;
Best Local Similarity 34.6%; Pred. No. 4.7e-12;
Matches 37; Conservative 22; Mismatches 42; Indels 6; Gaps 4;

QY 10 NLENCVRLPYIDFRODLGW-KWHEPKGYANFCGPGPYLRSAD---TTHSTVLGL 65
Db 355 NSDWQCKRKNLFVNF-EDLDWQEWIIAPLGVAFYQCGECAFPLGHANATNHAIVOTLV 413

QY 66 NTLNPEASAPCCVPQDLEPLTILYY-VGRTPKVEQLSNMVVVKSCCK 111
Db 414 HHMSPSHVQPCCAPTKLSPITVLYYDDSRNVVLYKKYKNMVVRCGC 460

RESULT 72
IHBC_HUMAN STANDARD; PRT; 352 AA.
ID IHBC_HUMAN
AC P55103;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE INHIBIN BETA C CHAIN PRECURSOR (ACTIVIN BETA-C CHAIN).
GN INHBC.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Medline=95126961; PubMed=7826378;
RX Hoetten G., Neidhardt H., Schneider C., Pohl J.;
RT "Cloning of a new member of the TGF-beta family: a putative new
RT activin beta C chain.";
RL Biochem. Biophys. Res. Commun. 206:608-613(1995).
CC -1- FUNCTION: INHIBINS ARE GONADAL GLYCOPROTEIDS THAT INHIBIT THE
CC SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND. ON THE OTHER HAND
CC ACTIVINS ACTIVATE THE SECRETION OF FOLLITROPIN. ACTIVINS REGULATE
CC GROWTH AND DIFFERENTIATION OF EMBRYONAL CARCINOMA CELLS, INDUCE
CC ERYTHROPOIESIS, STIMULATE INSULIN SECRETION, AND PROMOTE NEURAL
CC CELL SURVIVAL. ACTIVINS ARE ALSO IMPORTANT IN EMBRYONIC AXIAL
CC DEVELOPMENT.
CC -1- SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE BONDS.
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC -----
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CC -----
CC EMBL; X82540; CAA57890.1; -
CC HSSP; P18075; LBMP.
CC MIM; 601233; -
CC InterPro; IPR001318; -
CC InterPro; IPR001839; -
CC InterPro; IPR002400; -
CC Pfam; PF00019; TGF-beta; 1.
CC PRINTS; PR00438; GFCYSKNOT.
CC PRINTS; PR00672; INHIBINBC.
CC PROSITE; PS00250; TGF_BETA_1; 1.

```

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KW Follitropin inhibitor; Contrapeptive; Hormone; Glycoprotein; Signal.
FT SIGNAL 1 18 POTENTIAL.
FT PROPEP 19 236
FT CHAIN 237 352 INHIBIN BETA C CHAIN.
FT DISULFID 240 248 BY SIMILARITY.
FT DISULFID 247 317 BY SIMILARITY.
FT DISULFID 276 349 BY SIMILARITY.
FT DISULFID 280 351 BY SIMILARITY.
FT DISULFID 316 316 INTERCHAIN (BY SIMILARITY).
FT CARBOHYD 110 110 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 143 143 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 161 161 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 352 AA; 38238 MW; 496476AD82562D3E CRC64;

Query Match 28.4%; Score 180; DB 1; Length 352;
Best Local Similarity 37.4%; Pred. No. 4.5e-12;
Matches 40; Conservative 19; Mismatches 38; Indels 10; Gaps 5;

QY 15 CCVRPLIDFRODLGW-KWHEPKGYANFCGCPYLRSD-ADTHSTVLGLY--N 66
|| : :||| :|| : :||| :||| :||| :||| :||| :||| :||| :|||
Dd 247 CCQREFFVDFR-EIGWHDWIIQEGYAMNFCIGQCPGLHAGMPGIAASFHTAVLNLLKAN 305

QY 67 TLNPEASPCVQDLEPLTILYVGRTPKVE-QLSNMVKSKCS 112
| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Dd 306 TAAGTGGSCCVPTARRPLSLLYDRDSNVKTDIPDMVVEACGCS 352

RESULT 73
IHBC_MOUSE
ID IHBC_MOUSE STANDARD; PRT; 352 AA.
AC P55104; Q61452;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE INHIBIN BETA C CHAIN PRECURSOR (ACTIVIN BETA-C CHAIN).
GN INHBC.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129; TISSUE=Liver;
RX MEDLINE=96435913; PubMed=8838799;
RA Schmitt J., Hoeten G., Jenkins N.A., Gilbert D.J., Copeland N.G.,
RA Pohl J., Schrewe H.;
RT "Structure, chromosomal localization, and expression analysis of the
RT mouse inhibin/activin beta C (Inhbc) gene.";
RL Genomics 32:358-366(1996).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96283807; PubMed=8679697;
RA Lau A.L., Nishimori K., Matzuk M.M.;
RT "Structural analysis of the mouse activin beta C gene.";
RL Biochim. Biophys. Acta 1307:145-148(1996).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=97224404; PubMed=9070865;
RA Fang J., Wang S.O., Smiley E., Bonadio J.;
RT "Genes coding for mouse activin beta C and beta E are closely linked
RT and exhibit a liver-specific expression pattern in adult tissues.";
RL Biochem. Biophys. Res. Commun. 231:655-661(1997).
CC -!- FUNCTION: INHIBINS ARE GONADAL GLYCOPROTEIDS THAT INHIBIT THE
CC SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND. ON THE OTHER HAND
CC ACTIVINS ACTIVATE THE SECRETION OF FOLLITROPIN. ACTIVINS REGULATE
CC GROWTH AND DIFFERENTIATION OF EMBRYONAL CARCINOMA CELLS, INDUCE
CC ERYTHROPOIESIS, STIMULATE INSULIN SECRETION, AND PROMOTE NEURAL
CC CELL SURVIVAL. ACTIVINS ARE ALSO IMPORTANT IN EMBRYONIC AXIAL
CC DEVELOPMENT.
CC -!- SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE BONDS.
CC -!- TISSUE SPECIFICITY: MAINLY EXPRESSED IN THE ADULT LIVER.
CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
```

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CC -----
CC EMBL; X90841; CAA62347.1; -.
CC EMBL; X90842; CAA62347.1; JOINED.
CC EMBL; X90819; CAA62333.1; -.
CC EMBL; U40773; AAC52723.1; -.
CC EMBL; U40772; AAC52723.1; JOINED.
CC EMBL; U95962; AAC53164.1; -.
CC HSSP; P18075; 1BMP.
CC MGD; MGI:105932; Inhbc.
CC InterPro; IPR001318; -.
CC InterPro; IPR001839; -.
CC InterPro; IPR002400; -.
CC Pfam; PF00019; TGF-beta; 1.
CC PRINTS; PR00438; GFCYSKNOT.
CC PRINTS; PR00672; INHIBINC.
CC PROSITE; PS00250; TGF_BETA_1; 1.
KW Follitropin inhibitor; Contrapeptive; Hormone; Glycoprotein; Signal.
FT SIGNAL 1 18 POTENTIAL.
FT PROPEP 19 236
FT CHAIN 237 352 INHIBIN BETA C CHAIN.
FT DISULFID 240 248 BY SIMILARITY.
FT DISULFID 247 317 BY SIMILARITY.
FT DISULFID 276 349 BY SIMILARITY.
FT DISULFID 280 351 BY SIMILARITY.
FT DISULFID 316 316 INTERCHAIN (BY SIMILARITY).
FT CARBOHYD 111 111 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 143 143 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 161 161 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 173 173 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 243 243 A -> G (IN REF. 1).
SQ SEQUENCE 352 AA; 39401 MW; 220812FD73717185 CRC64;

Query Match 28.4%; Score 180; DB 1; Length 352;
Best Local Similarity 37.8%; Pred. No. 4.5e-12;
Matches 42; Conservative 20; Mismatches 31; Indels 18; Gaps 7;

QY 15 CCVRPLIDFRODLGW-KWHEPKGYANFCGCPYLRSD-----TTSTVLGLYNT 67
|| : :||| :|| : :||| :||| :||| :||| :||| :||| :||| :|||
Dd 247 CCQREFFVDFR-EIGWHDWIIQEGYAMNFCIGQCP-LHVAGMPGISASFHTAVL---NL 301

QY 68 LNPEASA-----SPCCVPQDLEPLTILYVGRTPKVE-QLSNMVKSKCS 112
| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Dd 302 LKANAAGTGRGSCCVPTARRPLSLLYDRDSNVKTDIPDMVVEACGCS 352

RESULT 74
DECA_DROPS STANDARD; PRT; 621 AA.
AC P91699;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE DECAPENTAPLEGIC PROTEIN PRECURSOR (DPP-C PROTEIN).
GN DPP.
OS Drosophila pseudoobscura (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7237;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97225212; PubMed=9071585;
RA Newfield S.J., Padgett R.W., Findley S.D., Richter B.G., Sanicola M.,
RA de Cuevas M., Gelbart W.M.;
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RT "Molecular evolution at the decapentaplegic locus in Drosophila.";
CC GN 145:297-309(1997).
CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CC OX NCBI_TaxID=10090;
CC RN [1]
CC RP SEQUENCE FROM N.A.
CC RC STRAIN=BALE/C; TISSUE=Liver;
CC RX MEDLINE=94195427; PubMed=8145850;
CC RA Storm E.E., Huynh T.V., Copeland N.G., Jenkins N.A., Kingsley D.M.,
CC RA Lee S.-J.;
CC RT "Limb alterations in brachypodism mice due to mutations in a new
CC RT member of the TGF beta-superfamily.";
CC RL Nature 368:639-643(1994).
CC CC -!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
CC CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC CC -----
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CC CC -----
CC DR EMBL; U08338; AAA18779.1; .
CC DR HSSP; P18075; LBMP.
CC DR MGD; MGI:95689; Gdf6.
CC DR InterPro; IPR001839; .
CC DR Pfam; PF00019; TGF-beta; 1.
CC DR PROSITE; PS00250; TGF_BETA_1; 1.
CC KW Growth factor; Developmental protein; Differentiation; Glycoprotein;
CC KW Signal.
CC FT SIGNAL 1 15 POTENTIAL.
CC FT PROPEP 16 479 BY SIMILARITY.
CC FT CHAIN 480 621 DECAPENTAPLEGIC PROTEIN.
CC FT DISULFID 520 586 BY SIMILARITY.
CC FT DISULFID 549 618 BY SIMILARITY.
CC FT DISULFID 553 620 BY SIMILARITY.
CC FT DISULFID 585 585 INTERCHAIN (BY SIMILARITY).
CC FT DOMAIN 45 57 POLY-ALA.
CC FT DOMAIN 88 92 POLY-ASN.
CC FT DOMAIN 95 104 POLY-ASN.
CC FT DOMAIN 163 173 POLY-GLN.
CC FT DOMAIN 149 149 POLY-GLY.
CC FT CARBOHYD 149 149 N-LINKED (GLCNAC. .) (POTENTIAL).
CC FT CARBOHYD 365 365 N-LINKED (GLCNAC. .) (POTENTIAL).
CC FT CARBOHYD 400 400 N-LINKED (GLCNAC. .) (POTENTIAL).
CC FT CARBOHYD 562 562 N-LINKED (GLCNAC. .) (POTENTIAL).
CC SQ SEQUENCE 621 AA; 69038 MW; 3FD7141FB5509651 CRC64;

Query Match 28.4%; Score 180; DB 1; Length 621;
Best Local Similarity 38.5%; Pred. No. 8.2e-12;
Matches 42; Conservative 13; Mismatches 46; Indels 8; Gaps 5;

QY 9 RNLENCVRLYIDFRODLGW-KWVHEPKGYANFCGPGPYLRSD-THSTHTVLG 63
Db 514 KNEETCRRLHYVDF-ADVGDWDWIVAPPGYDAYCHGKCPF-PLADHFNSTNHAVQT 571

QY 64 LYNTINPEASPCVPODLEPLTILYVGR-TPKVEQLSNMVKSKC 111
Db 572 LVNNLPKVKPCVPTQLDSVAMLYLNDQSTVVLYKNYQEMTVVVGCG 620

RESULT 75
GDF6_MOUSE ID GDF6_MOUSE STANDARD; PRT; 125 AA.
AC P43028;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE GROWTH/DIFFERENTIATION FACTOR 6 PRECURSOR (GDF-6) (FRAGMENT).

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GN GDF6 OR GDF-6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALE/C; TISSUE=Liver;
RX MEDLINE=94195427; PubMed=8145850;
RA Storm E.E., Huynh T.V., Copeland N.G., Jenkins N.A., Kingsley D.M.,
RA Lee S.-J.;
RT "Limb alterations in brachypodism mice due to mutations in a new
RT member of the TGF beta-superfamily.";
RL Nature 368:639-643(1994).
CC CC -!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
CC CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
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CC CC -----
CC DR EMBL; U08338; AAA18779.1; .
CC DR HSSP; P18075; LBMP.
CC DR MGD; MGI:95689; Gdf6.
CC DR InterPro; IPR001839; .
CC DR Pfam; PF00019; TGF-beta; 1.
CC DR PROSITE; PS00250; TGF_BETA_1; 1.
CC KW Growth factor; Cytokine; Glycoprotein.
CC FT NON_TER 1 1
CC FT PROPEP <1 5 POTENTIAL.
CC FT CHAIN 6 125 GROWTH/DIFFERENTIATION FACTOR 6.
CC FT DISULFID 24 90 BY SIMILARITY.
CC FT DISULFID 53 122 BY SIMILARITY.
CC FT DISULFID 57 124 BY SIMILARITY.
CC FT DISULFID 89 89 INTERCHAIN (BY SIMILARITY).
CC SQ SEQUENCE 125 AA; 14373 MW; 10FA2A5B7748DA32 CRC64;

Query Match 28.2%; Score 179; DB 1; Length 125;
Best Local Similarity 38.2%; Pred. No. 2e-12;
Matches 39; Conservative 20; Mismatches 37; Indels 6; Gaps 5;

QY 15 CCVRPLYIDFRODLGW-KWVHEPKGYANFCGPGPY-LRS--ADTHSTVLGLYNTLP 70
Db 24 CSRKPLHVNFK-ELGWDWDWIAPLEAYVHCEGVCDFPLRSHLEPTNHAITQTLMSMDP 82

QY 71 EASAPCCVPODLEPLTILYI-VGRTPKVEQLSNMVKSKC 111
Db 83 GSTPSCCVPTKLTPTISILYIDAGNNVYKQYEDMVVESC 124

RESULT 76
BMP5_MOUSE ID BMP5_MOUSE STANDARD; PRT; 452 AA.
AC P49003;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE BONE MORPHOGENETIC PROTEIN 5 PRECURSOR (BMP-5).
GN BMP5 OR BMP-5.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C3H/KW;
RX MEDLINE=95046894; PubMed=7958439;
RA King J.A., Marker P.C., Seung K.J., Kingsley D.M.;

```

"BMP5 and the molecular, skeletal, and soft-tissue alterations in short ear mice.";
 Dev. Biol. 166:112-122(1994).
 CC -!- FUNCTION: INDUCES CARTILAGE AND BONE FORMATION.
 CC -!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
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 CC -----

DR EMBL; L41145; AAA64612.1; -;
 DR HSSP; P18075; BMP.
 DR MGD; MGI:88181; Bmp5.
 DR InterPro; IPR001111; -;
 DR InterPro; IPR001839; -;
 DR Pfam; PF00019; TGF-beta; 1.
 DR Pfam; PF00688; TGF-beta; 1.
 DR PRINTS; PR00438; GFCYSKNOT.
 DR PROSITE; PS00250; TGF_BETA_1; 1.
 DR Signal; Growth factor; Cytokine; Bone; Cartilage; Glycoprotein.
 FT SIGNAL 1 25 POTENTIAL.
 FT PROPEP 26 320 POTENTIAL.
 FT CHAIN 321 452 BONE MORPHOGENETIC PROTEIN 5.
 FT DISULFID 351 417 BY SIMILARITY.
 FT DISULFID 380 449 BY SIMILARITY.
 FT DISULFID 384 451 BY SIMILARITY.
 FT DISULFID 416 416 INTERCHAIN (BY SIMILARITY).
 FT CARBOHYD 209. 329 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 325 325 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 343 343 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 393 393 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 452 AA; 51511 MW; AAD9521EC94A78D5 CRC64;

Query Match 28.2%; Score 179; DB 1; Length 452;
 Best Local Similarity 35.2%; Pred. No. 7.5e-12;
 Matches 37; Conservative 22; Mismatches 40; Indels 6; Gaps 4;

QY 12 EENCCVRPLIDFRQDLGWK-WVHEPKGYANFCSPGCPYLRSD---TTHSTVLGLYNT 67
 Db 348 KOACKKHELYVSR-DLGWDQWIIAPEGYAFYCDGECFPLNAHNMATNHAIVQTLVHL 406
 QY 68 LNPEASASPCVPQDLPTILYVVGRTPKV-EOLSNMVKSKC 111
 Db 407 MFPDHPKCCAPTCLNAISLVYFDSSNVILKKYRNWVRSCGC 451

RESULT 77
 BMP5_HUMAN
 ID BMP5_HUMAN STANDARD; PRT; 454 AA.
 AC P22003; Q9NTW5;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE BONE MORPHOGENETIC PROTEIN 5 PRECURSOR (BMP-5).
 GN BMP5.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Bone;
 RX MEDLINE=91088608; PubMed=2263636;
 RA Celeste A.J., Iannaz J.A., Taylor R.C., Hewick R.M., Rosen V.,
 RA Wang E.A., Wozney J.M.;
 RT "Identification of transforming growth factor beta family members

RT present in bone-inductive protein purified from bovine bone.";
 RL Proc. Natl. Acad. Sci. U.S.A. 87:9843-9847(1990).
 RN [2]
 RP SEQUENCE OF 279-454 FROM N.A.
 RA Tracey A.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: INDUCES CARTILAGE AND BONE FORMATION.
 CC -!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
 CC -!- TISSUE SPECIFICITY: EXPRESSED IN THE LUNGS AND LIVER.
 CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
 CC
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 CC -----

DR EMBL; M60314; AAA36736.1; -;
 DR EMBL; AL133386; CAB81657.1; -;
 DR PIR; A39263; A39263.
 DR HSSP; P18075; BMP.
 DR MIM; I12265; -;
 DR InterPro; IPR001111; -;
 DR InterPro; IPR001839; -;
 DR InterPro; IPR002400; -;
 DR Pfam; PF00019; TGF-beta; 1.
 DR Pfam; PF00688; TGF-beta; 1.
 DR PRINTS; PR00438; GFCYSKNOT.
 DR PROSITE; PS00250; TGF_BETA_1; 1.
 DR Signal; Growth factor; Cytokine; Bone; Cartilage; Glycoprotein.
 FT SIGNAL 1 30 POTENTIAL.
 FT PROPEP 31 322 POTENTIAL.
 FT CHAIN 323 454 BONE MORPHOGENETIC PROTEIN 5.
 FT DISULFID 353 419 BY SIMILARITY.
 FT DISULFID 382 451 BY SIMILARITY.
 FT DISULFID 386 453 BY SIMILARITY.
 FT DISULFID 418 418 INTERCHAIN (BY SIMILARITY).
 FT CARBOHYD 211 211 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 327 327 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 345 345 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 395 395 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 454 AA; 51736 MW; 631277413CCC22EE CRC64;

Query Match 28.2%; Score 179; DB 1; Length 454;
 Best Local Similarity 35.2%; Pred. No. 7.5e-12;
 Matches 37; Conservative 22; Mismatches 40; Indels 6; Gaps 4;

QY 12 EENCCVRPLIDFRQDLGWK-WVHEPKGYANFCSPGCPYLRSD---TTHSTVLGLYNT 67
 Db 350 KOACKKHELYVSR-DLGWDQWIIAPEGYAFYCDGECFPLNAHNMATNHAIVQTLVHL 408

QY 68 LNPEASASPCVPQDLPTILYVVGRTPKV-EOLSNMVKSKC 111
 Db 409 MFPDHPKCCAPTCLNAISLVYFDSSNVILKKYRNWVRSCGC 453

RESULT 78
 GDF7_MOUSE
 ID GDF7_MOUSE STANDARD; PRT; 151 AA.
 AC P43029;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE GROWTH/DIFFERENTIATION FACTOR 7 PRECURSOR (GDF-7) (FRAGMENT).
 GN GDF7 OR GDF-7.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]


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CC -----
DR EMBL; AF101441; AAC77462.1; -.
DR HSSP; P18075; IBMP.
DR InterPro; IPR001111; -.
DR InterPro; IPR001839; -.
DR InterPro; IPR002405; -.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGF-beta-propeptide; 1.
DR PRINTS; PR00669; INHIBIN.
DR PROSITE; PS00250; TGF_BETA_1.
KW Signal; Growth factor; Cytokine; Glycoprotein.
KW SIGNAL 21 POTENTIAL.
FT PROPEP 22 316 POTENTIAL.
FT CHAIN 317 424 BONE MORPHOGENETIC PROTEIN 10.
FT DISULFID 323 389 BY SIMILARITY.
FT DISULFID 352 421 BY SIMILARITY.
FT DISULFID 356 423 BY SIMILARITY.
FT DISULFID 388 388 INTERCHAIN (BY SIMILARITY).
FT CARBOHYD 67 67 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 131 131 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 424 AA; 48047 MW; 3FDB3B7221BB2254 CRC64;

Query Match 27.5%; Score 174.5; DB 1; Length 424;
Best Local Similarity 37.6%; Pred. No. 2.1e-11;
Matches 41; Conservative 15; Mismatches 46; Indels 7; Gaps 5;

QY 9 RNLENCVVR-PLYIDFQDLGW-KWHEPKGYANFGSGPCPYLRS---ADTHTSTVLG 63
DB 316 RNAKGKRTPLLYIDFQ-ETGWDSWIAPPGEYAEKRGVGNVPLAEHLTPTKHAIQA 374
QY 64 LYNTLNPEASPCVCPQDLPLETLTY-VGRTPKVEQLSNMVKSKC 111
DB 375 LVHLKNSOKASACVPTKLEPISILYLDKGVVYTKYEGMAVSECGC 423

RESULT 81
DECA_TRICA STANDARD; PRT; 372 AA.
AC Q26974;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE DECAPENTAPLEGIC PROTEIN PRECURSOR.
GN DPP.
OS Tribolium castaneum (Red flour beetle).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga;
OC Cucujiformia; Tenebrionidae; Tribolium.
OX NCBI_TaxID=7070;
RN [1]
RP SEQUENCE FROM N.A.
RA Sanchez-Salazar J., Pletcher M.T., Bennett R.L., Brown S.J.,
RA Dandamudi T.J., Denell R.E., Doctor J.S.;
RA "The Tribolium decapentaplegic gene is similar in sequence, structure,
FT and expression to the Drosophila dpp gene.";
RL Dev. Genes Evol. 206:237-246(1996).
CC -!- FUNCTION: ACTS AS AN EXTRACELLULAR MORPHOGEN TO ESTABLISH AT LEAST
CC TWO CELLULAR RESPONSE THRESHOLDS WITHIN THE DORSAL HALF OF THE
CC DROSOPHILA EMBRYO. REQUIRED FOR THE PROPER DEVELOPMENT OF THE
CC EMBRYONIC DORSAL HYPODERM, FOR VIABILITY OF LARVAE AND FOR CELL
CC VIABILITY OF THE EPITHELIAL CELLS IN THE IMAGINAL DISKS. ACTS
CC TOGETHER WITH SCW (BY SIMILARITY).
CC -!- SUBUNIT: HOMODIMER OR HETERODIMER, DISULFIDE-LINKED (BY
CC SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC -----
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CC -----
DR EMBL; U63132; AAB38392.1; -.
DR HSSP; P18075; IBMP.
DR InterPro; IPR001111; -.
DR InterPro; IPR001839; -.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGF-beta-propeptide; 1.
DR PROSITE; PS00250; TGF_BETA_1.
KW Growth factor; Developmental protein; Differentiation; Glycoprotein;
KW SIGNAL 21 POTENTIAL.
FT PROPEP 21 ? POTENTIAL.
FT CHAIN 271 372 DECAPENTAPLEGIC PROTEIN.
FT DISULFID 271 337 BY SIMILARITY.
FT DISULFID 300 369 BY SIMILARITY.
FT DISULFID 304 371 BY SIMILARITY.
FT DISULFID 336 336 INTERCHAIN (BY SIMILARITY).
FT CARBOHYD 110 110 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 134 134 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 173 173 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 313 313 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 372 AA; 42435 MW; C9991AB75D2E3173 CRC64;

Query Match 27.4%; Score 174; DB 1; Length 372;
Best Local Similarity 35.8%; Pred. No. 2.1e-11;
Matches 39; Conservative 17; Mismatches 45; Indels 8; Gaps 5;

QY 9 RNLENCVVR-PLYIDFQDLGW-KWHEPKGYANFGSGPCPYL---RSADTHTSTVLG 64
DB 265 KNLKDCRRRQMYVDF-GSVGNDWIAPLGLDAYCGEGCEYPIDHMTTINHAIVQSL 323
QY 65 YNTLNPEASPCVCPQDLPLETLTYVVGRTPKV--EQLSNMVKSKC 111
DB 324 VNSMKPEVPGPCVPTQLGQMSML-YLGSDGSVILNKYKEMVYVCGC 371

RESULT 82
GDF1_HUMAN STANDARD; PRT; 372 AA.
AC P27539; O43344;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE EMBRYONIC GROWTH/DIFFERENTIATION FACTOR 1 PRECURSOR (GDF-1).
GN GDF1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=91239545; PubMed=2034669;
RA Lee S.-J.;
RT "Expression of growth/differentiation factor 1 in the nervous system:
RT conservation of a bicistronic structure.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:4250-4254(1991).
RN [2]
RP SEQUENCE FROM N.A.
RA Lamerdin J.E., McCreedy P.M., Adamson A.W., Burkhardt-Schultz K.,
RA Gordon L., Christensen M., Kyle A., Ramirez M., Stillwagen S.,
RA Gurnes J., Danganan L., Bruce R., Quan G., Montgomery M., Ow D.,
RA Kobayashi A., Nolan M., Trong S., Olsen A.O., Carrano A.V.;
RA Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: MAY MEDIATE CELL DIFFERENTIATION EVENTS DURING EMBRYONIC
CC DEVELOPMENT.
CC -!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: SECRETED.
CC -!- TISSUE SPECIFICITY: EXPRESSED IN THE BRAIN.
CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.

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RESULT 84
DECA_DROSI STANDARD; PRT; 593 AA.
AC P91706;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE DECAPENTAPLEGIC PROTEIN PRECURSOR (DPP-C PROTEIN).
GN DPP.
OS Drosophila simulans (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7240;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NET DPI;
RX MEDLINE=97225212; PubMed=9071585;
RA Newfield S.J., Padgett R.W., Findley S.D., Richter B.G., Sanicola M.,
RA de Cuevas M., Gelbart W.M.;
RT "Molecular evolution at the decapentaplegic locus in Drosophila.";
RL Genetics 145:297-309(1997).
CC -!- FUNCTION: ACTS AS AN EXTRACELLULAR MORPHOGEN TO ESTABLISH AT LEAST
CC TWO CELLULAR RESPONSE THRESHOLDS WITHIN THE DORSAL HALF OF THE
CC DROSOPHILA EMBRYO. REQUIRED FOR THE PROPER DEVELOPMENT OF THE
CC EMBRYONIC DORSAL HYPODERM, FOR VIABILITY OF LARVAE AND FOR CELL
CC VIABILITY OF THE EPITHELIAL CELLS IN THE IMAGINAL DISKS. ACTS
CC TOGETHER WITH SCW (BY SIMILARITY).
CC -!- SUBUNIT: HETERODIMERS OF SCW/DPP ARE THE ACTIVE SUBUNIT, DPP/DPP
CC HOMODIMERS ELICIT A BASAL RESPONSE AND SCW/SCW HOMODIMERS ALONE
CC ARE INEFFECTIVE IN SPECIFYING A DORSAL PATTERN (BY SIMILARITY).
CC -!- TISSUE SPECIFICITY: EXPRESSED IN THE IMAGINAL DISCS ASSOCIATED
CC WITH ESTABLISHMENT OF THE PROXIMAL-DISTAL AXIS OF THE APPENDAGES,
CC AND MIDGUT MESODERM (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
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EMBL; U63854; AAC47554.1; -
DR FlyBase; FBgn0013673; Ds1m\dpp.
DR InterPro; IPR001111; -
DR InterPro; IPR001839; -
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00888; TGFb_propeptide; 1.
DR PROSITE; PS00250; TGF_BETA_1; 1.
KW Growth factor; Developmental protein; Differentiation; Glycoprotein;
Signal.
FT SIGNAL 1 15 POTENTIAL.
FT PROPEP 16 461 BY SIMILARITY.
FT CHAIN 462 593 DECAPENTAPLEGIC PROTEIN.
FT DISULFID 492 558 BY SIMILARITY.
FT DISULFID 521 590 BY SIMILARITY.
FT DISULFID 525 592 BY SIMILARITY.
FT DISULFID 557 557 INTERCHAIN (BY SIMILARITY).
FT CARBOHYD 122 122 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 347 347 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 382 382 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 534 534 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 593 AA; 66248 MW; F0BDB21209F44380 CRC64;

Query Match 27.1%; Score 172; DB 1; Length 593;
Best Local Similarity 35.8%; Pred. No. 5.6e-11;
Matches 39; Conservative 16; Mismatches 46; Indels 8; Gaps 5;

QY 9 RNLEENCCVRPLYIDPRDLGW-KWVHEPKGYANFCGPGCYLRSD-----TTHSTVLG 63
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Db 486 KNHDDTCRRHSLYVDF-SDVGWDDWIVAPLGVDAYCHGKCF-PLADHFNSTNHAVQT 543
QY 64 LYLTLNPEASAPCCVQDLEPLTILYVYVGR-TPKVEQLSNMVKSKC 111
Db 544 LVNNMFGKVPKACCVPTQLDSVAMLYLNDQSTVVLKMYQEMTVVGGCG 592

RESULT 85
BMP2_CHICK STANDARD; PRT; 353 AA.
ID BMP2_CHICK
AC Q90751;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE BONE MORPHOGENETIC PROTEIN 2 PRECURSOR (BMP-2) (FRAGMENT).
GN BMP2 OR BMP-2.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WHITE LEGHORN;
RX MEDLINE=94163974; PubMed=8119128;
RA Francis P.H., Richardson M.K., Brickell P.M., Tickle C.;
RT "Bone morphogenetic proteins and a signalling pathway that controls
RT patterning in the developing chick limb.";
RL Development 120:209-218(1994).
CC -!- FUNCTION: INDUCES CARTILAGE AND BONE FORMATION (BY SIMILARITY).
CC -!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
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EMBL; X75914; CAA53513.1; -
DR HSPSP; P18075; IBMP.
DR InterPro; IPR001111; -
DR InterPro; IPR001839; -
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGFb_propeptide; 1.
DR PROSITE; PS00250; TGF_BETA_1; 1.
KW Growth factor; Cytokine; Bone; Cartilage; Glycoprotein.
FT NON_TER 1 1
FT PROPEP <1 239 BY SIMILARITY.
FT CHAIN 240 353 BONE MORPHOGENETIC PROTEIN 2.
FT DISULFID 253 318 BY SIMILARITY.
FT DISULFID 282 350 BY SIMILARITY.
FT DISULFID 286 352 BY SIMILARITY.
FT DISULFID 317 317 INTERCHAIN (BY SIMILARITY).
FT CARBOHYD 91 91 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 121 121 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 157 157 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 353 AA; 40347 MW; 8DBB46CD0EBD769B CRC64;

Query Match 27.1%; Score 171.5; DB 1; Length 353;
Best Local Similarity 38.5%; Pred. No. 3.7e-11;
Matches 42; Conservative 18; Mismatches 30; Indels 19; Gaps 8;

QY 14 NCCVRPLYIDPRDLGWK-WVHEPKGYANFCGPGCY-----LRSDTHTSTVLGLYNT 67
Db 252 SCKRHPLYVDF-NDVGWWDWIVAPPGYSFAFYCHGCEPPLADHLNS--TNHAIIVQTLVNS 308
QY 68 LN---PEASAPCCVQDLEPLTILYVYVGRTPKV--EQLSNMVVSKC 111
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Db 309 VNSKIPKA-----CCVPTLSAISML-YLDENEKVLKNYQDMVVEGCGC 352

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RESULT 86
ID BM8B_MOUSE
AC P55105;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE BONE MORPHOGENETIC PROTEIN 8B PRECURSOR (BMP-8B).
GN BMP8B.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ICR; TISSUE=Placenta;
RX MEDLINE=97000308; PubMed=8843393;
RA Zhao G.Q., Hogan B.L.;
RT "Evidence that mouse Bmp8a (Op2) and Bmp8b are duplicated genes that
RL Mech. Dev. 57:158-168(1996).
CC -!- FUNCTION: INDUCES CARTILAGE AND BONE FORMATION. MAY BE THE
CC OSTEOINDUCTIVE FACTOR RESPONSIBLE FOR THE PHENOMENON OF
CC EPITHELIAL OSTEOGENESIS. PLAYS A ROLE IN CALCIUM REGULATION
CC AND BONE HOMEOSTASIS (BY SIMILARITY).
CC -!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED.
CC -!- SUBCELLULAR LOCATION: SECRETED (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
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CC -----
DR EMBL; U39545; AB17573.1; -
DR HSSP; P18075; IBMP.
DR MGD; MGI:107335; Bmp8b.
DR InterPro; IPR001111; -
DR InterPro; IPR001839; -
DR InterPro; IPR002400; -
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGF-beta-propeptide; 1.
DR PRINTS; PR00438; GFCYSKNOT.
DR PROSITE; PS00250; TGF_BETA_1; 1.
DR Signal; Growth factor; Cytokine; Bone; Cartilage; Glycoprotein.
FT SIGNAL 1 19
FT PROPEP 20 260
FT CHAIN 261 399
FT DISULFID 298 364
FT DISULFID 327 396
FT DISULFID 331 398
FT DISULFID 363 363
FT CARBOHYD 155 155
FT CARBOHYD 340 340
FT SEQUENCE 399 AA; 44752 MW; EFA0B7B8C7EC4839 CRC64;

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Query Match 27.0%; Score 171; DB 1; Length 399;
 Best Local Similarity 40.0%; Pred. No. 4.7e-11;
 Matches 42; Conservative 16; Mismatches 39; Indels 8; Gaps 6;

QY 13 ENCCVRLPYIDFRDLGW-KWHEPKGYANFCGCPY-LRSA--DTHSTVLGLYNTL 68
 Db 296 EVCRTGELYVFR-DLGWLDSDIAPQGYSAAYGECIYPLNSMNSNTHATMQALVHLM 354
 QY 69 NPEASAPCCVPQDLPLTILYVGRTPKV--EQLSNMVKSKC 111

Db 355 KPDIIPKVCVPTELSAISLYI-DRNNVILRRRNMVVOACGC 398

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RESULT 87
ID BMP4_CHICK
AC Q90752;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE BONE MORPHOGENETIC PROTEIN 4 PRECURSOR (BMP-4).
GN BMP4 OR BMP-4.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WHITE LEGHORN;
RX MEDLINE=94163974; PubMed=8119128;
RA Francis P.H., Richardson M.K., Brickell P.M., Tickle C.;
RT "Bone morphogenetic proteins and a signalling pathway that controls
RL patterning in the developing chick limb.";
CC Development 120:209-218(1994).
CC -!- FUNCTION: INDUCES CARTILAGE AND BONE FORMATION.
CC -!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
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CC -----
DR EMBL; X75915; CAA53514.1; -
DR HSSP; P18075; IBMP.
DR InterPro; IPR001111; -
DR InterPro; IPR001839; -
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGF-beta-propeptide; 1.
DR PROSITE; PS00250; TGF_BETA_1; 1.
DR Signal; Growth factor; Cytokine; Bone; Cartilage; Glycoprotein.
FT SIGNAL 1 19
FT PROPEP 20 291
FT CHAIN 292 405
FT DISULFID 305 370
FT DISULFID 334 402
FT DISULFID 338 404
FT DISULFID 369 369
FT CARBOHYD 144 144
FT CARBOHYD 208 208
FT CARBOHYD 347 347
FT CARBOHYD 362 362
FT SEQUENCE 405 AA; 46057 MW; 544302DBA0A40F81 CRC64;

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Query Match 26.9%; Score 170.5; DB 1; Length 405;
 Best Local Similarity 37.7%; Pred. No. 5.4e-11;
 Matches 43; Conservative 18; Mismatches 34; Indels 19; Gaps 8;

QY 9 RNLEENCVRPLYIDFRDLGMK-WVHEPKGYANFCGCPY-----LRSADTHSTVL 62
 Db 299 RKNKNCRRHRLYVDF-SDVGWNDWIVAPGYQAFYCHGDCPPPLADHLNS--TNHAIQ 355

QY 63 GLYNTLN----PEASAPCCVPQDLPLTILYVGRTPKV--EQLSNMVKSKC 111
 Db 356 TLVNSYNSSIPKA-----CCVPTLSAISML-YLDEYDKVVLKKNYQDMVVEGCGC 404


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FT CARBOHYD 350 350 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 365 365 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 152 152 V -> A (IN REF. 2).
SQ SEQUENCE 408 AA; 46555 MW; 79801179DBB98204 CRC64;

Query Match 26.9%; Score 170.5; DB 1; Length 408;
Best Local Similarity 37.7%; Pred. No. 5.5e-11;
Matches 43; Conservative 17; Mismatches 35; Indels 19; Gaps 8;

Qy 9 RNLENCVVRPLYIDFRODLGK-WVHEPKGYANFCSPGCPY-----LRSADTTHSTVL 62
Db 302 RKKKNCRHRSYVDF-SDVGWNDWIVAPPGYQAFYCHGDCFPPLADHLNS--TNHAIQV 358

Qy 63 GLYNTLN---PEASAPCCVPDLEPLTILYVGRTPKV--EQLSNMVVKSKC 111
Db 359 TLVNSVNSIPKA-----CCVPTLSAISML-YLDEYDKVVLKNYQEMVVEGCGC 407

RESULT 90
BMP4_MOUSE
ID BMP4_MOUSE STANDARD; PRT; 408 AA.
AC P21275;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE BONE MORPHOGENETIC PROTEIN 4 PRECURSOR (BMP-4) (BMP-2B).
GN BMP4 OR BMP-4 OR DVR-4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Dickinson M.E., van der Meer-De Jong R., Hogan B.L.M.;
RL Submitted (XXX-1992) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=9328803; PubMed=8507180;
RA Kurihara T., Kitamura K., Takaoka K., Nakazato H.;
RT "Murine bone morphogenetic protein-4 gene: existence of multiple promoters and exons for the 5'-untranslated region.";
RL Biochem. Biophys. Res. Commun. 192:1049-1056(1993).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=93365172; PubMed=8358941;
RA Takaoka K., Yoshikawa H., Hashimoto J., Masuhara K., Miyamoto S.,
RA Suzuki S., Ono K., Matsui M., Oikawa S., Tsuruoka N.;
RT "Gene cloning and expression of a bone morphogenetic protein derived from a murine osteosarcoma.";
RL Clin. Orthop. Relat. Res. 294:344-352(1993).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SV; TISSUE=Liver;
RX MEDLINE=96081880; PubMed=7499338;
RA Feng J.Q., Chen D., Cooney A.J., Tsai M., Harris M.A., Tsai S.Y.,
RA Feng M., Mundy G.R., Harris S.E.;
RT "The mouse bone morphogenetic protein-4 gene. Analysis of promoter utilization in fetal rat calvarial osteoblasts and regulation by COUP-TFI orphan receptor.";
RL J. Biol. Chem. 270:28364-28373(1995).
RN [5]
RP SEQUENCE OF 241-408 FROM N.A.
RX MEDLINE=90228966; PubMed=1970330;
RA Dickinson M.E., Kobrin M.S., Silan C.M., Kingsley D.M., Justice M.J.,
RA Miller D.A., Ceci J.D., Lock L.F., Lee A., Buchberg A.M.,
RA Stracusa L.D., Lyons K.M., Derynck R., Hogan B.L.M., Copeland N.G.,
RA Jenkins N.A.;
RT "Chromosomal localization of seven members of the murine TGF-beta superfamily suggests close linkage to several morphogenetic mutant loci.";
RT Genomics 6:505-520(1990).
CC -1- FUNCTION: INDUCES CARTILAGE AND BONE FORMATION.

-1- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
-1- SUBCELLULAR LOCATION: SECRETED INTO THE EXTRACELLULAR MATRIX.
-1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.

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EMBL; X56848; CAA40179.1; -
EMBL; S65032; AAB28021.1; -
EMBL; L47480; AAC37698.1; ALT_INIT.
EMBL; D14814; BAA03555.1; -
PIR; B34201; B34201.
PIR; S29523; S29523.
HSP; P18075; IBM.
MGD; MGI:88180; Bmp4.
InterPro; IPR001111; -
InterPro; IPR001839; -
Pfam; PF00019; TGF-beta; 1.
Pfam; PF00688; TGF-beta; 1.
PROSITE; PS00250; TGF_BETA_1; 1.
Signal; Growth factor; Cytokine; Bone; Cartilage; Glycoprotein.
FT SIGNAL 1 19
FT PROPEP 20 292
FT CHAIN 293 408
FT DISULFID 308 373
FT DISULFID 337 405
FT DISULFID 341 407
FT DISULFID 372 372 INTERCHAIN (BY SIMILARITY).
FT CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 209 209 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 350 350 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 365 365 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 407 407 C -> S (IN REF. 2).
SQ SEQUENCE 408 AA; 46496 MW; 35053D844624EF9D CRC64;

Query Match 26.9%; Score 170.5; DB 1; Length 408;
Best Local Similarity 37.7%; Pred. No. 5.5e-11;
Matches 43; Conservative 17; Mismatches 35; Indels 19; Gaps 8;

Qy 9 RNLENCVVRPLYIDFRODLGK-WVHEPKGYANFCSPGCPY-----LRSADTTHSTVL 62
Db 302 RKKKNCRHRSYVDF-SDVGWNDWIVAPPGYQAFYCHGDCFPPLADHLNS--TNHAIQV 358

Qy 63 GLYNTLN---PEASAPCCVPDLEPLTILYVGRTPKV--EQLSNMVVKSKC 111
Db 359 TLVNSVNSIPKA-----CCVPTLSAISML-YLDEYDKVVLKNYQEMVVEGCGC 407

RESULT 91
BMP4_RAT
ID BMP4_RAT STANDARD; PRT; 408 AA.
AC Q06826;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE BONE MORPHOGENETIC PROTEIN 4 PRECURSOR (BMP-4) (BMP-2B).
GN BMP4 OR BMP-4 OR DVR-4.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93385158; PubMed=8373807;
RA Chen D., Feng J.Q., Mundy G.R., Harris M.A., Mundy G.R., Harris S.E.;
RT "Cloning and sequence of bone morphogenetic protein 4 cDNA from fetal rat calvarial cell.";

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RL Biochim. Biophys. Acta 1174:289-292(1993).
CC -1- FUNCTION: INDUCES CARTILAGE AND BONE FORMATION.
CC -1- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: SECRETED INTO THE EXTRACELLULAR MATRIX.
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC -----
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: Z22607; CAA80329.1; -.
CC InterPro: IPR001839; -.
CC PIR: S33173; S33173.
CC PIR: S38343; S38343.
CC HSP: P18075; LBMP.
CC InterPro: IPR001111; -.
CC InterPro: IPR001839; -.
CC Pfam: PF00019; TGF-beta; 1.
CC PROSITE: PS00250; TGF_BETA.1; 1.
CC Signal: Growth factor; Cytokine; Bone; Cartilage; Glycoprotein.
CC SIGNAL 1 19
CC PROPEP 20 292
CC CHAIN 293 408
CC DISULFID 308 373
CC DISULFID 337 405
CC DISULFID 341 407
CC DISULFID 372 372
CC CARBOHYD 144 144
CC CARBOHYD 209 209
CC CARBOHYD 350 350
CC CARBOHYD 365 365
CC SEQUENCE 408 AA; 46540 MW; 61E92B48D5624F3 CRC64;
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CC Query Match 26.9%; Score 170.5; DB 1; Length 408;
CC Best Local Similarity 37.7%; Pred. No. 5.5e-11;
CC Matches 43; Conservative 17; Mismatches 35; Indels 19; Gaps 8;
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CC QY 9 RNLEENCVRPLYLIDFRQDLGK-WVHEPKGYANFCGPGPY-----LRASDTHSTVL 62
CC Db 302 RKKKNCRRHSLYVDF-SDVGNDWIVAPGYQAFYCHGDCPPLADHLNS--TNHAIQV 358
CC -----
CC QY 63 GLYNTLN---PEASAPCCVPQDLEPLTILYVGRTPKV--EQLSNMVKSKC 111
CC Db 359 TLVNSVNSIPKA---CCVPTLSAISML-YLDEYDKVVLKKNYQEMVVEGCGC 407
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CC RESULT 92
CC BMP4_RABIT
CC ID BMP4_RABIT STANDARD; PRT; 409 AA.
CC AC O46576;
CC DT 15-JUL-1999 (Rel. 38, Created)
CC DT 15-JUL-1999 (Rel. 38, Last sequence update)
CC DT 15-JUL-1999 (Rel. 38, Last annotation update)
CC DE BONE MORPHOGENETIC PROTEIN 4 PRECURSOR (BMP-4).
CC GN BMP4 OR BMP-4.
CC OS Oryctolagus cuniculus (Rabbit).
CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
CC OX NCBI_TaxID=9986;
CC RN [1]
CC RP SEQUENCE FROM N.A.
CC RC STRAIN=NEW ZEALAND WHITE; TISSUE=Ocular ciliary epithelium;
CC RA Wan X.L., Sears J., Chen S., Sears M.;
CC RT "Cloning and expression of BMP-2/-4 from rabbit ocular ciliary
CC RT epithelium."
CC RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
CC CC -1- FUNCTION: INDUCES CARTILAGE AND BONE FORMATION (BY SIMILARITY).
CC -1- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).

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CC -1- SUBCELLULAR LOCATION: SECRETED INTO THE EXTRACELLULAR MATRIX.
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: AF042497; AAB97467.1; -.
CC InterPro: IPR001111; -.
CC InterPro: IPR001839; -.
CC Pfam: PF00019; TGF-beta; 1.
CC Pfam: PF00688; TGF-beta; 1.
CC PROSITE: PS00250; TGF_BETA.1; 1.
CC Signal: Growth factor; Cytokine; Bone; Cartilage; Glycoprotein.
CC SIGNAL 1 19
CC PROPEP 20 293
CC CHAIN 294 409
CC DISULFID 309 374
CC DISULFID 338 406
CC DISULFID 342 408
CC DISULFID 373 373
CC CARBOHYD 144 144
CC CARBOHYD 209 209
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CC Query Match 26.7%; Score 169.5; DB 1; Length 409;
CC Best Local Similarity 38.1%; Pred. No. 7e-11;
CC Matches 43; Conservative 17; Mismatches 36; Indels 17; Gaps 8;
CC -----
CC QY 9 RNLEENCVRPLYLIDFRQDLGK-WVHEPKGYANFCGPGPYLRASD---TTHSTVLG 63
CC Db 303 RKKKNCRRHSLYVDF-SDVGNDWIVAPGYQAFYCHGDCPFLADHFNSTHAIQV 360
CC -----
CC QY 64 LYNTLN---PEASAPCCVPQDLEPLTILYVGRTPKV--EQLSNMVKSKC 111
CC Db 361 LVNSVNSIPKA---CCVPTLSAISML-YLDEYDKVVLKKNYQEMVVEGCGC 408
CC -----
CC RESULT 93
CC UNIV_STRPU
CC ID UNIV_STRPU STANDARD; PRT; 383 AA.
CC AC P48970;
CC DT 01-FEB-1996 (Rel. 33, Created)
CC DT 01-FEB-1996 (Rel. 33, Last sequence update)
CC DT 01-OCT-1996 (Rel. 33, Last annotation update)
CC DE UNIVIN PRECURSOR.
CC OS Strongylocentrotus purpuratus (Purple sea urchin).
CC OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
CC OC Echinoidea; Euechinoidea; Echinacea; Echinoidea; Strongylocentrotidae;
CC OC Strongylocentrotus.
CC OX NCBI_TaxID=7668;
CC RN [1]
CC RP SEQUENCE FROM N.A.
CC RX MEDLINE=95046897; PubMed=7958442;
CC RA Stenzel P., Angerer L.M., Smith B.J., Angerer R.C., Vale W.W.;
CC RT "The univin gene encodes a member of the transforming growth
CC RT factor-beta superfamily with restricted expression in the sea urchin
CC RT embryo."
CC RL Dev. Biol. 166:149-158(1994).
CC CC -1- FUNCTION: COULD HAVE A CRITICAL ROLE IN EARLY DEVELOPMENTAL
CC CC DECISIONS IN THE SEA URCHIN EMBRYO.
CC -1- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (PROBABLE).
CC -1- DEVELOPMENTAL STAGE: HIGHEST LEVELS OF EXPRESSION IN THE EGG AND
CC PREHATCHING BLASTULA. DURING LATE CLEAVAGE STAGES, IT ACCUMULATES
CC PROGRESSIVELY TO A CIRCUMEQATORIAL BAND. DURING GASTRULATION IT
CC IS DETECTED PRIMARILY IN THE PRESUMPTIVE FOREGUT AND CILIATED

```

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: October 30, 2001, 08:52:11 ; Search time 18.1 Seconds
 (without alignments)
 825,993 Million cell updates/sec

Title: TGFB3P
 Perfect score: 634
 Sequence: 1 ALDTNCFRNLENCVRL.....RTPKVEQLSNMVKSCRSX 113

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 100 summaries

Database : SPTREMBL16.*
 1: sp.archaea.*
 2: sp.bacteria.*
 3: sp.fungi.*
 4: sp.human.*
 5: sp.invertebrate.*
 6: sp.mammal.*
 7: sp.mhc.*
 8: sp.organelle.*
 9: sp.phage.*
 10: sp.plant.*
 11: sp.rodent.*
 12: sp.unclassified.*
 13: sp.vertibrate.*
 14: sp.virus.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	535	84.4	442	Q15579	Q15579 homo sapien
2	530	83.6	414	Q9R298	Q9R298 rattus norv
3	530	83.6	414	Q9R281	Q9R281 rattus norv
4	530	83.6	442	Q9WU08	Q9WU08 rattus norv
5	528	83.3	414	Q9R2B8	Q9R2B8 rattus norv
6	500	78.9	112	Q02730	Q02730 oryctolagus
7	491	77.4	390	Q08TUM8	Q08TUM8 equus caball
8	489	77.1	361	Q398854	Q398854 cyprinus ca
9	488	77.0	130	Q08714	Q08714 mesocricetu
10	482	76.0	399	Q11QER7	Q11QER7 mesocricetu
11	463	73.0	81	Q9N1S3	Q9N1S3 capreolus c
12	435	68.6	91	Q6QWZ1	Q6QWZ1 capra hircu
13	422	66.6	101	Q11Q9R184	Q11Q9R184 meriones un
14	412	65.0	86	Q28241	Q28241 cervus elap
15	404	63.7	382	Q33449	Q33449 oncorhynch
16	396	62.5	382	Q9PWA9	Q9PWA9 morone chry
17	375	59.1	376	Q39PT02	Q39PT02 cyprinus ca
18	339	53.5	76	Q11Q9W26	Q11Q9W26 rattus sp.
19	329	51.9	87	Q42306	Q42306 carassius a

20	230	36.3	50	6	Q28240	Q28240 cervus elap
21	223	35.2	62	13	Q9DEP5	Q9DEP5 scophthalmu
22	213.5	33.7	373	13	Q9DD18	Q9DD18 salar
23	208	32.8	354	13	Q9YGV1	Q9YGV1 xenopus lae
24	207	32.6	373	13	Q90723	Q90723 gallus gall
25	207	32.6	373	13	Q98950	Q98950 gallus gall
26	204.5	32.3	162	6	Q9TSK2	Q9TSK2 sus scrofa
27	204.5	32.3	375	6	Q9GM97	Q9GM97 equus caball
28	204	32.2	361	5	Q96504	Q96504 branchiosto
29	204	32.2	411	5	Q9U418	Q9U418 branchiosto
30	200	31.5	426	4	Q9HBP0	Q9HBP0 homo sapien
31	198	31.2	404	13	Q9PW65	Q9PW65 carassius a
32	197.5	31.2	367	13	Q91696	Q91696 xenopus lae
33	196.5	31.0	185	6	Q9MZ18	Q9MZ18 ovis aries
34	193	30.4	413	13	Q98860	Q98860 cynops pyrr
35	192	30.3	614	5	P91720	P91720 drosophila
36	191.5	30.2	365	5	O02424	O02424 caenorhabdi
37	191.5	30.2	365	5	O76514	O76514 caenorhabdi
38	190	30.0	313	13	Q91403	Q91403 gallus gall
39	190	30.0	398	13	Q918T6	Q918T6 gallus gall
40	190	30.0	412	13	O12938	O12938 brachydanio
41	189	29.8	115	13	Q9DGF2	Q9DGF2 cyprinus ca
42	189	29.8	115	13	Q9DGE8	Q9DGE8 oryzias lat
43	189	29.8	177	4	Q9H512	Q9H512 homo sapien
44	189	29.8	438	5	Q9GT26	Q9GT26 anopheles s
45	188.5	29.7	370	13	Q91350	Q91350 xenopus lae
46	188	29.7	96	13	Q9W759	Q9W759 cairina mos
47	188	29.7	399	13	Q9W753	Q9W753 xenopus lae
48	188	29.7	405	5	Q9U5E8	Q9U5E8 ptychodera
49	188	29.7	432	13	Q9PTF9	Q9PTF9 brachydanio
50	187	29.5	345	13	Q9DFV1	Q9DFV1 eleutheroda
51	187	29.5	413	13	Q9DGN4	Q9DGN4 xenopus lae
52	186	29.3	178	5	Q25211	Q25211 junonia coe
53	186	29.3	261	13	Q9W6C0	Q9W6C0 brachydanio
54	185.5	29.3	115	13	Q9DGE9	Q9DGE9 cyprinus ca
55	185.5	29.3	390	13	Q91597	Q91597 xenopus lae
56	185.5	29.3	683	5	Q94580	Q94580 halocynthia
57	185	29.2	126	13	Q93573	Q93573 gallus gall
58	185	29.2	204	5	Q9XZ69	Q9XZ69 tripeustes
59	185	29.2	351	11	Q9WUK5	Q9WUK5 rattus norv
60	184.5	29.1	352	13	Q9PWR8	Q9PWR8 carassius a
61	184.5	29.1	393	13	Q90261	Q90261 brachydanio
62	183.5	28.9	115	13	Q9DGF1	Q9DGF1 cyprinus ca
63	183.5	28.9	115	13	Q9DGE6	Q9DGE6 oryzias lat
64	183.5	28.9	138	13	Q9W6T9	Q9W6T9 brachydanio
65	183	28.9	424	13	Q9TGH7	Q9TGH7 xenopus lae
66	183	28.9	500	13	Q9W6G0	Q9W6G0 gallus gall
67	182.5	28.8	99	13	Q93254	Q93254 pagrus majo
68	181.5	28.6	115	13	Q9DGF0	Q9DGF0 cyprinus ca
69	179.5	28.3	395	13	Q9PWG6	Q9PWG6 anguilla ja
70	179.5	28.3	411	13	O57573	O57573 brachydanio
71	179.5	28.3	411	13	O13108	O13108 brachydanio
72	179.5	28.3	411	13	O93369	O93369 brachydanio
73	179	28.2	443	5	O76851	O76851 halocynthia
74	179	28.2	453	13	P87373	P87373 gallus gall
75	178	28.1	115	13	Q9DGE7	Q9DGE7 oryzias lat
76	178	28.1	417	5	O9XXQ7	O9XXQ7 lytechinus
77	177.5	28.0	364	13	Q9PVK1	Q9PVK1 gallus gall
78	177.5	28.0	386	13	O13109	O13109 brachydanio
79	177	27.9	289	5	O9XQ8	O9XQ8 strongyloce
80	174.5	27.5	400	13	O57574	O57574 brachydanio
81	173	27.3	191	5	Q26468	Q26468 schistocerc
82	173	27.3	400	5	O76147	O76147 dugesia jap
83	172.5	27.2	586	5	O9VQ99	O9VQ99 drosophila
84	172	27.1	301	5	O97390	O97390 crassostrea
85	172	27.1	428	5	O16123	O16123 brugia paha
86	172	27.1	428	5	O16134	O16134 brugia mala
87	172	27.1	588	5	O9VQ66	O9VQ66 drosophila
88	171.5	27.1	102	13	Q90390	Q90390 carassius a
89	170.5	26.9	337	6	Q9MZV5	Q9MZV5 canis famli
90	169	26.7	120	13	Q9W6T8	Q9W6T8 brachydanio
91	169	26.7	257	13	O42303	O42303 brachydanio
92	168.5	26.6	104	13	Q98861	Q98861 cynops pyrr

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93 168.5 26.6 400 13 013107 Q13107 brachydanio
94 168.5 26.6 421 11 0921V8 Q921V8 mus musculus
95 167.5 26.4 102 13 09DE11 Q9DE11 oncorhynchus
96 165.5 26.1 400 13 073818 O73818 xenopus lae
97 165.5 26.1 400 13 091703 Q91703 xenopus lae
98 165 26.0 324 13 09YHW9 Q9YHW9 gallus gall
99 164 25.9 102 13 090388 Q90388 carassius a
100 162 25.6 83 13 P79707 P79707 cynops pyrri

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ALIGNMENTS

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RESULT 1
Q15579 ID Q15579 PRELIMINARY; PRT; 442 AA.
AC Q15579;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE TRANSFORMING GROWTH FACTOR-BETA-2 PRECURSOR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=TAMOXIFEN-TREATED PROSTATIC ADENOCARCINOMA;
RX MEDLINE=88166349; PubMed=3162414;
RA Madisen L., Webb N.R., Rose T.M., Marquardt H., Ikeda T., Twardzik D.,
RA Seyedin S., Purchio A.F.;
RT "Transforming growth factor-beta 2: cDNA cloning and sequence
RT analysis."
RL DNA 7:1-8(1988).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=TAMOXIFEN-TREATED PROSTATIC ADENOCARCINOMA;
RX MEDLINE=89090808; PubMed=2850146;
RA Webb N.R., Madisen L., Rose T.M., Purchio A.F.;
RT "Structural and sequence analysis of TGF-beta 2 cDNA clones predicts
RT two different precursor proteins produced by alternative mRNA
RT splicing."
RL DNA 7:493-497(1988).
CC -1- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
DR EMBL; M19154; AAA50404.1; -.
DR HSP; P08112; 2TGI.
DR InterPro; IPR001111; -.
DR InterPro; IPR001839; -.
DR InterPro; IPR002400; -.
DR Pfam; PF00019; TGF-beta; 1.
DR PRINTS; PR00438; GFCYSKNOT.
DR PRODOM; PD000357; -.
DR PROSITE; PS00250; TGF_BETA; 1.
DR SMART; SM00204; TGF; 1.
KW Glycoprotein; Signal.
FT SIGNAL 1 20 POTENTIAL.
FT CHAIN 331 442 POTENTIAL.
SQ SEQUENCE 442 AA; 50573 MW; 5D7A3C2ED51753D5 CRC64;

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Query Match 84.4%; Score 535; DB 4; Length 442;
Best Local Similarity 79.5%; Pred. No. 1.8e-52;
Matches 89; Conservative 14; Mismatches 9; Indels 0; Gaps 0;

QY 1 ALDITNYCFRNLENCVRLPYIDFQDLGKWKVHEPKGYANFCGCPYLRSDATTHST 60
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Db 331 ALDAAVCFRNVDNCLRLPYIDFQDLGKWKVHEPKGYANFCACPYLWSSDTQHSR 390

QY 61 VLGLYNTLNPEASPCVPPQDLPLTILYVGRTPKVEQLSNMVKSKCS 112
||| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 391 VLSLYNTLNPEASPCVQDLEPLTILYIGTKPTKIEQLSNMIVKSKCS 442

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RESULT 2
Q9R298 ID Q9R298 PRELIMINARY; PRT; 414 AA.
AC Q9R298;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE TGF-BETA 2 SHORT FORM PRECURSOR.
GN TGF-BETA2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WISTAR; TISSUE=MUSCLE;
RA Koishi K., Dalzell K.G.B., McLennan I.S.;
RT "Structure and expression of TGF-beta 2 messages in the rat muscle."
RT Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
DR EMBL; AF153013; AAD34160.1; -.
DR HSP; P08112; 2TGI.
DR InterPro; IPR001111; -.
DR InterPro; IPR001839; -.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGFb_propeptide; 1.
DR PROSITE; PS00250; TGF_BETA; 1.
DR SMART; SM00204; TGF; 1.
KW Glycoprotein.
SQ SEQUENCE 414 AA; 47727 MW; 485DFC04EC0CA291 CRC64;

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Query Match 83.6%; Score 530; DB 11; Length 414;
Best Local Similarity 78.6%; Pred. No. 6.3e-52;
Matches 88; Conservative 14; Mismatches 10; Indels 0; Gaps 0;

QY 1 ALDITNYCFRNLENCVRLPYIDFQDLGKWKVHEPKGYANFCGCPYLRSDATTHST 60
||| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 303 ALDAAVCFRNVDNCLRLPYIDFQDLGKWKVHEPKGYANFCACPYLWSSDTQHTK 362

QY 61 VLGLYNTLNPEASPCVPPQDLPLTILYVGRTPKVEQLSNMVKSKCS 112
||| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 363 VLSLYNTLNPEASPCVQDLEPLTILYIGTKPTKIEQLSNMIVKSKCS 414

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RESULT 3
Q9R281 ID Q9R281 PRELIMINARY; PRT; 414 AA.
AC Q9R281;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE TRANSFORMING GROWTH FACTOR BETA 2 PRECURSOR.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Plisov S.Y., Ivanov S.V., Plisova T.M., Lerman M., Perantoni A.O.;
RT "Rat transforming growth factor-beta2, complete coding sequence."
RT Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
DR EMBL; AF135598; AAD24484.1; -.
DR HSP; P08112; 2TGI.
DR InterPro; IPR001111; -.
DR InterPro; IPR001839; -.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGFb_propeptide; 1.
DR PROSITE; PS00250; TGF_BETA; 1.
DR SMART; SM00204; TGF; 1.
KW Glycoprotein.

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SQ SEQUENCE 414 AA; 47711 MW; 485DE768E720B2D1 CRC64;

Query Match 83.6%; Score 530; DB 11; Length 414;
Best Local Similarity 78.6%; Pred. No. 6.3e-52;
Matches 88; Conservative 14; Mismatches 10; Indels 0; Gaps 0;

QY 1 ALDNTYCFNLENCVRRPLYIDFRODLGKWKVHEPKGYANFCSPGCPYLSADTTHST 60
DB 303 ALDAAAYCFNVDNCCRLPYIDFKRDLGKWKVHEPKGYANFCACGACPYLWSSDTQHTK 362

QY 61 VLGLYNTLNPEASASPCVQDLEPLTILYVGRTPKVEQLSNMIVKSKCS 112
DB 363 VLSLYNTINPEASASPCVQDLEPLTILYVGRTPKVEQLSNMIVKSKCS 414

RESULT 4
Q9WUQ8 PRELIMINARY; PRT; 442 AA.
AC Q9WUQ8;
DT 01-NOV-1999 (Tremblrel. 12, Created)
DT 01-NOV-1999 (Tremblrel. 12, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE TGF-BETA 2 LONG FORM PRECURSOR.
GN TGF-BETA2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WISTAR;
RA Kishimoto K., Dalzell K.G.B., McLennan I.S.;
RT "Structure and expression of TGF-beta 2 messages in the rat muscle.";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
DR EMBL; AF153012; AAD34159.1; -.
DR HSP; P08112; 2TGI.
DR InterPro; IPR001111; -.
DR InterPro; IPR001839; -.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGF-beta; 1.
DR PROSITE; PS00250; TGF-BETA; 1.
DR SMART; SM00204; TGF-beta; 1.
KW Glycoprotein.
SQ SEQUENCE 442 AA; 50533 MW; 69C81A19CE06C253 CRC64;

Query Match 83.6%; Score 530; DB 11; Length 442;
Best Local Similarity 78.6%; Pred. No. 6.7e-52;
Matches 88; Conservative 14; Mismatches 10; Indels 0; Gaps 0;

QY 1 ALDNTYCFNLENCVRRPLYIDFRODLGKWKVHEPKGYANFCSPGCPYLSADTTHST 60
DB 331 ALDAAAYCFNVDNCCRLPYIDFKRDLGKWKVHEPKGYANFCACGACPYLWSSDTQHTK 390

QY 61 VLGLYNTLNPEASASPCVQDLEPLTILYVGRTPKVEQLSNMIVKSKCS 112
DB 391 VLSLYNTINPEASASPCVQDLEPLTILYVGRTPKVEQLSNMIVKSKCS 442

RESULT 5
Q9R2B8 PRELIMINARY; PRT; 414 AA.
AC Q9R2B8;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE TGF-BETA2 PROTEIN.
GN TGF-BETA2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WISTAR;
RA Konrad L., Albrecht M., Amueller G.;
RT "The rat TGF-beta2 gene: Sequence analysis and expression pattern in the rat testis.";
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
DR EMBL; AJ132718; CAB42003.1; -.
DR HSP; P08112; 2TGI.
DR InterPro; IPR001111; -.
DR InterPro; IPR001839; -.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGF-beta; 1.
DR PROSITE; PS00250; TGF-BETA; 1.
DR SMART; SM00204; TGF-beta; 1.
KW Glycoprotein.
SQ SEQUENCE 414 AA; 47689 MW; 3AEF0912F5B550D5 CRC64;

Query Match 83.3%; Score 528; DB 11; Length 414;
Best Local Similarity 78.6%; Pred. No. 1.1e-51;
Matches 88; Conservative 13; Mismatches 11; Indels 0; Gaps 0;

QY 1 ALDNTYCFNLENCVRRPLYIDFRODLGKWKVHEPKGYANFCSPGCPYLSADTTHST 60
DB 303 ALDAAAYCFNVDNCCRLPYIDFKRDLGKWKVHEPKGYANFCACGACPYLWSSDTQHTK 362

QY 61 VLGLYNTLNPEASASPCVQDLEPLTILYVGRTPKVEQLSNMIVKSKCS 112
DB 363 VLSLYNTINPEASASPCVQDLEPLTILYVGRTPKVEQLSNMIVKSKCS 414

RESULT 6
O02730 PRELIMINARY; PRT; 112 AA.
AC O02730; O97501;
DT 01-JUL-1997 (Tremblrel. 04, Created)
DT 01-JUL-1997 (Tremblrel. 04, Last sequence update)
DT 01-OCT-2000 (Tremblrel. 15, Last annotation update)
DE TRANSFORMING GROWTH FACTOR BETA 1 (TGF-BETA 1) (FRAGMENT).
GN TGFBI OR TGF-BETA-1.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RA Taylor T.K., James E.R., McGonigle S., Yoho E.R.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RN SEQUENCE OF 2-99 FROM N.A.
RA Inoue K., Kawabe Y., Kodama T.;
RA Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: TGF-BETA 1 IS A MULTIFUNCTIONAL PEPTIDE THAT CONTROLS PROLIFERATION, DIFFERENTIATION, AND OTHER FUNCTIONS IN MANY CELL TYPES. MANY CELLS SYNTHESIZE TGF-BETA 1 AND ESSENTIALLY ALL OF THEM HAVE SPECIFIC RECEPTORS FOR THIS PEPTIDE. TGF-BETA 1 REGULATES THE ACTIONS OF MANY OTHER PEPTIDE GROWTH FACTORS AND DETERMINES A POSITIVE OR NEGATIVE DIRECTION OF THEIR EFFECTS.
CC -!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR EMBL; AF000133; AAB53806.1; -.
DR EMBL; AB020217; BAA36950.1; -.
DR HSP; P01137; 1KLA.
DR InterPro; IPR001839; -.
DR InterPro; IPR002400; -.
DR Pfam; PF00019; TGF-beta; 1.
DR PRINTS; PR00438; GFCYSKNOT.
DR PROSITE; PS00250; TGF-BETA; 1.
KW Growth factor; Mitogen; Glycoprotein.
FT NON_TER 1 1

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FT CHAIN 1 112 TRANSFORMING GROWTH FACTOR BETA 1.
FT DISULFID 7 16 BY SIMILARITY.
FT DISULFID 15 78 BY SIMILARITY.
FT DISULFID 44 109 BY SIMILARITY.
FT DISULFID 48 111 BY SIMILARITY.
FT DISULFID 77 77 INTERCHAIN (BY SIMILARITY).
FT CONFLICT 2 3 LD -> FS (IN REF. 2).
FT CONFLICT 85 92 PLPIVYV -> AVAHRVTL (IN REF. 2).
SQ SEQUENCE 112 AA; 12795 MW; 53C5B7D4635A6F3 CRC64;

Query Match 78.9%; Score 500; DB 6; Length 112;
Best Local Similarity 76.8%; Pred. No. 4e-49;
Matches 86; Conservative 11; Mismatches 15; Indels 0; Gaps 0;

Qy 1 ALDNYCFRNLENCVRLYIDFRQDLGKWKVHEPKGYANFCGCPYLRSDTTHST 60
Db 1 ALDNYCFSSTEKNCVRLYIDFRKDLGKWKVHEPKGYHANFCLGCPYIWSLDTQYSK 60

Qy 61 VLGLYNTLNPEASPCVCPQDLEPLTILYVGRTPKVEQLSNMVVKSCKS 112
Db 61 VLALYNQHNPGASAPCCVPQALEPLIVYVGRKPKVEQLSNMIVRSCKS 112

RESULT 7
Q9TUM8 PRELIMINARY; PRT; 390 AA.
AC Q9TUM8;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE TRANSFORMING GROWTH FACTOR BETA 1.
GN TGFBI.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP NIXON A.J., Brower-Toland B.T., Sandell L.J.;
RA "Molecular cloning of equine transforming growth factor beta 1 reveals
RT a divergent nucleotide structure that encodes a novel bioactive
RT peptide among mammalian species."
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
DR EMBL; AF175709; AAD49431.1; -.
DR HSSP; P01137; 1K1A.
DR InterPro; IPR001111; -.
DR InterPro; IPR001839; -.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGFb_propeptide; 1.
DR PROSITE; PS00250; TGF_BETA; 1.
DR SMART; SM00204; TGFb; 1.
KW Glycoprotein.
SQ SEQUENCE 390 AA; 43860 MW; 220FE40DFCCA6016 CRC64;

Query Match 77.48%; Score 491; DB 6; Length 390;
Best Local Similarity 75.9%; Pred. No. 1.5e-47;
Matches 85; Conservative 11; Mismatches 16; Indels 0; Gaps 0;

Qy 1 ALDNYCFRNLENCVRLYIDFRQDLGKWKVHEPKGYANFCGCPYLRSDTTHST 60
Db 279 ALDNYCSSTKNCVRLYIDFRKDLGKWKVHEPKGYHANFCLGCPYIWSLDTQYSK 338

Qy 61 VLGLYNTLNPEASPCVCPQDLEPLTILYVGRTPKVEQLSNMVVKSCKS 112
Db 339 VLALYNQHNPGASAPCCVPQVLEPLIVYVGRKPKVEQLSNMIVRSCKS 390

RESULT 8
Q98854 PRELIMINARY; PRT; 361 AA.
ID Q98854

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AC Q98854;
DT 01-FEB-1997 (Tremblrel. 02, Created)
DT 01-FEB-1997 (Tremblrel. 02, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE TRANSFORMING GROWTH FACTOR BETA 2 (TGF-BETA 2) (FRAGMENT).
GN TGFb2.
OS Cyprinus carpio (Common carp).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Cyprininae; Cyprinus.
OX NCBI_TaxID=7962;
RN [1]
RP SEQUENCE FROM N.A.
TX TISSUE=HEART;
RX MEDLINE=97354301; PubMed=9210595;
RA Sumathy K., Desai K.V., Kondaiah P.;
RT "Isolation of transforming growth factor-beta2 cDNA from a fish,
RT Cyprinus carpio by RT-PCR."
RL Gene 191:103-107(1997).
CC -1- FUNCTION: TGF-BETA 2 HAS SUPPRESSIVE EFFECTS ON INTERLEUKIN-2
CC -1- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR EMBL; U66874; AAB62983.1; -.
DR HSSP; P08112; 2TGI.
DR InterPro; IPR001111; -.
DR InterPro; IPR001839; -.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGFb_propeptide; 1.
DR PROSITE; PS00250; TGF_BETA; 1.
DR SMART; SM00204; TGFb; 1.
KW Growth factor; Mitogen; Glycoprotein.
FT NON_TER 1
FT PROPEP <1 257
FT CHAIN 258 361 TRANSFORMING GROWTH FACTOR BETA 2.
FT DISULFID 264 273 BY SIMILARITY.
FT DISULFID 272 335 BY SIMILARITY.
FT DISULFID 334 334 INTERCHAIN (BY SIMILARITY).
FT CARBOHYD 30 30 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 98 98 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 199 199 N-LINKED (GLCNAC. .) (POTENTIAL).
FT NON_TER 361 361
SQ SEQUENCE 361 AA; 41931 MW; 94D930FA970A3FD3 CRC64;

Query Match 77.1%; Score 489; DB 13; Length 361;
Best Local Similarity 77.9%; Pred. No. 2.4e-47;
Matches 81; Conservative 14; Mismatches 9; Indels 0; Gaps 0;

Qy 1 ALDNYCFRNLENCVRLYIDFRQDLGKWKVHEPKGYANFCGCPYLRSDTTHST 60
Db 258 ALDAAFCFRNVQDNCRLSLYIDFRKDLGKWKVHEPKGYANFCAGACPYLWSADTQHSN 317

Qy 61 VLGLYNTLNPEASPCVCPQDLEPLTILYVGRTPKVEQLSNM 104
Db 318 ILGLYNTLNPEASPCVCSQDLEPLTILYIGTKPKIEQLSNM 361

RESULT 9
Q08714 PRELIMINARY; PRT; 130 AA.
ID Q08714
AC Q08714; O70331;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE TRANSFORMING GROWTH FACTOR BETA 1 (TGF-BETA 1) (FRAGMENT).
GN TGFb1.
OS Mesocricetus auratus (Golden hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Mesocricetus.
OX NCBI_TaxID=10036;
RN [1]

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RP SEQUENCE FROM N.A.
RC STRAIN=LVG (SYR);
RX MEDLINE=93304479; PubMed=8317544;
RA Wong D.T., Donoff R.B., Yang J., Song B.Z., Matossian K., Nagura N.,
RA Elovic A., McBride J., Gallagher G., Todd R.;
RT "Sequential expression of transforming growth factors alpha and beta 1
RT by eosinophils during cutaneous wound healing in the hamster.";
RL Am. J. Pathol. 143:130-142(1993).
RN [2]
RP SEQUENCE OF 26-115 FROM N.A.
RC STRAIN=SYRIAN; TISSUE=SPLEEN;
RX MEDLINE=98234044; PubMed=9573100;
RA Melby P.C., Tryon V.V., Chandrasekar B., Freeman G.L.;
RT "Cloning of Syrian hamster (Mesocricetus auratus) cytokine cDNAs and
RT analysis of cytokine mRNA expression in experimental visceral
RT leishmaniasis.";
RL Infect. Immun. 66:2135-2142(1998).
CC -!- FUNCTION: TGF-BETA 1 IS A MULTIFUNCTIONAL PEPTIDE THAT CONTROLS
CC PROLIFERATION, DIFFERENTIATION, AND OTHER FUNCTIONS IN MANY CELL
CC TYPES. MANY CELLS SYNTHESIZE TGF-BETA 1 AND ESSENTIALLY ALL OF
CC THEM HAVE SPECIFIC RECEPTORS FOR THIS PEPTIDE. TGF-BETA 1
CC REGULATES THE ACTIONS OF MANY OTHER PEPTIDE GROWTH FACTORS AND
CC DETERMINES A POSITIVE OR NEGATIVE DIRECTION OF THEIR EFFECTS.
CC -!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED.
CC -!- SIMILARITY: TO OTHER GROWTH FACTORS OF THE TGF-BETA FAMILY.
CC EMBL; X60296; CAA42838.1; -.
DR HSP; P01137; KLKA.
DR InterPro; IPR001839; -.
DR Pfam; PF000019; TGF-beta; 1.
DR ProDom; PD000357; -.
DR PROSITE; PS00250; TGF-BETA; 1.
DR SMART; SM00204; TGF-beta; 1.
KW Growth factor; Mitogen; Glycoprotein.
FT NON_TER 1 1
FT PROPEP <1 18
FT CHAIN 19 130 TRANSFORMING GROWTH FACTOR BETA 1.
FT DISULFID 25 34 BY SIMILARITY.
FT DISULFID 33 96 BY SIMILARITY.
FT DISULFID 66 129 BY SIMILARITY.
FT DISULFID 95 95 INTERCHAIN (BY SIMILARITY).
FT CONFLICT 93 93 G -> S (IN REF. 2).
SQ SEQUENCE 130 AA; 14997 MW; 8B41DD6CF39CCA77 CRC64;

Query Match 77.0%; Score 488; DB 11; Length 130;
Best Local Similarity 75.9%; Pred. No. 1.1e-47;
Matches 85; Conservative 10; Mismatches 17; Indels 0; Gaps 0;

QY 1 ALDNTNYCFRNLENCVVRPLYIDFRDLGKWKVHEPKGYANFCSGPCPYLRSADTTHST 60
Db 19 ALDNTNYCFSTERNCCVRQYIDFRDLGKWKVHEPKGYHANFCIGPCPYIWSLDTOYSK 78

QY 61 VLGLYNTLNPEASASCCVPQDLEPLTILYVGRTPKVEQLSNMVKRSCKS 112
Db 79 VLALYNHNPFGASGAGCCVPQALEPLPIVYVVGKPKVEQLSNMIVRSYKCS 130

RESULT 10
Q9ERB7 PRELIMINARY; PRT; 399 AA.
AC Q9ERB7;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DE 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE TRANSFORMING GROWTH FACTOR-BETA 2 (FRAGMENT).
OS Mesocricetus auratus (Golden hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Mesocricetus.
OX NCBI_TaxID=10036;
RN [1]
RP SEQUENCE FROM N.A.

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RA Ramesh G., Kondaiah P., Seshagiri P.B.;
RT "Differential expression and selective localization of transforming
RT growth factor-beta isoforms in the hamster uterus during estrous
RT cycle.";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY007214; AAG02247.1; -.
FT NON_TER 1 1
FT NON_TER 399 399
SQ SEQUENCE 399 AA; 46078 MW; AGFF8E65EAFD5148 CRC64;

Query Match 76.0%; Score 482; DB 11; Length 399;
Best Local Similarity 76.9%; Pred. No. 1.6e-46;
Matches 80; Conservative 13; Mismatches 11; Indels 0; Gaps 0;

QY 1 ALDNTNYCFRNLENCVVRPLYIDFRDLGKWKVHEPKGYANFCSGPCPYLRSADTTHST 60
Db 296 ALDRAAYCFRNVDNCLRLPLYIDFRDLGKWKVHEPKGYANFCAGACPYLWSSDTQHTK 355

QY 61 VLGLYNTLNPEASASCCVPQDLEPLTILYVGRTPKVEQLSNM 104
Db 356 VLSLYNTLNPEASASCCVSHDLEPLTILYIGNTPKIEQLSNM 399

RESULT 11
Q9NIS3 PRELIMINARY; PRT; 81 AA.
AC Q9NIS3;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE TRANSFORMING GROWTH FACTOR BETA 3 (FRAGMENT).
GN TGF-B3.
OS Capreolus capreolus (Roe deer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervidae;
OC Cervidae; Odocoileinae; Capreolus.
OX NCBI_TaxID=9858;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=TESTIS;
RA Wagener A., Blottner S., Fickel J.;
RT "Detection of growth factors in the testes of roe deer (Capreolus
RT capreolus)";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
DR EMBL; AF152592; AAF73231.1; -.
DR InterPro; IPR001839; -.
DR Pfam; PF000019; TGF-beta; 1.
DR PROSITE; PS00250; TGF-BETA; 1.
KW Glycoprotein.
FT NON_TER 1 1
FT NON_TER 81 81
SQ SEQUENCE 81 AA; 9250 MW; 8515C856478E4BCC CRC64;

Query Match 73.0%; Score 463; DB 6; Length 81;
Best Local Similarity 98.8%; Pred. No. 4.4e-45;
Matches 80; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 12 EENCVRPLYIDFRDLGKWKVHEPKGYANFCSGPCPYLRSADTTHSTVLGLYNTLNPE 71
Db 1 EENCVRPLYIDFRDLGKWKVHEPKGYANFCSGPCPYLRSADTTHSTVLGLYNTLNPE 60

QY 72 ASASPCCVQDLEPLTILYV 92
Db 61 ASASPCCVQDLEPLTILYV 81

RESULT 12
Q9MYZ1 PRELIMINARY; PRT; 91 AA.
AC Q9MYZ1;

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DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE TGF BETA 2 (FRAGMENT).
OS Capra hircus (Goat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Capra.
OX NCBI_TaxID=9925;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=OVARIAN FOLLICLE;
RA Wang B., Zhang Y.;
RT "Goat ovarian TGF beta 2 cDNA sequence.";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
DR EMBL; AF276986; AAF87742.1; -.
DR InterPro; IPR001839; -.
DR Pfam; PF00019; TGF-beta; 1.
DR PROSITE; PS00250; TGF-BETA; 1.
KW Glycoprotein.
FT NON_TER 1 1
FT SEQUENCE 91 AA; 10412 MW; 59694PF30EAA1FAA CRC64;

Query Match 68.6%; Score 435; DB 6; Length 91;
Best Local Similarity 79.1%; Pred. No. 7.2e-42;
Matches 72; Conservative 11; Mismatches 8; Indels 0; Gaps 0;

QY 9 RNLENCVVRPLYIDFRDLGKWKVHEPKGYANFCSPCYLRSADTHTSTVLGLYNTL 68
Db 1 RNVQDNCCLRLPYIDFRDLGKWKVHEPKGYANFCAGCPYLWSDTQHSRVLNLYNTI 60

QY 69 NPEASAPCCVPQDLEPLTILYVGRTPKVE 99
Db 61 NPEASAPCCVSQDLEPLTILYIGTPKIE 91

RESULT 13
Q9R184 PRELIMINARY; PRT; 101 AA.
AC Q9R184;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE TRANSFORMING GROWTH FACTOR BETA 1 (TGF-BETA 1) (FRAGMENT).
GN TGFBI OR TGF-BETA.
OS Meriones unguiculatus (Mongolian jird).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Gerbillinae;
OC Meriones.
OX NCBI_TaxID=10047;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LYMPH NODE;
RA Rao U.R., Klei T.R.;
RT "cDNA cloning of gerbil transforming growth factor-beta by PCR.";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: TGF-BETA 1 IS A MULTIFUNCTIONAL PEPTIDE THAT CONTROLS
CC PROLIFERATION, DIFFERENTIATION, AND OTHER FUNCTIONS IN MANY CELL
CC TYPES. MANY CELLS SYNTHESIZE TGF-BETA 1 AND ESSENTIALLY ALL OF
CC THEM HAVE SPECIFIC RECEPTORS FOR THIS PEPTIDE. TGF-BETA 1
CC REGULATES THE ACTIONS OF MANY OTHER PEPTIDE GROWTH FACTORS AND
CC DETERMINES A POSITIVE OR NEGATIVE DIRECTION OF THEIR EFFECTS.
CC -1- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
CC EMBL; AF161218; AAD45726.1; -.
DR HSP; P01137; 1KIA
DR InterPro; IPR001839; -.
DR Pfam; PF00019; TGF-beta; 1.
DR PROSITE; PS00250; TGF-BETA; 1.
DR SMART; SM00204; TGFBI; 1.

KW Growth factor; Mitogen; Glycoprotein.
FT NON_TER 1 1
FT CHAIN <1 >86 TRANSFORMING GROWTH FACTOR BETA 2.
FT DISULFID 4 67 BY SIMILARITY.
FT DISULFID 66 66 INTERCHAIN (BY SIMILARITY).
FT NON_TER 86 86
FT SEQUENCE 86 AA; 9848 MW; A5AE8B62D78E80E5 CRC64;

Query Match 65.0%; Score 412; DB 6; Length 86;
Best Local Similarity 79.1%; Pred. No. 2.7e-39;
Matches 68; Conservative 11; Mismatches 7; Indels 0; Gaps 0;

QY 12 ENCCVVRPLYIDFRDLGKWKVHEPKGYANFCSPCYLRSADTHTSTVLGLYNTLNPE 71
Db 1 QDNCCLRLPYIDFRDLGKWKVHEPKGYANFCAGCPYLWSSDTQHSRVLNLYNTINPE 60

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KW Growth factor; Mitogen; Glycoprotein.
FT NON_TER 1 1
FT CHAIN <1 >101 TRANSFORMING GROWTH FACTOR BETA 1.
FT DISULFID 1 10 BY SIMILARITY.
FT DISULFID 9 72 BY SIMILARITY.
FT DISULFID 71 71 INTERCHAIN (BY SIMILARITY).
FT NON_TER 101 101
FT SEQUENCE 101 AA; 11724 MW; ABF1CFDA264AEFD CRC64;

Query Match 66.6%; Score 422; DB 11; Length 101;
Best Local Similarity 73.3%; Pred. No. 2.4e-40;
Matches 74; Conservative 9; Mismatches 18; Indels 0; Gaps 0;

QY 7 CERNLENCVVRPLYIDFRDLGKWKVHEPKGYANFCSPCYLRSADTHTSTVLGLYN 66
Db 1 CFSSTKNCVVRQLYRDKDLGKWKVHEPKGYANFCGLGPCPYINSLHTQYSKVLALYN 60

QY 67 TLNPEASAPCCVPQDLEPLTILYVGRTPKVEQLSNMVK 107
Db 61 QHNPASAPCCVPQALEPLPIVYVGRPKVEQLSNMFEVR 101

RESULT 14
Q28241 PRELIMINARY; PRT; 86 AA.
AC Q28241;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE TRANSFORMING GROWTH FACTOR BETA 2 (TGF-BETA 2) (FRAGMENT).
GN TGFBI OR TGF-BETA-2.
OS Cervus elaphus (Red deer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervidae;
OC Cervidae; Cervinae; Cervus.
OX NCBI_TaxID=9860;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=ANTLER;
RA Francis S.M., Suttie J.M.;
RT "Detection of growth factors and proto-oncogene mRNA in the growing
RT tip of red deer (Cervus elaphus) antler using reverse-transcriptase
RT polymerase chain reaction (RT-PCR).";
RL J. Exp. Zool. 281:36-42(1998).
CC -1- FUNCTION: TGF-BETA 2 HAS SUPPRESSIVE EFFECTS ON INTERLEUKIN-2
CC DEPENDENT T-CELL GROWTH.
CC -1- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR EMBL; U62111; AAB05257.1; -.
DR HSP; P08112; 2TGI.
DR InterPro; IPR001839; -.
DR Pfam; PF00019; TGF-beta; 1.
DR PROSITE; PS00250; TGF-BETA; 1.
DR SMART; SM00204; TGFBI; 1.
KW Growth factor; Mitogen; Glycoprotein.
FT NON_TER 1 1
FT CHAIN <1 >86 TRANSFORMING GROWTH FACTOR BETA 2.
FT DISULFID 4 67 BY SIMILARITY.
FT DISULFID 66 66 INTERCHAIN (BY SIMILARITY).
FT NON_TER 86 86
FT SEQUENCE 86 AA; 9848 MW; A5AE8B62D78E80E5 CRC64;

Query Match 65.0%; Score 412; DB 6; Length 86;
Best Local Similarity 79.1%; Pred. No. 2.7e-39;
Matches 68; Conservative 11; Mismatches 7; Indels 0; Gaps 0;

QY 12 ENCCVVRPLYIDFRDLGKWKVHEPKGYANFCSPCYLRSADTHTSTVLGLYNTLNPE 71
Db 1 QDNCCLRLPYIDFRDLGKWKVHEPKGYANFCAGCPYLWSSDTQHSRVLNLYNTINPE 60

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Best Local Similarity 69.0%; Pred. No. 8.3e-37;
Matches 69; Conservative 10; Mismatches 21; Indels 0; Gaps 0;

Qy 13 ENCCVRPLYIDFRODLGKWKWHEPKGYANFCSGPCPYLRSDTTHSVGLYNTLNPEA 72
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 283 ETCCVRSYIDFRDLGKWKIHKPTGYNANYCMGSCCTIYWAENKYSQILAYKHHNPCA 342

Qy 73 SASPCCVQDLEPLTILYVGRTPKVEQLSNMVKSKCS 112
    || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 343 SAOPCCVPQALEPLILYVGRQHKVEQLSNMVKSKCS 382

RESULT 17
Q9PTQ2 PRELIMINARY; PRT; 376 AA.
AC Q9PTQ2;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE TRANSFORMING GROWTH FACTOR BETA PRECURSOR.
OS Cyprinus carpio (Common carp).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Cyprininae; Cyprinus.
OX NCBI_TaxID=7962;
RN [1]
RP SEQUENCE FROM N.A.
RA Yin Z., Kuang J.;
RT "Molecular cloning of carp transforming growth factor beta 1.";
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: IS LIKELY TO BE AN IMPORTANT CYTOKINE REGULATING IMMUNE
CC RESPONSE. MAY ALSO HAVE A ROLE IN OTHER PHYSIOLOGICAL SYSTEMS.
CC -!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR EMBL; AF136947; AAF22573.1; -.
DR HSP; P01137; IKLA.
DR InterPro; IPR001111; -.
DR InterPro; IPR001839; -.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGF-beta; 1.
DR PRODOM; PD000357; -.
DR PROSITE; PS00250; TGF-BETA; 1.
DR SMART; SM00204; TGFB; 1.
DR Growth factor; Mitogen; Glycoprotein; Signal.
FT SIGNAL 1 22
FT PROPEP 23 264
FT CHAIN 265 376
FT DISULFID 272 280
FT DISULFID 308 373
FT DISULFID 312 375
FT DISULFID 341 341
FT CARBOHYD 76 76
FT CARBOHYD 125 125
FT CARBOHYD 167 167
FT SITE 230 232
FT SITE 232 232
SQ SEQUENCE 376 AA; 43329 MW; 7F7FC4DA58B69681 CRC64;

Query Match 59.1%; Score 375; DB 13; Length 376;
Best Local Similarity 59.6%; Pred. No. 1.9e-34;
Matches 65; Conservative 16; Mismatches 28; Indels 0; Gaps 0;

Qy 3 DTNYCFRNLENCVRLPYIDFRODLGKWKWHEPKGYANFCSGPCPYLRSDTTHSVL 62
    :||: : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 267 ETQVCTDKSGCCVRSYIDFRODLGKWKIHKPTGYNANYCMGSCCTIYWAENKYSQVL 326

Qy 63 GLYNTLNPEASPCVQDLEPLTILYVGRTPKVEQLSNMVKSKC 111
    || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 327 ALYKHHNPASQRCVRFQVNLNPLPIFYVGRQHKVEQLSNMVKTKC 375

RESULT 18
Q9QW26 PRELIMINARY; PRT; 76 AA.
AC Q9QW26;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE TRANSFORMING GROWTH FACTOR BETA ISOFORM 2 (FRAGMENT).
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10118;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93253033; PubMed=8486763;
RA Nishida M., Springhorn J.P., Kelly R.A., Smith T.W.;
RL J. Clin. Invest. 91:1934-1941(1993).
DR HSP; P08112; 2TGT.
DR InterPro; IPR001839; -.
DR Pfam; PF00019; TGF-beta; 1.
DR PRODOM; PD000357; -.
DR SMART; SM00204; TGFB; 1.
DR Growth factor; Mitogen; Glycoprotein.
FT NON_TER 1 1
FT CHAIN <1 >87
FT DISULFID 22 87
FT DISULFID 55 55
FT NON_TER 87 87
SQ SEQUENCE 87 AA; 10007 MW; 525465C4E8A70771 CRC64;
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Q9QW26 PRELIMINARY; PRT; 76 AA.
AC Q9QW26;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE TRANSFORMING GROWTH FACTOR BETA ISOFORM 2 (FRAGMENT).
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10118;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93253033; PubMed=8486763;
RA Nishida M., Springhorn J.P., Kelly R.A., Smith T.W.;
RL J. Clin. Invest. 91:1934-1941(1993).
DR HSP; P08112; 2TGT.
DR InterPro; IPR001839; -.
DR Pfam; PF00019; TGF-beta; 1.
DR PRODOM; PD000357; -.
DR SMART; SM00204; TGFB; 1.
DR Growth factor; Mitogen; Glycoprotein.
FT NON_TER 1 1
FT CHAIN <1 >87
FT DISULFID 22 87
FT DISULFID 55 55
FT NON_TER 87 87
SQ SEQUENCE 87 AA; 10007 MW; 525465C4E8A70771 CRC64;

Query Match 53.5%; Score 339; DB 11; Length 76;
Best Local Similarity 76.3%; Pred. No. 4.3e-31;
Matches 58; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

Qy 36 PKGYANFCSGPCPYLRSDTTHSVGLYNTLNPEASPCVQDLEPLTILYVGR 95
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 PKGYANFCSGPCPYLRSDTTHSVGLYNTLNPEASPCVQDLEPLTILYVGR 60

Qy 96 PKVEQLSNMVKSKC 111
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 PKIEQLSNMIVRACNC 76

RESULT 19
Q42306 PRELIMINARY; PRT; 87 AA.
AC Q42306;
DT 01-JAN-1998 (Tremblrel. 05, Created)
DT 01-JAN-1998 (Tremblrel. 05, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE TRANSFORMING GROWTH FACTOR BETA (FRAGMENT).
OS Carassius auratus (Goldfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Cyprininae; Carassius.
OX NCBI_TaxID=7957;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=MACROPHAGE;
RA Daniels G.D., Belosevic M., Secombes C.J.;
RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: IS LIKELY TO BE AN IMPORTANT CYTOKINE REGULATING IMMUNE
CC RESPONSE. MAY ALSO HAVE A ROLE IN OTHER PHYSIOLOGICAL SYSTEMS.
CC -!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR EMBL; AJ001040; CAA04494.1; -.
DR HSP; P01137; IKLA.
DR InterPro; IPR001839; -.
DR Pfam; PF00019; TGF-beta; 1.
DR PROSITE; PS00250; TGF-BETA; 1.
DR SMART; SM00204; TGFB; 1.
DR Growth factor; Mitogen; Glycoprotein.
FT NON_TER 1 1
FT CHAIN <1 >87
FT DISULFID 22 87
FT DISULFID 55 55
FT NON_TER 87 87
SQ SEQUENCE 87 AA; 10007 MW; 525465C4E8A70771 CRC64;
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Query Match          51.9%; Score 329; DB 13; Length 87;
Best Local Similarity 64.4%; Pred. No. 6.7e-30;
Matches 56; Conservative 13; Mismatches 18; Indels 0; Gaps 0;

QY 23 DFRQDLGKWKVHEPKGYANFCGPGCPYLRSADTHTSTVLGLYNTLNPEASASPCCVPOD 82
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 DFRKDLGKWKVHEPKGYANFCGPGCPYLRSADTHTSTVLGLYNTLNPEASASPCCVPOV 60

QY 83 LEPLTLYVGRTPKVEQLSNMVKSC 109
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 LNPLPIVYVGRQHKVEQLSNMIVRSC 87

RESULT 20
Q28240 ID Q28240 PRELIMINARY; PRT; 50 AA.
AC Q28240;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-OCT-2000 (Tremblrel. 15, Last annotation update)
DE TRANSFORMING GROWTH FACTOR BETA 1 (TGF-BETA 1) (TRANSFORMING GROWTH
DE FACTOR B1) (FRAGMENT).
GN TGFBI OR TGF BETA-1 OR TGF-B1.
OS Cervus elaphus (Red deer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidae;
OC Cervidae; Cervinae; Cervus.
OX NCBI_TaxID=9860;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=ANTLER;
RX MEDLINE=98233260; PubMed=9571767;
RA Francis S.M., Suttie J.M.;
RT "Detection of growth factors and proto-oncogene mRNA in the growing
RT tip of red deer (Cervus elaphus) antler using reverse-transcriptase
RT polymerase chain reaction (RT-PCR).";
RL J. Exp. Zool. 281:36-42(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=TESTIS;
RA Wagener A., Blottner S., Fickel J.;
RT "Detection of growth factors in the testes of roe deer (Capreolus
RT capreolus).";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: TGF-BETA 1 IS A MULTIFUNCTIONAL PEPTIDE THAT CONTROLS
CC PROLIFERATION, DIFFERENTIATION, AND OTHER FUNCTIONS IN MANY CELL
CC TYPES. MANY CELLS SYNTHESIZE TGF-BETA 1 AND ESSENTIALLY ALL OF
CC THEM HAVE SPECIFIC RECEPTORS FOR THIS PEPTIDE. TGF-BETA 1
CC REGULATES THE ACTIONS OF MANY OTHER PEPTIDE GROWTH FACTORS AND
CC DETERMINES A POSITIVE OR NEGATIVE DIRECTION OF THEIR EFFECTS.
CC -!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR EMBL; U62110; AA805256.1; -.
DR EMBL; AF152591; AAF73230.1; -.
DR HSP; P01137; 1KLA.
DR InterPro; IPR001839; -.
DR Pfam; PF00019; TGF-beta; 1.
DR PROSITE; PS00250; TGF_BETA; 1.
KW Growth factor; Mitogen; Glycoprotein.
FT NON_TER 1
FT CHAIN <1 >50 TRANSFORMING GROWTH FACTOR BETA 1.
FT NON_TER 50
FT SEQUENCE 50 AA; 6012 MW; 0DDDAE48C640759f CRC64;

Query Match          36.3%; Score 230; DB 6; Length 50;
Best Local Similarity 76.6%; Pred. No. 6e-19;
Matches 36; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 12 EBNCCVRQLYIDFRQDLGKWKVHEPKGYANFCGPGCPYLRSADTHT 58
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 4 EKNCCVRQLYIDFRKDLGKWKVHEPKGYANFCGLGCPYIWSLDTOY 50

Query Match          35.2%; Score 223; DB 13; Length 62;
Best Local Similarity 58.1%; Pred. No. 4.6e-18;
Matches 36; Conservative 10; Mismatches 16; Indels 0; Gaps 0;

QY 23 DFRQDLGKWKVHEPKGYANFCGPGCPYLRSADTHTSTVLGLYNTLNPEASASPCCVPOD 82
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 DFRKDLGKWKVHEPKGYANFCGPGCPYLRSADTHTSTVLGLYNTLNPEASASPCCVPOA 60

QY 83 LE 84
      ||
Db 61 LE 62

RESULT 22
Q9DDI8 ID Q9DDI8 PRELIMINARY; PRT; 373 AA.
AC Q9DDI8;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE MYOSTATIN PRECURSOR.
OS Salmo salar (Atlantic salmon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
OX NCBI_TaxID=8030;
RN [1]
RP SEQUENCE FROM N.A.
RA Andersen O.;
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Ostbye T.K.;
RT "The myostatin gene is expressed in multiple organs of Atlantic
RT salmon.";
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ297267; CAC19541.1; -.
KW Signal.
FT CHAIN 1 21 POTENTIAL.
FT CHAIN 265 373 MYOSTATIN.
FT SEQUENCE 373 AA; 41878 MW; C355D71D83E66C4D CRC64;

Query Match          33.7%; Score 213.5; DB 13; Length 373;

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Best Local Similarity 38.0%; Pred. No. 3.6e-16;
Matches 41; Conservative 13; Mismatches 37; Indels 17; Gaps 4;

QY 12 EENCVRPLYIDFRODLGWKWWHEPKGYANFCGPGCPYLSADTHSTVLGLYNTLNP 71
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 276 ESRCCRYPLTVDF-EDFGWDLIAPKRYKANYCSECEYMHQKYPHT---HLVKNANPR 331
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 72 ASASPCCVQDLEPLTILY-----VGRTPKVEQLSNMVMVVKSCKS 112
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 332 GTAGPCCPTTKMSPINMLYFNKKEQIIYKIPSI-----VVDRCGCS 373

RESULT 23
Q9YGV1
ID Q9YGV1 PRELIMINARY; PRT; 354 AA.
AC Q9YGV1;
DT 01-MAY-1999 (Tremblrel. 10, Created)
DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE DERRIERE.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99169090; PubMed=10068640;
RA Sun B.I., Bush S.M., Collins-Racie L.A., Lavallie E.R.,
RA DiBalsio-Smith E.A., Wolfman N.M., McCoy J.M., Sive H.L.;
RT "derriere: a TGF-beta family member required for posterior development
RT in Xenopus.";
RL Development 126:1467-1482(1999).
CC -!- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
DR EMBL: AF065135; AAD19837.1;
DR HSSP: P18075; IBMP.
DR InterPro; IPR001111;
DR InterPro; IPR001839;
DR InterPro; IPR002405;
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGF-beta; 1.
DR PRINTS; PR00669; INHIBINA.
DR PRODOM; PD000357; -; 1.
DR PROSITE; PS00250; TGF_BETA; 1.
DR SMART; SM00204; TGFB; 1.
KW Glycoprotein.
SQ SEQUENCE 354 AA; 40316 MW; 879CAE9A23F2E42F CRC64;

Query Match 32.8%; Score 208; DB 13; Length 354;
Best Local Similarity 42.3%; Pred. No. 1.4e-15;
Matches 44; Conservative 15; Mismatches 35; Indels 10; Gaps 5;

QY 15 CCVRPLYIDFRODLGWK-WVHEPKGYANFCGPGCPY-----LRSADTHSTVLGLYNTL 68
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 253 CKRRRLYIDFK-DVGQWQNIAPRGYMANYGCHGCPYPLTEMLRG--TNHVLQTLVHSV 309
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 69 NPEASPCCVQDLEPLTILYVGRTPKV-EQLSNMVMVVKSCKC 111
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 310 EPENTPLPCCAPTLPISMLYDNNVLRHYEDMVDVDEGC 353

RESULT 24
Q90723
ID Q90723 PRELIMINARY; PRT; 373 AA.
AC Q90723;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE GROWTH FACTOR CVGL.
GN CVGL.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-WHITE LEGHORN;
RA Shah S.B., Hume C.R., Dodd J.;
RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
DR EMBL; U55871; AAB01194.1;
DR HSSP; P18075; IBMP.
DR InterPro; IPR001111;
DR InterPro; IPR001839;
DR InterPro; IPR002400;
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGF-beta; 1.
DR PRINTS; PR00438; GFCYSKNOT.
DR PRODOM; PD000357; -; 1.
DR PROSITE; PS00250; TGF_BETA; 1.
DR SMART; SM00204; TGFB; 1.
KW Glycoprotein.
SQ SEQUENCE 373 AA; 41405 MW; E2ACFCCCD3A4C8B5 CRC64;

Query Match 32.6%; Score 207; DB 13; Length 373;
Best Local Similarity 41.2%; Pred. No. 1.9e-15;
Matches 42; Conservative 18; Mismatches 36; Indels 6; Gaps 4;

QY 15 CCVRPLYIDFRODLGWK-WVHEPKGYANFCGPGCPYLSAD---TTHSTVLGLYNTLNP 70
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 272 CKPRRLYISF-SDVGWQNIAPRGYMANYGCHGCPYPLTEMLNSTHAILQTMVHSLDP 330
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 71 EASASPCCVQDLEPLTILYVGRTPKV-EQLSNMVMVVKSCKC 111
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 331 EGTPOPCCVPRLSPLISILYDNNVLRHYEDMVDVDEGC 372

RESULT 25
Q98950
ID Q98950 PRELIMINARY; PRT; 373 AA.
AC Q98950;
DT 01-FEB-1997 (Tremblrel. 02, Created)
DT 01-FEB-1997 (Tremblrel. 02, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE VGL.
GN CVGL.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97147815; PubMed=8939612;
RA Seleiro E.A.P., Connolly D.J., Cooke J.;
RT "Early developmental expression and experimental axis determination by
RT the chicken Vgl gene.";
RL Curr. Biol. 6:1476-1486(1996).
CC -!- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
DR EMBL; U73003; AAC60038.1;
DR HSSP; P18075; IBMP.
DR InterPro; IPR001111;
DR InterPro; IPR001839;
DR InterPro; IPR002400;
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGF-beta; 1.
DR PRINTS; PR00438; GFCYSKNOT.
DR PRODOM; PD000357; -; 1.
DR PROSITE; PS00250; TGF_BETA; 1.
DR SMART; SM00204; TGFB; 1.
KW Glycoprotein.
SQ SEQUENCE 373 AA; 41503 MW; 9FAD8C212145602E CRC64;

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OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=THROUGHBRED;
RA HOSoyama T., Yamanouchi K., Tojo H., Tachi C.;
RT "Molecular cloning of equine myostatin cDNA and serum level of
  myostatin in horse.";
RL Submitted (Oct-1999) to the EMBL/GenBank/DBJ databases.
RE EMBL; AB033541; BAB16046.1; -
SQ SEQUENCE 375 AA; 42736 MW; 6F424ECBEE4D9936 CRC64;

Query Match 32.3%; Score 204.5; DB 6; Length 375;
Best Local Similarity 39.4%; Pred. No. 3,7e-15;
Matches 41; Conservative 15; Mismatches 39; Indels 9; Gaps

QY 12 EENCVRPLYIDFRQDLGKWKVHEPKGYANFCGGPCP--YLRSDTTHSTVLGLYNTLN 69
DB 278 ESCRCPPLVDFP-EATGWDWITAPKRYKANYSGCEGFVFLQKYPITH-----LVHQAN 331
QY 70 PEASAPCCVPQDLPLETLILYYVGRTEPKV-EQLSNMVMVSKCS 112
DB 332 PRGSAGPCCPTPKMSPINMLYFNKGKQIIVYKIPAMVVDRCGS 375

RESULT 28
O96504 PRELIMINARY; PRT; 361 AA.
ID O96504
AC O96504;
DT 01-MAY-1999 (Tremblrel. 10, Created)
DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE BONE MORPHOGENETIC PROTEIN 2/4.
GN AMPHIBMP2/4.
OS Branchiostoma floridae (Florida lancelet) (Amphioxus).
OC Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
OC Branchiostoma.
OX NCBI_TaxID=7739;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=98401944; PubMed=9733108;
RA Panopoulou G.D., Clark M.D., Holland L.Z., Lehrach H., Holland N.D.;
RT "AmphibMP2/4, an amphioxus bone morphogenetic protein closely related
  to Drosophila decapentaplegic and vertebrate BMP2 and BMP4: insights
  into evolution of dorsoventral axis specification.";
RL Dev. Dyn. 213:130-139(1998).
CC -1- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
DB EMBL; AF068750; AAC97488.1; -
DB HSP; P18075; IBMP.
DR InterPro; IPR001111; -
DR InterPro; IPR001839; -
DR InterPro; IPR002405; -
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGF-beta-propeptide; 1.
DR PRINTS; PR00669; INHIBIN.
DR PRODOM; PD000357; -; 1.
DR PROSITE; PS00250; TGF_BETA; 1.
DR SMART; SM00204; TGF-beta; 1.
KW Glycoprotein.
SQ SEQUENCE 361 AA; 41517 MW; 09FF5FE6C9785DD1 CRC64;

Query Match 32.2%; Score 204; DB 5; Length 361;
Best Local Similarity 40.9%; Pred. No. 4.1e-15;
Matches 45; Conservative 15; Mismatches 40; Indels 10; Gaps

QY 9 RNLEENCVRPLYIDFRQDLGKWKVHEPKGYANFCGGPCPY-----LRSADTTHSTVL 62
DB 254 RRLKANCRRHSLYVDF-SDVGWNDWIVAPPGYQAYYCHGCEPFLADHLNS--TNHAIQV 310
QY 63 GLYNTLNPEASAPCCVPQDLPLETLILYYVGRTEPKV-EQLSNMVMVSKCK 111
DB 311 TLVNSVPLAVPRACCCVPTDLSIFMILYNENDQVVLKNTQDMVREGCGG 360

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RESULT 29
Q9U418
ID Q9U418 PRELIMINARY; PRT; 411 AA.
AC Q9U418;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE BONE MORPHOGENETIC PROTEIN 2/4.
GN BMP2/4.
OS Branchiostoma belcheri.
OC Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
OC Branchiostoma.
OX NCBI_TaxID=7741;
RN [1]
RP SEQUENCE FROM N.A.
RA Yasui K., Saiga H., Uemura M., Samba I.;
RT "Early body formation and expression pattern of genes encoding
secreted proteins, BbBMP2/4, BbWnt7, and BbWnt8 in lancelets.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
DR EMBL; AF206325; AAF19841.1; -.
DR HSP; P18075; IBMP.
DR InterPro; IPR001111; -.
DR InterPro; IPR001839; -.
DR InterPro; IPR002405; -.
DR Pfam; PF00019; TGF-beta; 1.
DR PRINTS; PR00688; TGFb_propeptide; 1.
DR PRINTS; PR00669; INHIBINA.
DR PROSITE; PS00250; TGF_BETA; 1.
DR SMART; SM00204; TGFb; 1.
DR GlycoProtein.
KW Glycoprotein.
SQ SEQUENCE 411 AA; 46929 MW; F579898060F18355 CRC64;

Query Match 32.28; Score 204; DB 5; Length 411;
Best Local Similarity 40.98; Pred. No. 4.7e-15;
Matches 45; Conservative 15; Mismatches 40; Indels 10; Gaps 5;

QY 9 RNLENCVRLYIDFRODLGKWK-WVHEPKGYANFCGPGCPY-----LRSDTTHSTVTL 62
DB 304 RRLKANCRRHSLYVDF-SDVGNDWIVAPGYQAYYCHGECFPPLADHLNS--TNHAIVQ 360
QY 63 GLYNTLNPEASASPCVPODLEPLTILYVGRTPKV--EQLSNMVVKSKC 111
DB 361 TLVNSVNPVLPKACCVPTDLSPLSMVLYNENDQVVLKNYQDMVVEGCGC 410

RESULT 30
Q9HBPO
ID Q9HBPO PRELIMINARY; PRT; 426 AA.
AC Q9HBPO;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE HYPOTHETICAL 47.5 KDA PROTEIN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Gu J.R., Wan D.F., Zhao X.T., Zhou X.M., Jiang H.Q., Zhang P.P.,
RA Qiu W.X., Huang Y., Qiu X.K., Qian L.F., He L.P., Li H.N., Yu Y.,
RA Yu J., Han L.H.;
RT "Novel Human cDNA clones with function of inhibiting cancer cell
growth.";
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF218018; AAG17260.1; -.
KW Hypothetical protein.
SQ SEQUENCE 426 AA; 47454 MW; 339276317B5B408 CRC64;
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Query Match 31.58; Score 200; DB 4; Length 426;
Best Local Similarity 37.48; Pred. No. 1.4e-14;
Matches 40; Conservative 21; Mismatches 36; Indels 10; Gaps 5;

QY 15 CCVRPLYIDFRODLGKWK-WVHEPKGYANFCGPGCP-----YLRSADTTHSTVGLYNTL 68
DB 321 CCKKQFFVSKF-DIGWNDWIIAPSGYHANYCEGCPSPHSTVGINHYRMR 379
QY 69 --NPEASASPCVPODLEPLTILYVGRTPKVEQLSNMVVKSKC 112
DB 380 GHSPPFANLSCCVPTKLRPMSMLYYDQGNIIKKDIQNMIIVEGCGS 426

RESULT 31
Q9PW65
ID Q9PW65 PRELIMINARY; PRT; 404 AA.
AC Q9PW65;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE ACTIVIN BETA A PRECURSOR.
OS Carassius auratus (Goldfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Cyprininae; Carassius.
OX NCBI_TaxID=7957;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN, PITUITARY;
RA Yam K.M., Yu K.L., Ge W.;
RT "Cloning and characterization of activin beta A subunit.";
RL Mol. Cell. Endocrinol. 0:0-0(1999).
CC -1- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
DR EMBL; AF159032; AAD50448.1; -.
DR HSP; P18075; IBMP.
DR InterPro; IPR000491; -.
DR InterPro; IPR001111; -.
DR InterPro; IPR001839; -.
DR InterPro; IPR002405; -.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGFb_propeptide; 1.
DR PRINTS; PR00669; INHIBINA.
DR PRINTS; PR00670; INHIBINA.
DR PROSITE; PS00250; TGF_BETA; 1.
DR SMART; SM00204; TGFb; 1.
KW Glycoprotein; Signal.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 289 404 ACTIVIN BETA A.
SQ SEQUENCE 404 AA; 44799 MW; 3AFB41BE62A8C0DC CRC64;

Query Match 31.28; Score 198; DB 13; Length 404;
Best Local Similarity 38.08; Pred. No. 2.2e-14;
Matches 41; Conservative 19; Mismatches 36; Indels 12; Gaps 6;

QY 15 CCVRPLYIDFRODLGKWK-WVHEPKGYANFCGPGCP-----YLRSADTTHSTVGLYNT- 67
DB 299 CCKKQFFVSKF-DIGWSDWIIAPSGYHANYCEGCPSPHSTVGINHYRMR 357
QY 68 -LNPEASASPCVPODLEPLTILYVGRTPKV--EQLSNMVVKSKC 112
DB 358 GYSPFNNKSCCVPTLRMSMLYV-NESQIKKDIQNMIIVEGCGS 404

RESULT 32
Q91696
ID Q91696 PRELIMINARY; PRT; 367 AA.
AC Q91696;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE ACTIVIN D PRECURSOR.
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OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RX MEDLINE=95275314; PubMed=7755637;
RA Oda S., Nishimatsu S., Murakami K., Ueno N.;
RT "Molecular cloning and functional analysis of a new activin beta
subunit: a dorsal mesoderm-inducing activity in Xenopus.";
RL Biochem. Biophys. Res. Commun. 210:581-588(1995).
CC -!- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
DR EMBL; D49543; BAA08494.1; -.
DR HSSP; P18075; 1BMP.
DR InterPro; IPR001111; -.
DR InterPro; IPR001839; -.
DR InterPro; IPR002400; -.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGF-beta-propeptide; 1.
DR PRINTS; PR00438; GFCYSKNOT.
DR ProDom; PD000357; -; 1.
DR PROSITE; PS00250; TGF_BETA; 1.
DR SMART; SM00204; TGF-beta; 1.
DR Glycoprotein; Signal.
FT SIGNAL 1 253 POTENTIAL.
FT CHAIN 254 367 'ACTIVIN D'.
FT SEQUENCE 367 AA; 41729 MW; C7B6334BD606FA04 CRC64;

Query Match 31.2%; Score 197.5; DB 13; Length 367;
Best Local Similarity 36.0%; Pred. No. 2.3e-14;
Matches 41; Conservative 25; Mismatches 35; Indels 13; Gaps 6;

QY 10 NLEEN---CCVRPLIDFRQDLGWK-WVHEPKGYANFCGPGPYLRS-----ADTHST 60
DB 256 NCDQSNLCCKRDYVDFK-DIGWMDWIIPKGYQINCYCMGLCPMHIAAGPAGMAASFHTT 314

QY 61 VLGLYNTLNPEASAPCCVPQDLEPLTILYVGRTPKV--EQLSNMVKSKCS 112
DB 315 VLNLKANNIQAVNSCCVPTRRPLMLYF-DRNNVLKTDIADMIVEACGCS 367

RESULT 33
Q9MZ18 PRELIMINARY; PRT; 185 AA.
AC Q9MZ18;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE MYOSTATIN (FRAGMENT).
GN MSTN.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RA Lian Z., Jin H., Li N.;
RT "Cloning of intron 2 of the myostatin gene in sheep.";
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
DR EMBL; AF266758; AAF78069.1; -.
DR InterPro; IPR001839; -.
DR Pfam; PF00019; TGF-beta; 1.
DR PROSITE; PS00250; TGF_BETA; 1.
DR Glycoprotein.
KW NON_TER 1 185
FT NON_TER 185
FT SEQUENCE 185 AA; 20923 MW; BA9634203A552850 CRC64;

Query Match 31.0%; Score 196.5; DB 6; Length 185;
Best Local Similarity 38.4%; Pred. No. 1.4e-14;
Matches 38; Conservative 16; Mismatches 40; Indels 5; Gaps 3;

QY 12 EENCVRPLIDFRQDLGWK-WVHEPKGYANFCGPGPYLRSADTHSTHVLGLYNTLPE 71
DB 90 ESRCCRYPLTVDF-EAFGWDWIIPKRYKANYCCEFLFLQKYPHT---HLVHOANPK 145

QY 72 ASASPCCPVQDLEPLTILYVGRTPKV-EQLSNMVKSKC 109
DB 146 GSAGPCCTPKMSPINMLYFNKGKEIYKIPGMVVDR 184

RESULT 34
Q98860 PRELIMINARY; PRT; 413 AA.
AC Q98860;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE ACTIVIN BETA-A SUBUNIT.
OS Cynops pyrrhogaster (Japanese common newt).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Caudata; Salamandridae; Cynops.
OX NCBI_TaxID=8330;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=TESTIS;
RX MEDLINE=96295508; PubMed=8702409;
RA Yamamoto T., Nakayama Y., Abe S.;
RT "Expression of activin beta subunit genes in Sertoli cells of newt
testes".
RL Biochem. Biophys. Res. Commun. 224:451-456(1996).
CC -!- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
DR EMBL; D84516; BAA12693.1; -.
DR HSSP; P18075; 1BMP.
DR InterPro; IPR000491; -.
DR InterPro; IPR001111; -.
DR InterPro; IPR001839; -.
DR InterPro; IPR002400; -.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGF-beta-propeptide; 1.
DR PRINTS; PR00438; GFCYSKNOT.
DR PRINTS; PR00670; INHIBINB.
DR ProDom; PD000357; -; 1.
DR PROSITE; PS00250; TGF_BETA; 1.
DR SMART; SM00204; TGF-beta; 1.
DR Glycoprotein.
KW SEQUENCE 413 AA; 46303 MW; 46F66D112AALB010 CRC64;

Query Match 30.4%; Score 193; DB 13; Length 413;
Best Local Similarity 38.3%; Pred. No. 8.2e-14;
Matches 41; Conservative 17; Mismatches 39; Indels 10; Gaps 6;

QY 15 CCVRPLIDFRQDLGWK-WVHEPKGYANFCGPGCP-YLR----SADTHSTHVLGLYNT- 67
DB 308 CCKKQFYVSEK-DIGWSDWVIAPPGYTANYCEGDCPMYITGSGSPSFHAAVINOYRMR 366

QY 68 -LNPEASAPCCVPQDLEPLTILYV-VGRTPKQSLNMVKSKCS 112
DB 367 GYSPFTSVKSCVPTKLRAMSLYDDGQNIKKDIQNMVVEGCS 413

RESULT 35
P91720 PRELIMINARY; PRT; 614 AA.
AC P91720;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE DECAPENTAPLEGIC PROTEIN.

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GN DPP.
OS Drosophila virilis (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta.
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7244;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97225212; PubMed=9071585;
RA Newfield S.J., Padgett R.W., Findley S.D., Richter B.G., Sanicola M.,
RA de Cuevas M., Gelbart W.M.;
RT "Molecular evolution at the decapentaplegic locus in Drosophila.";
RL Genetics 145:297-309(1997).
CC -!- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
DR EMBL; U63855; AAC47555.1; -.
DR HSSP; P18075; 1BMP.
DR FlyBase; FBgn0013109; Dvir\dpp.
DR InterPro; IPR001111; -.
DR InterPro; IPR001839; -.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGFb_propeptide; 1.
DR ProDom; PD000357; -. 1.
DR PROSITE; PS00250; TGF_BETA; 1.
DR SMART; SM00204; TGFB; 1.
KW Glycoprotein.
SQ SEQUENCE 614 AA; 69055 MW; D0F20A4093403DCE CRC64;

Query Match 30.3%; Score 192; DB 5; Length 614;
Best Local Similarity 40.0%; Pred. No. 1.6e-13;
Matches 44; Conservative 14; Mismatches 42; Indels 10; Gaps 5;

QY 9 RNLENCVRLYIDFRDLGK-WVHEPKGYANFCGCPY-----LRSDTTHSTVL 62
DB 507 KNEEDNCRRHSLYVDF-ODVGSWDIVAPPGYDAYCHGKQFPLADHLNS--TNHAVVQ 563
QY 63 GLYNTLNPEASAPCCVPQDLEPLTILYVGRTPKVEQLSNMVVKSCK 111
DB 564 TLVNLNLPKGVKACCVPTQLEGISMLYLNQRTVVLKYNQDMTVVGGCG 613

RESULT 36
O02424 SEQUENCE FROM N.A.
ID O02424 PRELIMINARY; PRT; 365 AA.
AC O02424;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE DECAPENTAPLEGIC PROTEIN HOMOLOG.
GN DBL-1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=N2;
RA Yandell M.D., Ross R.M., Suzuki Y., Wood W.B.;
RT "Characteristics of dbl-1, a C. elegans decapentaplegic homologue,
RT support a conserved role for BMP-family signaling in bilaterian
RT development.";
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
DR EMBL; AF004395; AAC27729.1; -.
DR HSSP; P18075; 1BMP.
DR InterPro; IPR001111; -.
DR InterPro; IPR001839; -.
DR InterPro; IPR002400; -.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGFb_propeptide; 1.
DR PRINTS; PR00438; GFCYSKNOT.
DR PROSITE; PS000357; -. 1.
DR PROSITE; PS00250; TGF_BETA; UNKNOWN_1.

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DR SMART; SM00204; TGFB; 1.
KW Glycoprotein.
SQ SEQUENCE 365 AA; 41768 MW; 937BFF3459F02C7E CRC64;

Query Match 30.2%; Score 191.5; DB 5; Length 365;
Best Local Similarity 39.6%; Pred. No. 1.1e-13;
Matches 42; Conservative 16; Mismatches 41; Indels 7; Gaps 5;

QY 12 ENCCVVR-PLYIDFRDLGK-WVHEPKGYANFCGCPYLRSD---TTHSTVLGLYN 66
DB 260 ESNLCRRDTDFYVDF-DDLNWQDWIMAPKGYDAYQCQSCPNPMPAQLNATNHAIQSLH 318
QY 67 TLNPEASAPCCVPQDLEPLTILYVGRTPKVEQLSNMVVKSCK 111
DB 319 SLRPDEVPPPCVPTETSPLSILYMDVKVIVIREYADMRVESC 364

RESULT 37
O76514 SEQUENCE FROM N.A.
ID O76514 PRELIMINARY; PRT; 365 AA.
AC O76514;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE CET-1.
GN CET-1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=N2;
RA Morita K., Chow K.L., Ueno N.;
RT "Body length and Male Tail Ray Pattern Formation of C. elegans are
RT Regulated by a Member of TGFb Family.";
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
DR EMBL; AF074395; AAC26791.1; -.
DR HSSP; P18075; 1BMP.
DR InterPro; IPR001111; -.
DR InterPro; IPR001839; -.
DR InterPro; IPR002400; -.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGFb_propeptide; 1.
DR PRINTS; PR00438; GFCYSKNOT.
DR ProDom; PD000357; -. 1.
DR PROSITE; PS00250; TGF_BETA; UNKNOWN_1.
DR SMART; SM00204; TGFB; 1.
KW Glycoprotein.
SQ SEQUENCE 365 AA; 41781 MW; 4DCE5C528BA3FF CRC64;

Query Match 30.2%; Score 191.5; DB 5; Length 365;
Best Local Similarity 39.6%; Pred. No. 1.1e-13;
Matches 42; Conservative 16; Mismatches 41; Indels 7; Gaps 5;

QY 12 ENCCVVR-PLYIDFRDLGK-WVHEPKGYANFCGCPYLRSD---TTHSTVLGLYN 66
DB 260 ESNLCRRDTDFYVDF-DDLNWQDWIMAPKGYDAYQCQSCPNPMPAQLNATNHAIQSLH 318
QY 67 TLNPEASAPCCVPQDLEPLTILYVGRTPKVEQLSNMVVKSCK 111
DB 319 SLRPDEVPPPCVPTETSPLSILYMDVKVIVIREYADMRVESC 364

RESULT 38
Q91403 SEQUENCE FROM N.A.
ID Q91403 PRELIMINARY; PRT; 313 AA.
AC Q91403;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)

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DR	Pfam:	PF00688;	TGFB_propeptide; 1.
DR	PRINTS;	PR00669;	INHIBINA.
DR	PROSITE;	PS00250;	TGF_BETA; 1.
KW	Glycoprotein.		
FT	NON_TER	1	
SQ	SEQUENCE	398 AA; 45459 MW; 9C3F625299DD0C37 CRC64;	
Query Match 30.0%; Score 190; DB 13; Length 398;			
Best Local Similarity 34.8%; Pred. No. 1.7e-13;			
Matches 40; Conservative 22; Mismatches 39; Indels 14; Gaps			
Qy	10 NLEEN-----CCVRPLVIDFRDQLGW-KWHEPKGYGANFCSPGPCPYLRSA---DTT 57		
Dd	284 NIAENSDDORQAQCKHELXYSER-DLGWDWIYIATPGEYAAYCYCEGACAPLNSYNMATN 342		
Qy	58 HSTVLGLYNTLNPEASPCCVQDLEPLILYVGRTPKV-EQLSNMVKSKCK 111		
Dd	343 HAIVQTLVHFINPTVPKPCAPTQLNAISLVIFDDSSNVILAKRYNMVVRRGCC 397		
RESULT	40		
O12938	PRELIMINARY;	PRT;	412 AA.
ID	O12938		
AC	012938;		
DT	01-JUL-1997 (TREMBLrel. 04, Created)		
DT	01-JUL-1997 (TREMBLrel. 04, Last sequence update)		
DI	01-MAR-2001 (TREMBLrel. 16, Last annotation update)		
DE	DYNAMO PROTEIN PRECURSOR.		
GN	DYNAMO.		
OS	Brachydanio rerio (zebrafish) (Zebra danio).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;		
OC	Cypriniformes; Cyprinidae; Rasborinae; Danio.		
OX	NCBI_TaxID=7955;		
[J]			
RN	SEQUENCE FROM N.A.		
RP	TISSUE-WHOLE EMBRYO;		
RX	MEDLINE=97231294; PubMed=9076689;		
RA	Bruneau S., Rosa F.;		
RT	"Dynamo, a new zebrafish DVR member of the TGF-beta superfamily is expressed in the posterior neural tube and is up-regulated by Sonic hedgehog.";		
RL	Mech. Dev. 61:199-212(1987).		
CC	-1- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.		
DR	ENBL; X95769; CAA68102.1; "		
DR	HSSP; P18075; IBM.		
DR	ZFIN; ZDB-GENE-980526-442; dynamo.		
DR	InterPro; IPR001111; "		
DR	InterPro; IPR001839; "		
DR	InterPro; IPR002400; "		
DR	Pfam; PF00019; TGF-beta; 1.		
DR	Pfam; PF00688; TGFB_propeptide; 1.		
DR	PRINTS; PR00438; GFCYSKNOT.		
DR	PRODOM; PD000357; -; 1.		
DR	PROSITE; PS00250; TGF_BETA; 1.		
DR	SMART; SM00204; TGFB; 1.		
KW	Glycoprotein; Signal.		
FT	SIGNAL	1	POTENTIAL.
FT	CHAIN	293	412 DYNAMO PROTEIN.
SQ	SEQUENCE	412 AA; 47071 MW; 4076E262C4A81121 CRC64;	
Query Match 30.0%; Score 190; DB 13; Length 412;			
Best Local Similarity 40.0%; Pred. No. 1.8e-13;			
Matches 42; Conservative 16; Mismatches 41; Indels 6; Gaps			
Qy	12 EENCVRPLVIDFRDQLGW-KWHEPKGYANFCSPGPCPY-LRS---ADTTHTSVLGLYNT 67		
Dd	308 KSRCSKKPLAVNER-ELGWDWDWIAPLDYRAYHCEGCMDFPLSHLEPTNHAIQTLMNS 366		
Qy	68 LNPEASPCPVQDLEPLILYVGRTPKEQLSNMVKSKCK 111		

Db 367 MNPSNPPSCCVPSKSLSPISILYIDAGNNVYKQYEDMVVESC GC 411

RESULT 41

Q9DGF2
ID Q9DGF2 PRELIMINARY; PRT; 115 AA.
AC Q9DGF2
DT 01-MAR-2001 (TremBLrel. 16, Created)
DT 01-MAR-2001 (TremBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TremBLrel. 16, Last annotation update)
DE INHIBIN/ACTIVIN (FRAGMENT).
OS Cyprinus carpio (Common carp).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Cyprininae; Cyprinidae; Cyprinus.
OX NCBI_TaxID=7962;
RN [1]
RP SEQUENCE FROM N.A.
RA Tada T., Hirono I., Aoki T., Takashima F.;
RT "Cloning and sequencing of carp and medaka activin subunit genes."
RL Fisheries Sci. 64:680-685(2000).
DR EMBL; AB009403; BAB17596.1; -.
FT NON_TER 1 115
FT NON_TER 115 115
SQ SEQUENCE 115 AA; 13139 MW; 8C8C7C7A784E51D2 CRC64;

Query Match 29.8%; Score 189; DB 13; Length 115;
Best Local Similarity 36.4%; Pred. No. 6.2e-14;
Matches 39; Conservative 20; Mismatches 36; Indels 12; Gaps 6;

Qy 15 CCVRPLYIDFRQDLGWK-WVHEPKGYANFCSGPCP-----YLRSDTTHSTVLGLYNT- 67

Db 11 CCKRQFYVNFK-DIGWSDWIIAPSGYHANYCEGDCPIHVASIMGSAFSFHTVINHYRMR 69

Qy 68 -LNPEASAPCCVPQDLPLTILYVGRTPKV--EQLSNMVVKSKC 111

Db 70 GYSPFNKSCCVPTLRAMSL-YCNEEQKIIRKIDQNNMIVECGC 115

RESULT 42

Q9DGE8
ID Q9DGE8 PRELIMINARY; PRT; 115 AA.
AC Q9DGE8
DT 01-MAR-2001 (TremBLrel. 16, Created)
DT 01-MAR-2001 (TremBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TremBLrel. 16, Last annotation update)
DE INHIBIN/ACTIVIN (FRAGMENT).
OS Oryzias latipes (Medaka fish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
OC Belontiiformes; Adrianichthyidae; Oryziinae; Oryzias.
OX NCBI_TaxID=8090;
RN [1]
RP SEQUENCE FROM N.A.
RA Tada T., Hirono I., Aoki T., Takashima F.;
RT "Cloning and sequencing of carp and medaka activin subunit genes."
RL Fisheries Sci. 64:680-685(2000).
DR EMBL; AB009407; BAB17600.1; -.
FT NON_TER 1 115
FT NON_TER 115 115
SQ SEQUENCE 115 AA; 13127 MW; 90628E7BC85BA432 CRC64;

Query Match 29.8%; Score 189; DB 13; Length 115;
Best Local Similarity 36.4%; Pred. No. 6.2e-14;
Matches 39; Conservative 20; Mismatches 36; Indels 12; Gaps 6;

Qy 15 CCVRPLYIDFRQDLGWK-WVHEPKGYANFCSGPCP-----YLRSDTTHSTVLGLYNT- 67

Db 11 CCKRQFYVNFK-DIGWSDWIIAPSGYHANYCEGDCPIHVASIMGSAFSFHTVINHYRMR 69

Qy 68 -LNPEASAPCCVPQDLPLTILYVGRTPKV--EQLSNMVVKSKC 111

Db 70 GYSPFNKSCCVPTLRAMSL-YCNEEQKIIRKIDQNNMIVECGC 115

RESULT 43

Q9H512
ID Q9H512 PRELIMINARY; PRT; 177 AA.
AC Q9H512
DT 01-MAR-2001 (TremBLrel. 16, Created)
DT 01-MAR-2001 (TremBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TremBLrel. 16, Last annotation update)
DE BA50A15.1 (BONE MORPHOGENETIC PROTEIN 7 (OSTEOGENIC PROTEIN 1))
DE (FRAGMENT).
GN BMP7.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Heath P.;
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL157414; CAC08434.1; -.
FT NON_TER 1 177
FT NON_TER 177 177
SQ SEQUENCE 177 AA; 19985 MW; 3DD2ABDD09D6323D CRC64;

Query Match 29.8%; Score 189; DB 4; Length 177;
Best Local Similarity 34.8%; Pred. No. 9.7e-14;
Matches 40; Conservative 22; Mismatches 39; Indels 14; Gaps 5;

Qy 10 NLEEN-----CCVRPLYIDFRQDLGWK-WVHEPKGYANFCSGPCPYLRSA---DTT 57

Db 63 NVAENSSDQRAQKHELYVSR-DLGWDWIIAPSGYHANYCEGDCAPPLNSYNMNTN 121

Qy 58 HSTVLGLYNTLNPEASAPCCVPQDLPLTILYVGRTPKV-EQLSNMVVKSKC 111

Db 122 HAIVQTLVHFNPETVPKCAPTQLNAISLVLYFDSSNVILKRYRMVVRACGC 176

RESULT 44

Q9GT26
ID Q9GT26 PRELIMINARY; PRT; 438 AA.
AC Q9GT26
DT 01-MAR-2001 (TremBLrel. 16, Created)
DT 01-MAR-2001 (TremBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TremBLrel. 16, Last annotation update)
DE GBB-60A-LIKE PROTEIN AS60A.
OS Anopheles stephensi (Indo-Pakistan malaria mosquito).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
OC Anopheles.
OX NCBI_TaxID=30069;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-WHOLE ANIMAL;
RA Crampton A.L., Luckhart S.;
RT "Isolation and characterization of As60A, a transforming growth factor
B gene, from the malaria vector Anopheles stephensi."
RL Cytokine 0:0-0(2000).
DR EMBL; AF284816; AAG13400.1; -.
SQ SEQUENCE 438 AA; 49824 MW; 124BA66DAA832E84 CRC64;

Query Match 29.8%; Score 189; DB 5; Length 438;
Best Local Similarity 36.5%; Pred. No. 2.5e-13;
Matches 38; Conservative 23; Mismatches 37; Indels 6; Gaps 4;

Qy 13 ENCCVRPLYIDFRQDLGW-KWHEPKGYANFCSGPCPYLRSA---TTHSTVLGLYNTL 68

Db 335 KSCRQIQLYVSKF-DLQWHEWIIAPSGYHANYCEGDCPFLNAHMTNHAIVQTLVHLN 393

QY 69 NPEASAPCCVPQDLEPLTILYVGR-TPKVEQLSNMVKSCKC 111
DB 394 HPTKVPKCCAPTKLIPISVLIHIDEANWLNKKYKNMVKSCGC 437

RESULT 45
Q91350 PRELIMINARY; PRT; 370 AA.
AC Q91350;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE ACTIVIN BETA B SUBUNIT.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93273083; PubMed=8500654;
RA Dohrmann C.E., Hemmati-Brivanlou A., Thomsen G.H., Fields A.,
RA Wolf T.M., Melton D.A.;
RT "Expression of activin mRNA during early development in Xenopus
RT laevis.";
RL Dev. Biol. 157:474-483(1993).
CC -1- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
DR EMBL; S61773; AAB26863.1; -;
DR HSP; P18075; 1BMP.
DR InterPro; IPR001111; -;
DR InterPro; IPR001839; -;
DR InterPro; IPR002400; -;
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGF-beta; 1.
DR PRINTS; PR00438; GFCYSKNOT.
DR ProDom; PD000357; -; 1.
DR PROSITE; PS00250; TGF-BETA; 1.
DR SMART; SM00204; TGF-beta; 1.
KW Glycoprotein.
SQ SEQUENCE 370 AA; 41678 MW; AD21502AC45FIDE9 CRC64;

Query Match 29.7%; Score 188.5; DB 13; Length 370;
Best Local Similarity 38.3%; Pred. No. 2.4e-13;
Matches 41; Conservative 19; Mismatches 36; Indels 11; Gaps 7;

QY 15 CCVRPLYIDFQDLGW-KWHEPKGYANFCSGPCP-YLR-----SADTHTSTVLGLYNT- 67
DB 266 CCRQFYIDFRL-IGWDDWIIAPLEYEAHHCVCDFPLRSHLEPTNHAIITLMSMNP 324

QY 68 -LNPEASAPCCVPQDLEPLTILYVGRTPKVEQ-LSNMVKVKSCKCS 112
DB 325 GLNP-GTVNSCCPTKLSTMSMLYFDDEYNIVKRDVPMIVDCGCA 370

RESULT 46
Q9W759 PRELIMINARY; PRT; 96 AA.
AC Q9W759;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE MYOSTATIN (FRAGMENT).
GN MSTN.
OS Cairina moschata (Muscovy duck).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Cairina.
OX NCBI_TaxID=8855;
RN [1]
RP SEQUENCE FROM N.A.
RA Barrios M., Pallova P., Karpisek M., Londynova J., Stankova I.,
RA Svoboda I., Vernerova N., Ruzicka V.;
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.

CC -1- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
DR EMBL; AF151692; AAD42221.1; -;
DR HSP; P18075; 1BMP.
DR InterPro; IPR001839; -;
DR Pfam; PF00019; TGF-beta; 1.
DR PROSITE; PS00250; TGF-BETA; 1.
DR SMART; SM00204; TGF-beta; 1.
KW Glycoprotein.
FT NON_TER 1
FT NON_TER 96
SQ SEQUENCE 96 AA; 11040 MW; 383BC564EBD6EF18 CRC64;

Query Match 29.7%; Score 188; DB 13; Length 96;
Best Local Similarity 41.2%; Pred. No. 6.6e-14;
Matches 35; Conservative 12; Mismatches 30; Indels 8; Gaps 3;

QY 12 EENCVRPLYIDFQDLGW-KWHEPKGYANFCSGPCP--YLRSDATHTSTVLGLYNTLN 69
DB 7 ESRCCRYPLTVDF-EAFGWDWIIAPLEYEAHHCVCDFPLRSHLEPTNHAIITLMSMNP 60

QY 70 PEASAPCCVPQDLEPLTILYVGR 94
DB 61 PRGSAGCCCTTKMSPINMLYFNGK 85

RESULT 47
Q9W753 PRELIMINARY; PRT; 399 AA.
AC Q9W753;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE GROWTH AND DIFFERENTIATION FACTOR 6.
GN GDF6.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Chang C., Hemmati-Brivanlou A.;
RT "Xenopus GDF6, a new antagonist of noggin and a partner of BMPs.";
RL Development 0:0-0(1999).
CC -1- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
DR EMBL; AF155125; AAD38402.1; -;
DR HSP; P18075; 1BMP.
DR InterPro; IPR001111; -;
DR InterPro; IPR001839; -;
DR InterPro; IPR002405; -;
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGF-beta; 1.
DR PRINTS; PR00669; INHIBINA.
DR PROSITE; PS00250; TGF-BETA; 1.
DR SMART; SM00204; TGF-beta; 1.
KW Glycoprotein.
SQ SEQUENCE 399 AA; 45571 MW; C549D973B50B8517 CRC64;

Query Match 29.7%; Score 188; DB 13; Length 399;
Best Local Similarity 39.2%; Pred. No. 2.9e-13;
Matches 40; Conservative 20; Mismatches 36; Indels 6; Gaps 5;

QY 15 CCVRPLYIDFQDLGW-KWHEPKGYANFCSGPCP-YLR--ADTHTSTVLGLYNTLN 70
DB 298 CSKPLHVNFK-ELGWDWIIAPLEYEAHHCVCDFPLRSHLEPTNHAIITLMSMNP 356

QY 71 EASAPCCVPQDLEPLTILYVGRTPKVEQLSNMVKVKSCKC 111
DB 357 GSTPPSCCVPKLTIPISILYIDAGNNVYKQYEDMNVVSCGC 398


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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX PUBMED=10906478;
RA Vokes S.A., Krieg P.A.;
RT "Gdf16, a novel member of the growth/differentiation factor subgroup
RT of the TGF-beta superfamily, is expressed in the hindbrain and
RT ephibranchial placodes.";
RL Mech. Dev. 95:279-282(2000).
DR EMBL: AF239676; AAF9597.1; -.
KW Signal.
FT SIGNAL.
FT SIGNAL.
SQ SEQUENCE 1 23 POTENTIAL.
SQ SEQUENCE 413 AA; 46510 MW; 5F1B0D7D97E591F6 CRC64;

Query Match 29.5%; Score 187; DB 13; Length 413;
Best Local Similarity 39.2%; Pred. No. 3.9e-13;
Matches 40; Conservative 19; Mismatches 37; Indels 6; Gaps 5;

QY 15 CCVRPLYIDFRDLGW-KWHEPKGYANFCSPCPY-LRS--ADTTHSTVLGLYNTLNP 70
DB 312 CSKKPLLVNFK-ELGWDWIIAPLDYEAHCEGVCDPLRSHLEPTNHAIQTLMNSMDP 370
QY 71 EASASPCVPQDLEPTILYY-VGRTPKVEQLSNMVKSCK 111
DB 371 ESTPPSCCVPSKLSILYIDSGNNVYKQYEDMWVESCSC 412

RESULT 52
Q25211 PRELIMINARY; PRT; 178 AA.
AC Q25211;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE DECAPENTAPLEGIC (FRAGMENT).
OS Junonia coenia (Peacock butterfly) (Precis coenia).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Papilionoidea; Nymphalidae; Nymphalinae; Junonia.
OX NCBI_TaxID=39708;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-WHOLE ANIMAL;
RX MEDLINE=94287189; PubMed=7912449;
RA Carroll S.B., Gates J., Keys D.N., Paddock S.W., Panganiban G.E.,
RA Selegue J.E., Williams J.A.;
RT "Pattern formation and eyespot determination in butterfly wings.";
RL Science 265:109-114(1994).
CC -1- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
DR EMBL: L42141; AAB46367.1; -.
DR HSSP: P18075; IAMP.
DR InterPro: IPR001839; -.
DR InterPro: IPR002405; -.
DR Pfam: PF00019; TGF-beta; 1.
DR PRINTS: PR00438; GFCYSKNOT.
DR PROSITE: PS00250; TGF_BETA; 1.
DR SMART: SM00204; TGFB; 1.
DR Glycoprotein.
FT NON_TER 1
SQ SEQUENCE 178 AA; 20443 MW; 30D3A7E55458EADAE CRC64;

Query Match 29.3%; Score 186; DB 5; Length 178;
Best Local Similarity 34.8%; Pred. No. 2.1e-13;
Matches 40; Conservative 21; Mismatches 34; Indels 20; Gaps 5;

QY 9 RNLENCVVRPLYIDFRDLGW-KWHEPKGYANFCSPCPY-LRS---ADTTHSTVLGL 64

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DB 71 KEAREICQRPLEFVDF-ADVGSWDIIVAPHGYDAYVCGDCCPFLPSDLHNGTNAIVOTL 129
QY 65 YNTLNPEASASPCVPQDLEPTILYYVGRTPKVEQLSNMVKSCK 111
DB 130 VNSVNPAAVPKACCVPTQLSSISMLY-----MDEVNNVVLKNYQDMVMVCCGC 177

RESULT 53
Q9W6C0 PRELIMINARY; PRT; 261 AA.
AC Q9W6C0;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE GROWTH/DIFFERENTIATION FACTOR 7 (FRAGMENT).
GN GDF7.
OS Brachydanio rerio (Zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Rasboridae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99148135; PubMed=10022976;
RA Davidson A.J., Postlethwait J.H., Yan Y.L., Beier D.R., van Doren C.,
RA Foerzler D., Celeste A.J., Crosier K.E., Crosier P.S.;
RT "Isolation of zebrafish gdf7 and comparative genetic mapping of genes
RT belonging to the growth/differentiation factor 5, 6, 7 subgroup of the
RT TGF-beta superfamily.";
RL Genome Res. 9:121-129(1999).
CC -1- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
DR EMBL: AF113023; AAD20829.1; -.
DR HSSP: P18075; IAMP.
DR InterPro: IPR001839; -.
DR InterPro: IPR002405; -.
DR InterPro: IPR002405; -.
DR Pfam: PF00019; TGF-beta; 1.
DR PRINTS: PR00438; GFCYSKNOT.
DR PROSITE: PS00250; TGF_BETA; 1.
DR SMART: SM00204; TGFB; 1.
DR Glycoprotein.
FT NON_TER 1
SQ SEQUENCE 261 AA; 29414 MW; 77346E977036A104 CRC64;

Query Match 29.3%; Score 186; DB 13; Length 261;
Best Local Similarity 39.2%; Pred. No. 3.2e-13;
Matches 40; Conservative 20; Mismatches 36; Indels 6; Gaps 5;

QY 15 CCVRPLYIDFRDLGW-KWHEPKGYANFCSPCPY-LRS--ADTTHSTVLGLYNTLNP 70
DB 160 CSRKPLHVNFK-ELGWDWIIAPLDYEAHCEGLCDPLRSHLEPTNHAIQTLMNSMDP 218
QY 71 EASASPCVPQDLEPTILYY-VGRTPKVEQLSNMVKSCK 111
DB 219 ESTPPSCCVPSKLSILYIDSGNNVYKQYEDMWVESCSC 260

RESULT 54
Q9DGE9 PRELIMINARY; PRT; 115 AA.
AC Q9DGE9;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE INHIBIN/ACTIVIN (FRAGMENT).
OS Cyprinus carpio (Common carp).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Cyprininae; Cyprinus.

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OX NCBI_TaxID=7962;
RN [1]
RP SEQUENCE FROM N.A.
RA Tada T., Hirono I., Aoki T., Takashima F.;
RT "Cloning and sequencing of carp and medaka activin subunit genes.";
RL Fisheries Sci. 64:680-685(2000).
DR EMBL: AB009406; BABI7599.1; -
FT NON_TER 1 115
FT NON_TER 115 115
SQ SEQUENCE 115 AA; 12666 MW; CD38FA0DD7BD52A6 CRC64;

Query Match 29.3%; Score 185.5; DB 13; Length 115;
Best Local Similarity 37.7%; Pred. No. 1.5e-13;
Matches 40; Conservative 20; Mismatches 35; Indels 11; Gaps 7;

QY 15 CCVRPLXIDFQDLGKWK-WHEPKGYANFCGPGCP-YLR-...-SADTTHSTVLGLYNT- 67
Db 12 CCROQFIDFRL-TGNDWIITAPAGYGNICEGSPAYLAGVPGSASSFHTAVVQYRMR 70
QY 68 -LNPEASASCCVPPQDLPLEPLTILYVGTPEQ-LSNMVVKSKC 111
Db 71 GMSPP-GSVNSCCITKLTSMLSMLYFDDYENIVKRDVPNMIIVECGC 115

RESULT 55
Q91597
ID Q91597 PRELIMINARY; PRT; 390 AA.
AC Q91597;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE ANTI-DORSALIZING MORPHOGENETIC PROTEIN 1 PRECURSOR.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipiloidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Moos M., Wang S., Krinks M.;
RT "Anti-dorsalizing morphogenetic protein is a novel TGF-beta homolog
expressed in the Spemann organizer.";
RL Development 121:4293-4301(1995).
CC -1- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
DR EMBL: U2155; AAC59736.1; -
DR HSP; P18075; IBMP.
DR InterPro: IPR001111; -
DR Pfam: PF00019; TGF-beta; 1.
DR PROSITE: PS00250; TGF-BETA; 1.
DR SMART: SM00204; TGFB; 1.
DR SIGNAL 1 17 POTENTIAL.
FT CHAIN 18 390 ANTI-DORSALIZING MORPHOGENETIC PROTEIN 1.
SQ SEQUENCE 390 AA; 44367 MW; DEC8IA001349C895 CRC64;

Query Match 29.3%; Score 185.5; DB 13; Length 390;
Best Local Similarity 36.3%; Pred. No. 5.5e-13;
Matches 41; Conservative 20; Mismatches 41; Indels 11; Gaps 6;

QY 9 RNLEEN---CCVRPLXIDFQDLGKWK-WHEPKGYANFCGPGCPY---LRSADTTHST 60
Db 278 RSVEDQLPCORPLIYDF-EETGWSGWIISPRGYNAHCKGSPFLGQNMPTNAT 336
QY 61 VLGLYNTLN-PEASASCCVPPQDLPLEPLTILYV-VGRTPKVEQLSNMVVKSKC 111
Db 337 VQSINALKLTGKVSSPCVPPDKLFSINLLYFDDDDNVVLKQYDDMVAGSCGC 389

Query Match 29.3%; Score 185.5; DB 13; Length 390;
Best Local Similarity 36.3%; Pred. No. 5.5e-13;
Matches 41; Conservative 20; Mismatches 41; Indels 11; Gaps 6;

QY 9 RNLEEN---CCVRPLXIDFQDLGKWK-WHEPKGYANFCGPGCPY---LRSADTTHST 60
Db 278 RSVEDQLPCORPLIYDF-EETGWSGWIISPRGYNAHCKGSPFLGQNMPTNAT 336
QY 61 VLGLYNTLN-PEASASCCVPPQDLPLEPLTILYV-VGRTPKVEQLSNMVVKSKC 111
Db 337 VQSINALKLTGKVSSPCVPPDKLFSINLLYFDDDDNVVLKQYDDMVAGSCGC 389

Query Match 29.3%; Score 185.5; DB 5; Length 683;
Best Local Similarity 38.7%; Pred. No. 9.8e-13;
Matches 43; Conservative 16; Mismatches 43; Indels 9; Gaps 5;

QY 9 RNLEEN---CCVRPLXIDFQDLGKWK-WHEPKGYANFCGPGCPYLRSD---TTHSTV 61
Db 573 KKLKGTQACHREELVSP-QDVNWEDWIIAPSGYMAVRCGECDFPLSANMNATNHAIV 631
QY 62 LGLYNTLNPEASASCCVPPQDLPLEPLTILYV-VGRTPKVEQLSNMVVKSKC 111
Db 632 QTLVHLKSLKFPCCCTPDLDLSISLVYDDHNNVYVYKRYNMVYLSCAC 682

RESULT 57
Q93573
ID Q93573 PRELIMINARY; PRT; 126 AA.
AC Q93573;
DT 01-NOV-1998 (Tremblrel. 08, Created)
DT 01-NOV-1998 (Tremblrel. 08, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE PUTATIVE GROWTH/DIFFERENTIATION FACTOR 6/7 (FRAGMENT).
GN GDF6/7.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Lee K.J., Mendelsohn M., Jessell T.M.;
RT "Neuronal patterning by BMPs: A requirement for GDF7 in the generation
of a discrete class of commissural interneurons in the mouse spinal
cord.";
RL Genes Dev. 0:0-0(1998).
CC -1- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
DR EMBL: AF089086; AAC97113.1; -
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RESULT 56
Q94580
ID Q94580 PRELIMINARY; PRT; 683 AA.
AC Q94580;
DT 01-FEB-1997 (Tremblrel. 02, Created)
DT 01-FEB-1997 (Tremblrel. 02, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE BONE MORPHOGENIC PROTEIN A.
OS Halocynthia roretzi (Sea squirt).
OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;
OC Stolidobranchia; Pyuridae; Halocynthia.
OX NCBI_TaxID=7729;
RN [1]
RP SEQUENCE FROM N.A.
RA Miya T., Morita K., Ueno N., Satoh N.;
RT "An ascidian homologue of vertebrate BMPs-5-8 is expressed in the
midline of the anterior neuroectoderm and in the midline of the
ventral epidermis of the embryo.";
RL Mech. Dev. 57:181-190(1996).
CC -1- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
DR EMBL: D83183; BAAL1835.1; -
DR HSP; P18075; IBMP.
DR InterPro: IPR001111; -
DR InterPro: IPR001839; -
DR InterPro: IPR002400; -
DR Pfam: PF00019; TGF-beta; 1.
DR PRINTS: PR00438; GFCYSKNOT.
DR PRODOM: PD000357; -; 1.
DR PROSITE: PS00250; TGF-BETA; 1.
DR SMART: SM00204; TGFB; 1.
DR Glycoprotein.
KW GDF6/7.
SQ SEQUENCE 683 AA; 78693 MW; A0A157AE2518B686 CRC64;

Query Match 29.3%; Score 185.5; DB 5; Length 683;
Best Local Similarity 38.7%; Pred. No. 9.8e-13;
Matches 43; Conservative 16; Mismatches 43; Indels 9; Gaps 5;

QY 9 RNLEEN---CCVRPLXIDFQDLGKWK-WHEPKGYANFCGPGCPYLRSD---TTHSTV 61
Db 573 KKLKGTQACHREELVSP-QDVNWEDWIIAPSGYMAVRCGECDFPLSANMNATNHAIV 631
QY 62 LGLYNTLNPEASASCCVPPQDLPLEPLTILYV-VGRTPKVEQLSNMVVKSKC 111
Db 632 QTLVHLKSLKFPCCCTPDLDLSISLVYDDHNNVYVYKRYNMVYLSCAC 682

RESULT 57
Q93573
ID Q93573 PRELIMINARY; PRT; 126 AA.
AC Q93573;
DT 01-NOV-1998 (Tremblrel. 08, Created)
DT 01-NOV-1998 (Tremblrel. 08, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE PUTATIVE GROWTH/DIFFERENTIATION FACTOR 6/7 (FRAGMENT).
GN GDF6/7.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Lee K.J., Mendelsohn M., Jessell T.M.;
RT "Neuronal patterning by BMPs: A requirement for GDF7 in the generation
of a discrete class of commissural interneurons in the mouse spinal
cord.";
RL Genes Dev. 0:0-0(1998).
CC -1- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
DR EMBL: AF089086; AAC97113.1; -
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DR HSP; P18075; 1BMP.
DR InterPro; IPR001839; -.
DR InterPro; IPR002400; -.
DR InterPro; IPR002405; -.
DR Pfam; PF00019; TGF-beta; 1.
DR PRINTS; PR00438; GFCYSKNOT.
DR PRINTS; PR00669; INHIBINA.
DR PROSITE; PS00250; TGF-BETA; 1.
DR SMART; SM00204; TGFB; 1.
KW Glycoprotein.
FT NON_TER
SQ SEQUENCE 126 AA; 14265 MW; CB824D280F44A394 CRC64;

Query Match 29.2%; Score 185; DB 13; Length 136;
Best Local Similarity 36.1%; Pred. No. 1.9e-13;
Matches 39; Conservative 23; Mismatches 40; Indels 6; Gaps 5;

QY 9 RNLEENCVRPLYIDFRDLGW-KWHEPKGYANFCGCPY-LRS--ADTTHSTVLGL 64
D : : : : : : : : : : : : : : : : : : : : : : : : : : : :
D 19 KKAATCRSKRPLHNFK-ELGWDWIIAPLDYEAHCEGVCDPLRSHLEPTNHAIQT 77

QY 65 YNTLNPEASPCCVQDLEPLTILYVGRTPKV--EQLSNMVVKSKC 111
D : : : : : : : : : : : : : : : : : : : : : : : : : : : :
D 78 MNSMPESTPPSCCVSKLSPISILYIDSGNNVYVQYEDMVVETCGC 125

RESULT 58
QYXZ69
ID Q9XZ69 PRELIMINARY; PRT; 204 AA.
AC Q9XZ69;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE BONE MORPHOGENETIC PROTEIN 2/4 HOMOLOG (FRAGMENT).
GN BMP2/4.
OS Tripneustes gratilla (Hawaiian sea urchin).
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC Echinoidea; Euechinoidea; Echinacea; Temnopleuroidea; Toxopneustidae;
OC Tripneustes.
OX NCBI_TaxID=7673;
RN [1]
RN SEQUENCE FROM N.A.
RP MEDLINE=99262121; PubMed=10329409;
RX Hwang S.-P.L., Chen C.A., Chen C.-P.;
RA "Sea urchin TgBMP2/4 gene encoding a bone morphogenetic protein
RT closely related to vertebrate BMP2 and BMP4 with maximal expression at
RT the later stages of embryonic development.";
RL Biochem. Biophys. Res. Commun. 258:457-463(1999).
CC -|- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
D EMBL; AF133305; AAD30538.1; -.
DR HSP; P18075; 1BMP.
DR InterPro; IPR001839; -.
DR InterPro; IPR002400; -.
DR InterPro; IPR002405; -.
DR Pfam; PF00019; TGF-beta; 1.
DR PRINTS; PR00438; GFCYSKNOT.
DR PRINTS; PR00669; INHIBINA.
DR PROSITE; PS00250; TGF-BETA; 1.
DR SMART; SM00204; TGFB; 1.
KW Glycoprotein.
FT NON_TER
SQ SEQUENCE 204 AA; 23697 MW; CE829BDC2AA9F077 CRC64;

Query Match 29.2%; Score 185; DB 5; Length 204;
Best Local Similarity 36.7%; Pred. No. 3.2e-13;
Matches 40; Conservative 19; Mismatches 42; Indels 8; Gaps 5;

QY 9 RNLEENCVRPLYIDFRDLGW-KWHEPKGYANFCGCPYLRSA--DTTHSTVLGL 64
D : : : : : : : : : : : : : : : : : : : : : : : : : : : :
D 97 KRLKANCRRHPLYVDF-SDVHNDWIVAPAGYQAYYCHGECPPFLAHLNTHAIVQTL 155

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QY 65 YNTLNPEASPCCVQDLEPLTILYVGRTPKV--EQLSNMVVKSKC 111
D : : : : : : : : : : : : : : : : : : : : : : : : : : : :
D 156 VNSVNPALVPRACCVPTLSAISML-YLDEYKVVLLKNYQDMVVEGCGC 203

RESULT 59
Q9WUK5
ID Q9WUK5 PRELIMINARY; PRT; 351 AA.
AC Q9WUK5;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE ACTIVIN BETA C.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RN SEQUENCE FROM N.A.
RP STRAIN=Wistar;
RC Rossmannith W., Peter B., Schulte-Hermann R.;
RA "Rat activin beta C and beta E: sequence and expression.";
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
CC -|- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
D EMBL; AF140031; AAD30132.1; -.
DR HSP; P18075; 1BMP.
DR InterPro; IPR001318; -.
DR InterPro; IPR001839; -.
DR InterPro; IPR002405; -.
DR Pfam; PF00019; TGF-beta; 1.
DR PRINTS; PR00669; INHIBINA.
DR PRINTS; PR00672; INHIBINBC.
DR PROSITE; PS00250; TGF-BETA; 1.
DR SMART; SM00204; TGFB; 1.
KW Glycoprotein.
SQ SEQUENCE 351 AA; 39335 MW; 6B219BF6C3E180A1 CRC64;

Query Match 29.2%; Score 185; DB 11; Length 351;
Best Local Similarity 37.7%; Pred. No. 5.6e-13;
Matches 43; Conservative 20; Mismatches 39; Indels 12; Gaps 6;

QY 9 RNLEENCVRPLYIDFRDLGW-KWHEPKGYANFCGCPYLRSA-----TTHSTV 61
D : : : : : : : : : : : : : : : : : : : : : : : : : : : :
D 240 QGLSRMCCRQEFFVDFR-EIGHWDWIIQEGYANMFCGQCP-LHVAGMPGISASFTAV 297

QY 62 LGLY--NTLNPEASPCCVQDLEPLTILYVGRTPKVE-QLSNMVVKSKCS 112
D : : : : : : : : : : : : : : : : : : : : : : : : : : : :
D 298 LNLKANTDAGTARRGSCVPTSRRLSLLYYDRDSNIVKTDIPDMVVEACGCS 351

RESULT 60
Q9PWR8
ID Q9PWR8 PRELIMINARY; PRT; 392 AA.
AC Q9PWR8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE ACTIVIN BETA B SUBUNIT PRECURSOR.
OS Carassius auratus (Goldfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Cyprininae; Carassius.
OX NCBI_TaxID=7957;
RN [1]
RN SEQUENCE FROM N.A.
RP TISSUE-Ovary;
RA Ge W., Miura T., Kobayashi H., Peter R.E., Nagahama Y.;
RT "Cloning of cDNA for goldfish activin beta B subunit, and the
RT expression of its messenger RNA in gonadal and non-gonadal tissues.";
RL J. Mol. Endocrinol. 0:0-0(0).
CC -|- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
D EMBL; AF004669; AAB61468.1; -.

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DR HSP; P18075; I BMP.
DR InterPro; IPR000381; -
DR InterPro; IPR001111; -
DR InterPro; IPR001318; -
DR InterPro; IPR001839; -
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGFB_propeptide; 1.
DR PRINTS; PR00671; INHIBINBB.
DR PRINTS; PR00672; INHIBINBC.
DR PROSITE; PS00250; TGF_BETA; 1.
DR SMART; SM00204; TGFB; 1.
KW Glycoprotein; Signal.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 277 392 ACTIVIN BETA B SUBUNIT.
SQ SEQUENCE 392 AA; 43853 MW; 73AAA7E1C0B2450B CRC64;

Query Match      29.1%; Score 184.5; DB 13; Length 392;
Best Local Similarity 36.4%; Pred. No. 7.2e-13;
Matches 39; Conservative 22; Mismatches 35; Indels 11; Gaps 7;

QY 15 CCVRPLYIDFQQDLGWK-WVHEPKGYANFCGGPCP-YLR-----SADTTHSTVLGLYNT- 67
DB 288 CCRQFYIDFLR-LGWNDWIITAPGYGNCEGSCPAYMAGVPGSASFHTAVNQYRMR 346
    ||| ||||| :|| :| | ||| ||| ||| ||| ||| :| :| :| :| :|
QY 68 -LNPEASASPCCPDQLPLILTYVGRTPKVEQ-LSNMVVKSKCS 112
    :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
DB 347 GISP-GSVNSCCIPKLTSMSLVFDDDEYNIVKRDPVNKIIVECGCA 392

RESULT 61
Q90261 PRELIMINARY; PRT; 393 AA.
AC O90261
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE ACTIVIN BETA B.
GN ZACTBB OR ZACTBETAB.
OS Brachydanio rerio (Zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Rasborinae; Danio.
NCBI_TaxId=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95011555; PubMed=7926744;
RA Wattbrodt J., Frederic R.M.;
RT "Distruption of mesoderm and axis formation in fish by ectopic
RL expression of activin variants: the role of maternal activin.";
RL Genes Dev. 8:1448-1462(1994).
CC -1- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
DR EMBL; X76051; CAAS3636.1; -.
DR HSP; P18075; I BMP.
DR ZFIN; ZDB-GENE-990415-2; zactbb.
DR InterPro; IPR001111; -
DR InterPro; IPR001839; -
DR InterPro; IPR002400; -.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGFB_propeptide; 1.
DR PRINTS; PR00438; GFCYSKNOT.
DR ProDom; PD000357; -. 1.
DR PROSITE; PS00250; TGF_BETA; 1.
DR SMART; SM00204; TGFB; 1.
KW Glycoprotein.
SQ SEQUENCE 393 AA; 43830 MW; FA769C4D9BE4D252 CRC64;

Query Match      29.1%; Score 184.5; DB 13; Length 393;
Best Local Similarity 36.4%; Pred. No. 7.2e-13;
Matches 39; Conservative 22; Mismatches 35; Indels 11; Gaps 7;

QY 15 CCVRPLYIDFQQDLGWK-WVHEPKGYANFCGGPCP-YLR-----SADTTHSTVLGLYNT- 67

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QY 15 CCVRPLYIDFRDLGWK-WVHEPKGYANFCGCP- YLR-----SADTTHSTVGLYNT- 67
 DB 12 CCRQCFYIDFRL-IGNWDIIAPAGYIGNYCEGCPAYMAGVPGSASFHTAVVGYRMR 70
 QY 68 -LNPEASAPCCVPDLEPLTILYVGRTPKVEQ-LSNMVVKSCCK 111
 DB 71 GMSP-GSVNSCCIPKLTMSMLYDFDEYNIVKRDVNPNMIVECGC 115

RESULT 64
 Q9W6T9 PRELIMINARY; PRT; 138 AA.
 AC Q9W6T9
 DT 01-NOV-1999 (Tremblrel. 12, Created)
 DT 01-NOV-1999 (Tremblrel. 12, Last sequence update)
 DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
 DE ACTIVIN BETA B PROTEIN (FRAGMENT).
 GN ACTIVIN BETA B.
 OS Brachydanio rerio (Zebrafish) (Zebra danio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
 OC Cypriniformes; Cyprinidae; Rasbora; Danio.
 OC NCBI_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Rodaway A., Takeda H., Koshida S., Price B.M., Smith J.C., Patient R.,
 RA Holder N.;
 RT "Activin is an inducer of mesoderm in the zebrafish germ ring."
 RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
 DB EMBL; AJ238981; CAB43092.1; -
 DR HSP; P18075; 1BMP.
 DR InterPro; IPR001839; -
 DR InterPro; IPR002400; -
 DR Pfam; PF00019; TGF-beta; 1.
 DR PRINTS; PR00438; GFCYSKNOT.
 DR PRINTS; PR00669; INHIBINA.
 DR PROSITE; PS00250; TGF_BETA; 1.
 DR SMART; SM00204; TGF-beta; 1.
 KW Glycoprotein.
 FT NON_TER 1
 FT NON_TER 138
 SQ SEQUENCE 138 AA; 15263 MW; 5BE38C763EDAC42B CRC64;

Query Match 28.9%; Score 183.5; DB 13; Length 138;
 Best Local Similarity 36.8%; Pred. No. 3.1e-13;
 Matches 39; Conservative 21; Mismatches 35; Indels 11; Gaps 7;

QY 15 CCVRPLYIDFRDLGWK-WVHEPKGYANFCGCP- YLR-----SADTTHSTVGLYNT- 67
 DB 29 CCRQCFYIDFRL-IGNWDIIAPAGYIGNYCEGCPAYMAGVPGSASFHTAVVGYRMR 87
 QY 68 -LNPEASAPCCVPDLEPLTILYVGRTPKVEQ-LSNMVVKSCCK 111
 DB 88 GMSP-GSVNSCCIPKLTMSMLYDFDEYNIVKRDVNPNMIVECGC 132

RESULT 65
 Q9YGH7 PRELIMINARY; PRT; 424 AA.
 AC Q9YGH7
 DT 01-MAY-1999 (Tremblrel. 10, Created)
 DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
 DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
 DE OSTEOGENIC PROTEIN-1 HOMOLOG PRECURSOR.
 GN XOP-1H.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus.

OX NCBI_TaxID=8355;
 RP SEQUENCE FROM N.A.
 RA Wang S., Krinks M., Kleinwaks L., Zapalo P., Moos M. Jr.;
 RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
 DB EMBL; U40034; AAD09399.1; -
 DR HSP; P18075; 1BMP.
 DR InterPro; IPR001111; -
 DR InterPro; IPR001839; -
 DR Pfam; PF00019; TGF-beta; 1.
 DR Pfam; PF00688; TGF-beta; 1.
 DR ProDom; PD000357; -; 1.
 DR PROSITE; PS00250; TGF_BETA; 1.
 DR SMART; SM00204; TGF-beta; 1.
 KW Glycoprotein; Signal.
 FT SIGNAL 9
 FT CHAIN 286 424 OSTEOGENIC PROTEIN-1 HOMOLOG.
 FT CHAIN 424 424
 SQ SEQUENCE 424 AA; 48917 MW; C4638C7D3D0A1DE4 CRC64;

Query Match 28.9%; Score 183; DB 13; Length 424;
 Best Local Similarity 33.0%; Pred. No. 1.1e-12;
 Matches 38; Conservative 24; Mismatches 39; Indels 14; Gaps 5;

QY 10 NLEEN-----CCVRPLYIDFRDLGWK-WVHEPKGYANFCGCPYLRSA---DTT 57
 DB 310 NIAENSTDKQACKKHELYVSK-DLGWDIITAPEGYAAFYCEGECAPPLNSYMNATN 368
 QY 58 HSTVGLYNTLNPEASAPCCVPDLEPLTILYVGRTPKV-EOLSNMVVKSCCK 111
 DB 369 HAIVQTLVHFINDTPKPCCAPTOLNAISLVYFDDSSNVILKKYRNWVRACGC 423

RESULT 66
 Q9W6G0 PRELIMINARY; PRT; 500 AA.
 AC Q9W6G0
 DT 01-NOV-1999 (Tremblrel. 12, Created)
 DT 01-NOV-1999 (Tremblrel. 12, Last sequence update)
 DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
 DE GDF-5 PROTEIN.
 GN GDF5.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OC NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE-99146893; PubMed-10021348;
 RA Francis-West P.H., Abdelfattah A., Chen P., Allen C., Parish J.,
 RA Lader R., Allen S., MacPherson S., Luyten F.P., Archer C.W.;
 RT "Mechanisms of GDF-5 action during skeletal development."
 RL Development 126:1305-1315(1999).
 CC -1- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
 DB EMBL; AF123389; AAD30451.1; -
 DR HSP; P18075; 1BMP.
 DR InterPro; IPR001111; -
 DR InterPro; IPR001839; -
 DR InterPro; IPR002405; -
 DR Pfam; PF00019; TGF-beta; 1.
 DR Pfam; PF00688; TGF-beta; 1.
 DR PRINTS; PR00669; INHIBINA.
 DR PROSITE; PS00250; TGF_BETA; 1.
 DR SMART; SM00204; TGF-beta; 1.
 KW Glycoprotein.
 SQ SEQUENCE 500 AA; 55952 MW; 1DE8385A3119A598 CRC64;

Query Match 28.9%; Score 183; DB 13; Length 500;
 Best Local Similarity 37.0%; Pred. No. 1.4e-12;
 Matches 40; Conservative 23; Mismatches 39; Indels 6; Gaps 5;


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AC O57573;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE BONE MORPHOGENETIC PROTEIN.
GN ZBMP-2.
OS Brachydanio rerio (Zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Rasbora; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=WHOLE EMBRYO;
RX MEDLINE=97231284; PubMed=9076679;
RA Nikaido M., Tada M., Saji T., Ueno N.;
RT "Conservation of BMP signaling in zebrafish mesoderm patterning.";
RL Mech. Dev. 61:75-88(1997).
CC -!- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
DR EMBL; D49971; BAA24406.1; -
DR HSP; P18075; IBMP.
DR InterPro; IPR001111; -
DR InterPro; IPR001839; -
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGF-beta; 1.
DR ProDom; PD000357; -; 1.
DR PROSITE; PS00250; TGF BETA; 1.
DR SMART; SM00204; TGF-beta; 1.
KW Glycoprotein.
SQ SEQUENCE 411 AA; 46845 MW; 049EC3BA083DEBDF CRC64;

Query Match 28.3%; Score 179.5; DB 13; Length 411;
Best Local Similarity 38.5%; Pred. No. 2.8e-12;
Matches 42; Conservative 20; Mismatches 28; Indels 19; Gaps 8;

QY 14 NCVRPLYIDFRDLGW-KWHEPKGYANFCGCPY-----LRSADTTHSTVLGLYNT 67
DB 310 NCRHLYVDF-SDVGWNEIVAPPGYHAFYCHGCPPLPDHLNS--TNHAIQTIVLNS 366
QY 68 LN---PEASAPCCVPQDLEPLTILYVGRTPKV--EQLSNMVVSKKC 111
DB 367 VNSNIPKA-----CCIPTLSPIALL-YLDEYEKVLKYNQDMVVEGCGC 410

RESULT 72
O93369 ID O93369 PRELIMINARY; PRT; 411 AA.
AC O93369
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE BONE MORPHOGENETIC PROTEIN 2.
GN BMP2.
OS Brachydanio rerio (Zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Rasbora; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FW;
RX MEDLINE=97231284; PubMed=9076679;
RA Nikaido M., Tada M., Saji T., Ueno N.;
RT "Conservation of BMP signaling in zebrafish mesoderm patterning.";
RL Mech. Dev. 61:75-88(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=FW;
RX MEDLINE=98072322; PubMed=9409664;
RA Kishimoto Y., Lee K.H., Zon L., Hammerschmidt M., Schulte-Merker S.;
RT "The molecular nature of zebrafish swirl: BMP2 function is essential during early dorsoventral patterning.";
RL Development 124:4457-4466(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=FW;
RA Lee K.H., Marden J.J., Thompson M.S., MacLennan H., Kishimoto Y., Pratt S.J., Schulte-Merker S., Hammerschmidt M., Johnson S.L., Postlethwaite J.H., Beier D.C., Zon L.I.;
RT "Cloning and Genetic Mapping of Zebrafish BMP-2.";
RL Dev. Genet. 23:0-0(1998).
CC -!- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
DR EMBL; AF072456; AAC25595.1; -
DR HSP; P18075; IBMP.
DR InterPro; IPR001111; -
DR InterPro; IPR001839; -
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGF-beta; 1.
DR ProDom; PD000357; -; 1.
DR PROSITE; PS00250; TGF BETA; 1.
DR SMART; SM00204; TGF-beta; 1.
KW Glycoprotein.
SQ SEQUENCE 411 AA; 46873 MW; 01A4C8CA012F1EDF CRC64;

Query Match 28.3%; Score 179.5; DB 13; Length 411;
Best Local Similarity 38.5%; Pred. No. 2.8e-12;

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AC O57573;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE BONE MORPHOGENETIC PROTEIN.
GN ZBMP-2.
OS Brachydanio rerio (Zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Rasbora; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=WHOLE EMBRYO;
RX MEDLINE=97231284; PubMed=9076679;
RA Nikaido M., Tada M., Saji T., Ueno N.;
RT "Conservation of BMP signaling in zebrafish mesoderm patterning.";
RL Mech. Dev. 61:75-88(1997).
CC -!- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
DR EMBL; D49971; BAA24406.1; -
DR HSP; P18075; IBMP.
DR InterPro; IPR001111; -
DR InterPro; IPR001839; -
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGF-beta; 1.
DR ProDom; PD000357; -; 1.
DR PROSITE; PS00250; TGF BETA; 1.
DR SMART; SM00204; TGF-beta; 1.
KW Glycoprotein.
SQ SEQUENCE 411 AA; 46845 MW; 049EC3BA083DEBDF CRC64;

Query Match 28.3%; Score 179.5; DB 13; Length 411;
Best Local Similarity 38.5%; Pred. No. 2.8e-12;
Matches 42; Conservative 20; Mismatches 28; Indels 19; Gaps 8;

QY 14 NCVRPLYIDFRDLGW-KWHEPKGYANFCGCPY-----LRSADTTHSTVLGLYNT 67
DB 310 NCRHLYVDF-SDVGWNEIVAPPGYHAFYCHGCPPLPDHLNS--TNHAIQTIVLNS 366
QY 68 LN---PEASAPCCVPQDLEPLTILYVGRTPKV--EQLSNMVVSKKC 111
DB 367 VNSNIPKA-----CCIPTLSPIALL-YLDEYEKVLKYNQDMVVEGCGC 410

RESULT 71
O13108 ID O13108 PRELIMINARY; PRT; 411 AA.
AC O13108
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE BMP2-4.
GN BMP2-4.
OS Brachydanio rerio (Zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Rasbora; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98036031; PubMed=9370264;
RA Martinez-Barbera J.P., Toresson H., Darocha S., Krauss S.;
RT "Cloning and expression of three members of the zebrafish Bmp family: Bmp2a, Bmp2b and Bmp4.";
RL Gene 198:53-59(1997).
CC -!- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
DR EMBL; U82232; AAC60286.1; -
DR HSP; P18075; IBMP.
DR InterPro; IPR001111; -
DR InterPro; IPR001839; -
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGF-beta; 1.

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Q9XYQ7
ID Q9XYQ7 PRELIMINARY; PRT; 417 AA.
AC Q9XYQ7
DT 01-NOV-1999 (Tremblrel. 12, Created)
DT 01-NOV-1999 (Tremblrel. 12, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE BONE MORPHOGENETIC PROTEIN BMP2/4.
GN BMP2/4.
OS Lytechinus variegatus (Sea urchin).
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC Echinozoa; Echinoidae; Echinacea; Temnopleuroidea; Toxopneustidae;
OC Lytechinus.
OX NCBI_TaxID=7654;
RN [1]
SEQUENCE FROM N.A.
RA Angerer L.M., Oleksyn D.W., Logan C.Y., McClay D.R., Dale L.,
RA Angerer R.C.;
RT "A BMP pathway regulates cell fate allocation along the sea urchin
animal-vegetal embryonic axis."
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
DR EMBL; AF119712; AAD28038.1; -.
DR HSP; P18075; 1BMP.
DR InterPro; IPR001111; -.
DR InterPro; IPR001839; -.
DR InterPro; IPR002405; -.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGFb_propeptide; 1.
DR PRINTS; PR00669; INHIBINA.
DR ProDom; PD000357; -; 1.
DR PROSITE; PS00250; TGF_BETA; 1.
DR SMART; SM00204; TGFB; 1.
KW Glycoprotein.
SQ SEQUENCE 417 AA; 47727 MW; 5EB93E3022BFC50F CRC64;

Query Match 28.1%; Score 178; DB 5; Length 417;
Best Local Similarity 35.8%; Pred. No. 4.1e-12;
Matches 39; Conservative 19; Mismatches 43; Indels 8; Gaps 5;
QY 9 RNLENCVRPLYIDFRQDLGK-WVHEPKGYANFCSGPCPYLRSA---DTTHSTVLGL 64
Db 310 KRLKNCRRHPLYVDF-SDVHNDWIVAPGYQAYVCHGECPPFLAEHLMTTTHAIVQTL 368
QY 65 YNTLNPASASPCCVQDLEPLTILYVGRTPKV--EQLSNMVKSKC 111
Db 369 VNSVPALVPKACCGTPELSAISML-YLDEYKVLKYNQDMVVEGCGC 416

RESULT 77
Q9PVK1
ID Q9PVK1 PRELIMINARY; PRT; 364 AA.
AC Q9PVK1
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE ANTI-DORSALIZING MORPHOGENETIC PROTEIN.
GN ADMP.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
SEQUENCE FROM N.A.
RA MEDLINE=99418628; PubMed=10490096;
RA Joulin K., Stern C.D.;
RT "Molecular Interactions Continuously Define the Organizer during the
Cell Movements of Gastrulation."
RL Cell 98:559-571(1999).
CC -!- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
DR EMBL; AF082178; AAD52011.1; -.
DR HSP; P18075; 1BMP.

DR InterPro; IPR001111; -.
DR InterPro; IPR001839; -.
DR InterPro; IPR002405; -.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGFb_propeptide; 1.
DR PRINTS; PR00669; INHIBINA.
DR ProDom; PD000357; -; 1.
DR PROSITE; PS00250; TGF_BETA; 1.
DR SMART; SM00204; TGFB; 1.
KW Glycoprotein.
SQ SEQUENCE 364 AA; 40071 MW; 76565716FBE78D8 CRC64;
Query Match 28.0%; Score 177.5; DB 13; Length 364;
Best Local Similarity 36.0%; Pred. No. 4.1e-12;
Matches 40; Conservative 20; Mismatches 42; Indels 9; Gaps 6;
QY 9 RNLE-ENCCVRPLYIDFRQDLGK-WVHEPKGYANFCSGPCPYLRSA---TTHSTVL 62
Db 254 RSLDRLPQCRHPLVSDF-EIEGSGWITISPRGYNAYHRCGSGPPPLGENMRPTNHAIVQ 312
QY 63 GLYNTLN-PEASASPCCVQDLEPLTILY-VGRTPKVEQLSNMVKSKC 111
Db 313 SIINALKSEGVSPCCVPDKLHSLINLLYFDDDENVVLKQYDDVAGSGCG 363

RESULT 78
O13109
ID O13109 PRELIMINARY; PRT; 386 AA.
AC O13109
DT 01-JUL-1997 (Tremblrel. 04, Created)
DT 01-JUL-1997 (Tremblrel. 04, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE BMP2.
GN BMP2.
OS Brachydanio rerio (zebrafish) (zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Rasbora; Danio.
OX NCBI_TaxID=7955;
RN [1]
SEQUENCE FROM N.A.
RP MEDLINE=98036031; PubMed=9370264;
RA Martinez-Barbera J.P., Toresson H., Darocha S., Krauss S.;
RT "Cloning and expression of three members of the zebrafish Bmp family:
Bmp2a, Bmp2b and Bmp4."
RL Gene 198:53-59(1997).
CC -!- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
DR EMBL; U82233; AAC60287.1; -.
DR HSP; P18075; 1BMP.
DR InterPro; IPR001111; -.
DR InterPro; IPR001839; -.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGFb_propeptide; 1.
DR ProDom; PD000357; -; 1.
DR PROSITE; PS00250; TGF_BETA; 1.
DR SMART; SM00204; TGFB; 1.
KW Glycoprotein.
SQ SEQUENCE 386 AA; 43374 MW; EA0954E7D3FBA1D7 CRC64;

Query Match 28.0%; Score 177.5; DB 13; Length 386;
Best Local Similarity 39.4%; Pred. No. 4.4e-12;
Matches 43; Conservative 18; Mismatches 29; Indels 19; Gaps 8;
QY 14 NCCVRPLYIDFRQDLGK-WVHEPKGYANFCSGPCPY----LRSAOTHTSTVLGKNT 67
Db 285 NCRHSIYVDF-SDVGWNDWIVAPGTHAFYCGECPPPLADHLNS--TTNHWOTLVNS 341
QY 68 LN---PEASASPCCVQDLEPLTILYVGRTPKV--EQLSNMVKSKC 111
Db 342 VNSNIPRA---CCVPTDLSVSL-LYLDEYERVLKYNQDMVVEGCGC 385

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RESULT 79
Q9XYQ8
ID Q9XYQ8 PRELIMINARY; PRT; 289 AA.
AC Q9XYQ8:
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE BONE MORPHOGENETIC PROTEIN BMP2/4 (FRAGMENT).
DE GN BMP2/4.
OS Strongylocentrotus purpuratus (Purple sea urchin).
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC Echinoidea; Euechinoidea; Echinacea; Echinoidea; Strongylocentrotidae;
OC Strongylocentrotus.
OX NCBI_TaxID=7668;
RN [1]
RP SEQUENCE FROM N.A.
RA Angerer L.M., Oleksyn D.W., Logan C.Y., McClay D.R., Dale L.,
RA Angerer R.C.;
RT "A BMP pathway regulates cell fate allocation along the sea urchin
RT animal-vegetal embryonic axis.";
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
DR EMBL: AF119713; AAC28039.1; -.
DR HSSP: P18075; 1BMP.
DR InterPro: IPR001839; -.
DR InterPro: IPR002400; -.
DR InterPro: IPR002405; -.
DR Pfam: PF00019; TGF-beta; 1.
DR PRINTS: PR00438; GFCYSKNOT.
DR PRINTS: PR00669; INHIBINA.
DR PROSITE: PS00250; TGF_BETA; 1.
DR SMART: SM00204; TGFB; 1.
DR Glycoprotein.
KW NON_TER 1
FT NON_TER 289
FT SEQUENCE 289 AA; 33599 MW; 99E175C7DBC3C58B CRC64;
SQ SEQUENCE 289 AA; 33599 MW; 99E175C7DBC3C58B CRC64;

Query Match 27.9%; Score 177; DB 5; Length 289;
Best Local Similarity 35.8%; Pred. No. 3.7e-12;
Matches 39; Conservative 19; Mismatches 43; Indels 8; Gaps 5;

QY 9 NLEENCVRPLIDFRODLGKW-WHPEPKGYANFCGPGCPYLRSA---DTTHSTVLGL 64
: :| | | | | | | | | | | | | | | | | | | | | | | | | |
Db 180 KRLKANCRRRHLYVDF-SDVHNDWIVAPAGYQAYCRGECGPLAEHLNLTNHAIVQTL 238
: :| | | | | | | | | | | | | | | | | | | | | | | | | |

QY 65 YNTLNPEASAPCCVPQDLEPLTILYVYGRTPKV--EQLSNWVYKSKC 111
: :| | | | | | | | | | | | | | | | | | | | | | | | | |
Db 239 VNSVNPALPKACCVPTSELSAISM-LYLDEYKVVVLKNYQDMVVEGCGC 286
: :| | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 80
O57574
ID O57574 PRELIMINARY; PRT; 400 AA.
AC O57574;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE BONE GENETIC PROTEIN 4.
DE GN BMP2-4 OR BMP4.
OS Brachydanio rerio (zebrafish) (zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Rasbora; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE-WHOLE EMBRYO;
RA MEDLINE-97231284; PubMed=9076679;
RA Nkaido M., Tada M., Saji T., Ueno N.;
RT "Conservation of BMP signaling in zebrafish mesoderm patterning.";
RL Mech. Dev. 61:75-88(1997).

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RL Science 242:1528-1534(1988).
CC -!- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
DR EMBL; U23785; AA811169.1; -.
DR HSP; P18075; 1BMP.
DR InterPro; IPR000169; -.
DR InterPro; IPR001839; -.
DR Pfam; PF00019; TGF-beta; 1.
DR PROSITE; PS00250; TGF-BETA; 1.
DR PROSITE; PS00639; THIOLEPROTEASE_HIS; UNKNOWN_1.
DR SMART; SM00204; TGFB; 1.
KW Glycoprotein.
FT NON_TER
SQ SEQUENCE 191 AA; 21879 MW; FA73DF060878F4C0 CRC64;

Query Match 27.3%; Score 173; DB 5; Length 191;
Best Local Similarity 34.3%; Pred. No. 6.7e-12;
Matches 37; Conservative 17; Mismatches 48; Indels 6; Gaps 4;

QY 9 RNLEENCVRPLYIDPRDLGW-KWHEPKGYANFCGPGPYLRS- --DTTHSTVLGL 64
   :: I ||| ||| ::| I | | | | | | | | | | | | | | | | | | | |
Db 84 KQORSTCRHRPLVDFR-EVGDDWIVAPPGYEGWICHGDCPPLSAHNMSTNHAVVQTL 142
   ::| | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 65 YNTLNPASASCCVPPQDLEPLTILYVGRTPKV-EQLSNMNVKSKC 111
   |::| | | | | | | | | | | | | | | | | | | | | | | | | |
Db 143 MNSMNLGVPKACCIPTQLTSTISMLYDESKVVLKNYHEMAYVGGCC 190

RESULT 82
O76147 PRELIMINARY; PRT; 400 AA.
AC O76147;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-WAR-2001 (TrEMBLrel. 16, Last annotation update)
DE BONE MORPHOGENETIC PROTEIN (FRAGMENT).
GN DJBMP.
OS Dugesia japonica (Planarian).
OC Eukaryota; Metazoa; Platyhelminthes; Rhabditophora; Turbellaria;
OC Tricladida; Paludicola; Dugesidae; Dugesia.
OX NCBI_TaxID=6161;
RN [1]
RC STRAIN=GI. TISSUE=WHOLE ANIMAL;
RA Oriti H., Kato K., Agata K., Watanabe K.;
RT "Molecular cloning of bone morphogenetic protein (BMP) gene from the
   planarian Dugesia japonica."
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
DR EMBL; AB010966; BAA32087.1; -.
DR HSP; P18075; 1BMP.
DR InterPro; IPR001839; -.
DR InterPro; IPR002405; -.
DR Pfam; PF00019; TGF-beta; 1.
DR PRINTS; PR00669; INHIBINA.
DR PROSITE; PS00250; TGF-BETA; 1.
DR SMART; SM00204; TGFB; 1.
KW Glycoprotein.
FT NON_TER
SQ SEQUENCE 400 AA; 47031 MW; 34220CB5140CB5A4 CRC64;

Query Match 27.3%; Score 173; DB 5; Length 400;
Best Local Similarity 35.1%; Pred. No. 1.5e-11;
Matches 40; Conservative 18; Mismatches 50; Indels 6; Gaps 4;

QY 3 DFNVCFRNLEENCVRPLYIDPRDLGW-KWHEPKGYANFCGPGPYLRSAD- --TTH 58
   ||: ||| | | | | | | | | | | | | | | | | | | | | | | | |
Db 287 DTSYMPGHEEDQRYPLIVTFK-EVGWSKWIIPQNIYAYCKGNCPPYPLSDNFNATNH 345
   ||: ||| | | | | | | | | | | | | | | | | | | | | | | | |

QY 59 STVGLGYNLTNPASASCCVPPQDLEPLTILYVGR-TPKVELSNMNVKSKC 111
   :: | | | | | | | | | | | | | | | | | | | | | | | | | |

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Db 346 AIIQLLVHGLKDLISIPKPCCVYHLHPETLLYLNNEGDAALLREFKDMVSVCSC 399

RESULT 83
Q9VQG9 PRELIMINARY; PRT; 586 AA.
AC Q9VQG9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE CG16987 PROTEIN.
GN CG16987.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Eohydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RC SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; Pubmed=10731132;
RA Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,
   Ananides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
   George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
   Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
   Brandon R.C., Rogers Y.-H.C., Blazek R.G., Champe M., Mikliff B.D.,
   Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
   Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
   Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
   Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
   Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
   Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
   Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
   de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
   Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
   Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
   Fodor C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
   Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
   Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
   Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwan C.,
   Jalaali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
   Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
   Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
   Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
   Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
   Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
   Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacle J.M.,
   Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
   Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
   Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
   Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
   Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
   Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
   Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
   Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
   Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
   Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
CC -!- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
CC -!- SIMILARITY: TO NEUTRAL ZINC METALLOPEPTIDASES, ZINC-BINDING REGION
   DOMAIN.
DR EMBL; AE003582; AAF51204.1; -.
DR HSP; P18075; 1BMP.
DR FlyBase; FBgn0031461; CG16987.
DR InterPro; IPR000130; -.
DR InterPro; IPR001111; -.
DR InterPro; IPR001839; -.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGFB_propeptide; 1.
DR ProDom; PD000357; -.
DR PROSITE; PS00250; TGF-BETA; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; 1.

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DR SMART; SM00204; TGFβ; 1.
KW Glycoprotein; Hydrolase; Metalloprotease; Zinc.
SQ SEQUENCE 586 AA; 67184 MW; 582582D7F370D549 CRC64;

Query Match 27.2%; Score 172.5; DB 5; Length 586;
Best Local Similarity 36.6%; Pred. No. 2.5e-11;
Matches 41; Conservative 17; Mismatches 45; Indels 9; Gaps

QY 7 CFRNLEENCCVRPLYIDFRQDLGW-KWHEPKGYANFCSGPCPYLRG---ADTTHSTVL 62
| : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 476 CSSGNT--CCEHLYISFR-DIGNSNWLKPEGYNAYFCRSCSSVASVTOAASHSSIM 533
| : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 63 GLYNT--LNPEASAPCCVPQDLEPLTILY-VGRTPKVEQLSNMVKSKC 111
| : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 534 KILSTSGANKSLELVPCCTAKQYSSLQLVMDSSNTATVKTLPNMVVEGCG 585
| : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 84
O97390 PRELIMINARY; PRT; 301 AA.
ID O97390 AC O97390;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
MGDF PRECURSOR.
GN MGDF.
OS Crassostrea gigas (Pacific oyster).
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Ostreoida;
OC Ostreoidae; Ostreidae; Crassostrea.
OX NCBI_TaxID=29159;
RN [1]
RP SEQUENCE FROM N.A.
RA LeLong C., Mathieu M., Favrel P.;
RT "Structure and expression of mgdf, a new member of the TGF-beta
RT superfamily in Crassostrea gigas (Mollusca Bivalvia).";
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
EMBL; AJ130967; CAA10268.1; -.
DR HSP; P18075; 1BMP.
DR InterPro; IPR001111; -.
DR InterPro; IPR001839; -.
DR InterPro; IPR002405; -.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGFβ_propeptide; 1.
DR PRINTS; PR00569; INHIBINA.
DR ProDom; PD000357; -. 1.
DR PROSITE; PS00250; TGF_BETA; 1.
DR SMART; SM00204; TGFβ; 1.
KW Glycoprotein; Signal.
FT SIGNAL 1 36
FT CHAIN 37 301
FT CHAIN 37 301 MGDF PRECURSOR.
SQ SEQUENCE 301 AA; 34723 MW; 5217AD88239C9009 CRC64;

Query Match 27.1%; Score 172; DB 5; Length 301;
Best Local Similarity 36.4%; Pred. No. 1.4e-11;
Matches 40; Conservative 19; Mismatches 41; Indels 10; Gaps

QY 9 RNLEENCCVRPLYIDFRQDLGW-KWHEPKGYANFCSGPC--PYLRSD-TTHSTVLGL 64
| : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 194 KKNYNCCRKELNVDFKA-VGMNDWIFAPPGYNAYICDGSCHWPYDDHMYNTHAIVQDL 252
| : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 65 YNTLNPEASAPCCVPQDLEPLTILY----YGRTPKVEQLSNMVKSKC 111
| : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 253 VNSIDPRAAPKPCVPTLSSLSLTYTDEHGAVLVKVIYQ--DMVVEGCGC 300
| : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 85
O16123 PRELIMINARY; PRT; 428 AA.
ID O16123 AC O16123;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)

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Query Match      27.1%; Score 172; DB 5; Length 428;
Best Local Similarity 36.0%; Pred. No. 2e-11;
Matches 41; Conservative 16; Mismatches 43; Indels 14; Gaps 5;

QY 3 DTWYCRNLNENCCVRLYIDFQDLGWK-WVHEPKGYANFCGPGPYLRSA---DTTH 58
      ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
Db 323 DKNYCRNT-----QLLVDF-NELNMWDWILAPSSYSAIQCGEGCPNPLTFHNTN 373
      ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
QY 59 STVLGYNTLNPEASAPCCVPQDLPLTILY-VGRTPKVEQLSNMVKSKC 111
      : || : : : : ||||| : : ||||| : : : : : ||||| : : : : :
Db 374 AIVOGLINSVDPLNVPAPCCVPTMESLAIYIDVEGKIVIKNYPDMEVLSGCG 427

RESULT 87
Q9VQC6 PRELIMINARY; PRT; 588 AA.
AC Q9VQC6;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE DPP PROTEIN.
GN DPP OR CG9885.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.C., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Aqbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K.J., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacieb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kianos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
CC -!- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
DR EMBL: AE003583; AAF51250.1; -.
DR HSSP: P18075; IBMP.

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FlyBase; FBgn0000490; dpp.
DR InterPro; IPR001111; -.
DR InterPro; IPR001839; -.
DR InterPro; IPR002405; -.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGF-beta-propeptide; 1.
DR PRINTS; PR00869; INHIBINA.
DR PROSITE; PS00250; TGF_BETA; 1.
DR SMART; SM00204; TGFb; 1.
KW Glycoprotein.
SQ SEQUENCE 588 AA; 65867 MW; 2C8166C1BD2F666B CRC64;

Query Match      27.1%; Score 172; DB 5; Length 588;
Best Local Similarity 35.8%; Pred. No. 2.8e-11;
Matches 39; Conservative 16; Mismatches 46; Indels 8; Gaps 5;

QY 9 RNLENCVRLYIDFQDLGW-KVHEPKGYANFCGPGPYLRSA-----TTHSTVLG 63
      : || : : : : ||||| : : ||||| : : : : : ||||| : : : : :
Db 481 KNHDDTCRRHSLYVDF-SDVGWDDWIVAPLGDAYDYCHGKCF-PLADHFNSTNHAVQT 538
      ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
QY 64 LYNTLNPEASAPCCVPQDLPLTILYVGR-TPKVEQLSNMVKSKC 111
      : || : : : : ||||| : : ||||| : : : : : ||||| : : : : :
Db 539 LVNNNPKVKACCCVPTQLDSVAMLYLNDQSTVVLKNYQEMTVVCGGC 587
      : || : : : : ||||| : : ||||| : : : : : ||||| : : : : :

RESULT 88
Q90390 PRELIMINARY; PRT; 102 AA.
AC Q90390;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE ACTIVIN BETA-A SUBUNIT (FRAGMENT).
OS Carassius auratus (Goldfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Cyprininae; Carassius.
OX NCBI_TaxID=7957;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BLOOD;
RX MEDLINE=93290666; PubMed=8512569;
RA Ge W., Gallin W.J., Strobeck C., Peter R.E.;
RT "Cloning and sequencing of goldfish activin subunit genes: strong
RT structural conservation during vertebrate evolution.";
RL Biochem. Biophys. Res. Commun. 193:711-717(1993).
CC -!- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
DR EMBL: L15339; AAA49162.1; -.
DR HSSP: P18075; IBMP.
DR InterPro; IPR001839; -.
DR Pfam; PF00019; TGF-beta; 1.
DR PROSITE; PS00250; TGF_BETA; 1.
DR SMART; SM00204; TGFb; 1.
KW Glycoprotein.
FT NON_TER 1
FT NON_TER 102
SQ SEQUENCE 102 AA; 11849 MW; 0F5E17FA198F94D9 CRC64;

Query Match      27.1%; Score 171.5; DB 13; Length 102;
Best Local Similarity 40.08; Pred. No. 5.2e-12;
Matches 34; Conservative 14; Mismatches 28; Indels 9; Gaps 4;

QY 15 CCVCPLYIDFQDLGWK-WVHEPKGYANFCGPGCP-----YLRADTTHSTVLGLYNT- 67
      ||||| : : : : : ||||| : : ||||| : : : : : ||||| : : : : :
Db 5 CCKRQFYVNFK-DIGSWDIAPSGYHANYCEGDCPSHVASITGSALSFIVNHYMR 63
      : || : : : : ||||| : : ||||| : : : : : ||||| : : : : :
QY 68 -LNPEASAPCCVPQDLPLTILY 91
      : || : : : : ||||| : : ||||| : : : : : ||||| : : : : :
Db 64 GYSPFNNIKCCVPTRLRAMSLY 88
      : || : : : : ||||| : : ||||| : : : : : ||||| : : : : :

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RESULT 89
Q9MZV5
ID Q9MZV5 PRELIMINARY; PRT; 337 AA.
AC Q9MZV5;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE BONE MORPHOGENETIC PROTEIN 4 (FRAGMENT).
GN BMP4.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RA Johanson J.A., Breen M., Lepine A., Murphy K.E.;
RT "Identification and chromosomal localization of the gene encoding
RT canine bone morphogenetic protein 4 (bmp4).";
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
DR EMBL; AF136233; AAF82188.1; -;
DR InterPro; IPR001111; -;
DR InterPro; IPR001839; -;
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGF-beta; 1.
DR PROSITE; PS00250; TGF_BETA; 1.
KW Glycoprotein.
FT NON_TER 1 1
SQ SEQUENCE 337 AA; 38792 MW; BC91231431FDCA27 CRC64;

Query Match 26.9%; Score 170.5; DB 6; Length 337;
Best Local Similarity 37.7%; Pred. No. 2.3e-11;
Matches 43; Conservative 17; Mismatches 35; Indels 19; Gaps 8;

QY 9 RNLENCVRLPYIDFRODLGK-WVHEPKGYANFCSPGCPY-----LRSADTHSTVL 62
Db 231 RKKKNKRRLHLYVDF-SDVGNWDWIVAPPGYQAFYCHGDCPFPLADHLNS--TNHAIQV 287
QY 63 GLYNTLN---PEASASPCVPQDLEPLTILYVGRTPKV--EOLSNMVVKSCKC 111
Db 288 TLVNSVNSIPKA----CCVPELSAISML-YLDEYDKVLKNYOEMVVEGCGC 336

RESULT 90
Q9W6T8
ID Q9W6T8 PRELIMINARY; PRT; 120 AA.
AC Q9W6T8;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE ACTIVIN BETA A PROTEIN (FRAGMENT).
GN ACTIVIN BETA A.
OS Brachydanio rerio (Zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Rasbora; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Rodaway A., Takeda H., Koshida S., Price B.M., Smith J.C., Patient R.,
RA Holder N.;
RT "Activin is an inducer of mesoderm in the zebrafish germ ring."
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
DR EMBL; AJ238980; CAB43091.1; -;
DR HSP; P18075; 1BMP.
DR InterPro; IPR001839; -;
DR InterPro; IPR002405; -;
DR Pfam; PF00019; TGF-beta; 1.
DR PRINTS; PR00669; INHIBINA.
DR PRODOM; PD000357; -; 1.
DR PROSITE; PS00250; TGF_BETA; 1.

DR SMART; SM00204; TGF-beta; 1.
KW Glycoprotein.
FT NON_TER 1 1
SQ SEQUENCE 120 AA; 13583 MW; D6B395EB4B40D705 CRC64;

Query Match 26.7%; Score 169; DB 13; Length 120;
Best Local Similarity 34.3%; Pred. No. 1.2e-11;
Matches 36; Conservative 21; Mismatches 36; Indels 12; Gaps 6;

QY 15 CCVRPLYIDFRODLGK-WVHEPKGYANFCSPGCPYLSADTH-----STVLGLYNT- 67
Db 11 CCKRQFYVNFK-DIGWNDWIIAPSGYHANYCEGDCASNVASITGNSLSRSTVISHYRIR 69
QY 68 -LNPEASAPCCVPQDLEPLTILYVGRTPKV--EOLSNMVVKSCKC 109
Db 70 GYSPFTNIKSCVPTLRAMSLY-NEEQKIVKDIQNMIVEEC 113

RESULT 91
O42303
ID O42303 PRELIMINARY; PRT; 257 AA.
AC O42303;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE CONTACT (FRAGMENT).
GN CONTACT.
OS Brachydanio rerio (Zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Rasbora; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97398455; PubMed=9256353;
RA Bruneau S., Mourrain P., Rosa F.M.;
RT "Expression of contact, a new zebrafish DVR member, marks mesenchymal
RT cell lineages in the developing pectoral fins and head and is
RT regulated by retinoic acid.";
RL Mech. Dev. 65:163-173(1997).
CC -!- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
DR EMBL; Y12005; CAA72733.1; -;
DR HSP; P18075; 1BMP.
DR ZFIN; ZDB-GENE-990415-39; contact.
DR InterPro; IPR001839; -;
DR InterPro; IPR002400; -;
DR Pfam; PF00019; TGF-beta; 1.
DR PRINTS; PR00438; GFCYSKNOT.
DR PROSITE; PS00250; TGF_BETA; 1.
DR SMART; SM00204; TGF-beta; 1.
KW Glycoprotein.
FT NON_TER 1 1
FT CHAIN 140 257 POTENTIAL.
SQ SEQUENCE 257 AA; 29787 MW; 6D64F0542F948849 CRC64;

Query Match 26.7%; Score 169; DB 13; Length 257;
Best Local Similarity 34.3%; Pred. No. 2.6e-11;
Matches 37; Conservative 25; Mismatches 40; Indels 6; Gaps 5;

QY 9 RNLENCVRLPYIDFRODLGK-WVHEPKGYANFCSPGCPY-LRS--ADTHSTVGL 64
Db 150 KNPCKRNCRLHVNFK-EMGWDDWIIAPLEYEAFHCDGVCDFPIRSHLEPTNHAIIQTL 208
QY 65 YNTLNPASASPCVPQDLEPLTILYVGRTPKV--EOLSNMVVKSCKC 111
Db 209 MNSMDPRSTPTCCVPTLRAMSLY-NEEQKIVKDIQNMIVEEC 256

RESULT 92
Q98861

DR	PROSITE; PS00250; TGF_BETA; 1.
DR	SMART; SM00204; TGFB; 1.
KW	Glycoprotein.
SQ	SEQUENCE 400 AA; 45757 MW; 427D1DB8FE12D025 CRC64;
Query Match	26.6%; Score 168.5; DB 13; Length 400;
Best Local Similarity	36.9%; Pred. No. 4.7e-11;
Matches	41; Conservative 16; Mismatches 41; Indels 13; Gaps 7;
Qy	9 RNLEENCVRRLYIDFRODLGKW-KWHPEKGYANFCSGPCPY-----LRSADTHTSTVL 62 : : : : : : : :
Dd	294 KRRNRNRRHAIYYDF-SDVGNWDIIVAPPGYQAYYGCEGFPFLADHLNS--TNHAIVQ 350 : : : : : : : : : : : : : : : : : :
Qy	63 GLYNLTNPASASCPCVPQDLPLTLILYVGRTPKV-EQLSNMVKSKC 111 : : : : : : : : : : : : : : : : : :
Dd	351 TLNVSVNTI-PKWCCVPTLSAISML-YLDETDRVVLKNYQMVEVGCG 399 : : : : : : : : : : : : : : : : : :
RESULT	94
Q9Z1V8	PRELIMINARY; PRT; 421 AA.
ID	Q9Z1V8 PRELIMINARY; PRT; 421 AA.
AC	Q9Z1V8; (TrEMBLrel. 10, Created)
DT	01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DI	01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE	BONE MORPHOGENETIC PROTEIN 10. BMP10.
GN	GN Mus musculus (Mouse).
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. OX NCBI_TaxId=10090; [1]
RN	SEQUENCE FROM N.A.
RP	Celeste A.;
RA	"Mouse Bone Morphogenetic Protein 10 (BMP-10) Genomic Sequence, Full Coding Region of Exon 2.";
RT	Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
RC	-1- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGFB) BETA FAMILY.
DR	EWEL; AF101440; AAC77461.1; JOINED.
DR	EWEL; AF101439; AAC77461.1; JOINED.
DR	HSP; PI8075; IBMP.
DR	InterPro; IPR001111; "
DR	InterPro; IPR001839; "
DR	InterPro; IPR002405; "
DR	pfam; PF00019; TGF-beta; 1.
DR	pfam; PF00688; TGFB-propeptide; 1.
DR	PRINTS; PR00669; INHIBINA.
DR	PRODOM; PD000357; -; 1.
DR	PROSITE; PS00250; TGF_BETA; 1.
DR	SMART; SM00204; TGFB; 1.
KW	Glycoprotein.
SQ	SEQUENCE 421 AA; 47917 MW; 703422876A64A18F CRC64;
Query Match	26.6%; Score 168.5; DB 11; Length 421;
Best Local Similarity	35.8%; Pred. No. 5e-11;
Matches	39; Conservative 17; Mismatches 46; Indels 7; Gaps 5;
Qy	9 RNLENCVR-RPLYIDPRODLGW-KWHPEKGYANFCSGPCPYLR-.-ADTHTSTVLG 63 : : : : : : : :
Dd	313 RNAKGNYCKRTPLYDPK-EIGWDSIIIPGEAYEBCRGVCNYPALAEHLTPTKHAIQA 371 : : : : : : : : : : : : : : : : : :
Qy	64 LYNLTNPASASCPCVPQDLPLTLILY-VGRTPKVQLSNMVKSKC 111 : : : : : : : : : : : : : : : : : :
Dd	372 LVHLKNSQASKACCVPKTLDPSILYLDRGVVTYFKFYEGMAVSEGC 420 : : : : : : : : : : : : : : : : : :
RESULT	95
Q9DET1	PRELIMINARY; PRT; 102 AA.
ID	Q9DET1 PRELIMINARY; PRT; 102 AA.
AC	Q9DET1; (TrEMBLrel. 16, Created)
DT	01-MAR-2001 (TrEMBLrel. 16, Created)

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DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DE 01-MAR-2001 (Tremblrel. 16, Last annotation update)
OS RAINBOW TROUT DNA FOR MATURE PEPTIDE, EXON2, PARTIAL CDS (FRAGMENT).
OC Oncorhynchus mykiss (rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BLOOD;
RA Aoki T.;
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=BLOOD;
RA Takashi T., Hirono I., Aoki T., Takashima F.;
RT "Structure and expression of activin genes in rainbow trout.";
RL Mol. Mar. Biol. Biotechnol. 7:72-77(1988).
DR EMBL; D88464; BAB16973.1; -.
FT NON_TER 102
FT NON_TER 102
SQ SEQUENCE 102 AA; 11562 MW; DB2745E872C93D48 CRC64;

Query Match 26.4%; Score 167.5; DB 13; Length 102;
Best Local Similarity 38.8%; Pred. No. 1.5e-11;
Matches 33; Conservative 14; Mismatches 29; Indels 9; Gaps 4;

QY 15 CCVRLPYIDFRQDLGWK-WVHEPKGYANFCSGPCPY-----YLRADTTHSTVLGLYNTL 68
DB 5 CCKQKQFYVNEK-DIGWSDIIAPGCGHYAHYEGDPCSHVASITGSLSFHSTVINHYRIT 63
QY 69 N--PEASASPCVPODLEPLTILYV 91
DB 64 GYAPFQNIKSCVPNALRAMSLIY 88

RESULT 96
O73818 ID O73818 PRELIMINARY; PRT; 400 AA.
AC O73818;
DT 01-AUG-1998 (Tremblrel. 07, Created)
DT 01-AUG-1998 (Tremblrel. 07, Last sequence update)
DE 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE BONE MORPHOGENETIC PROTEIN 4.
GN BMP-4.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Kim J., Chen H.-D., Roh D.-H., Ault K.T., Xu R.-H., Park M.-J.,
RA Kung H.-F.;
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
DR EMBL; AF058764; AAC61694.1; -.
DR HSSP; P18075; 1BMP.
DR InterPro; IPR001839; -.
DR InterPro; IPR001839; -.
DR Pfam; PF00019; TGF-beta; 1.
DR ProDom; PD000357; -.
DR PROSITE; PS00250; TGF_BETA; 1.
DR SMART; SM00204; TGFbeta; 1.
KW Glycoprotein.
RN [1]
RP SEQUENCE 400 AA; 45810 MW; A3147E4FACB4553F CRC64;

Query Match 26.1%; Score 165.5; DB 13; Length 400;
Best Local Similarity 36.8%; Pred. No. 1e-10;
Matches 42; Conservative 18; Mismatches 35; Indels 19; Gaps 8;

QY 9 RNLEENCVRPLYIDFRQDLGWK-WVHEPKGYANFCSGPCPY-----LRSADTTHSTVL 62
DB 294 RKKNHCRHRSLYVDF-SDVGWNDWIVAPPGYQAFYCHGDCPPLADHLNS--TNHAIQV 350
QY 63 GLYNTLN---PEASASPCVPODLEPLTILYVGRTPKV--EQLSNMVKSKCK 111
DB 351 TLVNSVNASIPKA----CCVPTELSAISML-YLDEYDKVVLKYNQEMVVEGCGC 399

RESULT 98
Q9YHW9 ID Q9YHW9 PRELIMINARY; PRT; 324 AA.
AC Q9YHW9;
DT 01-MAY-1999 (Tremblrel. 10, Created)

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Matches 42; Conservative 18; Mismatches 35; Indels 19; Gaps 8;

QY 9 RNLEENCVRPLYIDFRQDLGWK-WVHEPKGYANFCSGPCPY-----LRSADTTHSTVL 62
DB 294 RKKNHCRHRSLYVDF-SDVGWNDWIVAPPGYQAFYCHGDCPPLADHLNS--TNHAIQV 350
QY 63 GLYNTLN---PEASASPCVPODLEPLTILYVGRTPKV--EQLSNMVKSKCK 111
DB 351 TLVNSVNASIPKA----CCVPTELSAISML-YLDEYDKVVLKYNQEMVVEGCGC 399

RESULT 97
Q91703 ID Q91703 PRELIMINARY; PRT; 400 AA.
AC Q91703;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE PROTEIN 4.
GN BMP-4.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Smith J.C.;
RL Submitted (FEB-1992) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 1-20 FROM N.A.
RX MEDLINE=93048819; PubMed=1425340;
RA Dale L., Howes G., Price B.M., Smith J.C.;
RT "Bone morphogenetic protein 4: a ventralizing factor in early Xenopus
RT development.";
RL Development 115:573-585(1992).
RN [3]
RP SEQUENCE FROM N.A.
RA Metz A., Knoechel S., Buechler P., Koester M., Knoechel W.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
DR EMBL; X64538; CAA45836.1; -.
DR EMBL; AJ005076; CAA06333.1; -.
DR HSSP; P18075; 1BMP.
DR InterPro; IPR001111; -.
DR InterPro; IPR001839; -.
DR Pfam; PF00019; TGF-beta; 1.
DR ProDom; PD000357; -.
DR PROSITE; PS00250; TGF_BETA; 1.
DR SMART; SM00204; TGFbeta; 1.
KW Glycoprotein.
SQ SEQUENCE 400 AA; 45778 MW; B81472F9BCB4506E CRC64;

Query Match 26.1%; Score 165.5; DB 13; Length 400;
Best Local Similarity 36.8%; Pred. No. 1e-10;
Matches 42; Conservative 18; Mismatches 35; Indels 19; Gaps 8;

QY 9 RNLEENCVRPLYIDFRQDLGWK-WVHEPKGYANFCSGPCPY-----LRSADTTHSTVL 62
DB 294 RKKNHCRHRSLYVDF-SDVGWNDWIVAPPGYQAFYCHGDCPPLADHLNS--TNHAIQV 350
QY 63 GLYNTLN---PEASASPCVPODLEPLTILYVGRTPKV--EQLSNMVKSKCK 111
DB 351 TLVNSVNASIPKA----CCVPTELSAISML-YLDEYDKVVLKYNQEMVVEGCGC 399

RESULT 98
Q9YHW9 ID Q9YHW9 PRELIMINARY; PRT; 324 AA.
AC Q9YHW9;
DT 01-MAY-1999 (Tremblrel. 10, Created)

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DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
 DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
 DE GROWTH DIFFERENTIATION FACTOR 5 PRECURSOR (FRAGMENT).
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LEG BUD;
 RX MEDLINE=99119368; PubMed=9918693;
 RA Merino R., Macias D., Ganan Y., Economides A.N., Wang X., Wu Q.,
 RA Stahl N., Sampath K.T., Varona P., Hurlie J.M.;
 RT "Expression and function of Gdf-5 during digit skeletogenesis in the
 RT embryonic chick leg bud."
 RL Dev. Biol. 206:33-45(1999).
 CC -!- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
 DR EMBL; AF075441; AAD14569.1; -;
 DR HSSP; P18075; LBMP.
 DR InterPro; IPR001111; -;
 DR InterPro; IPR001839; -;
 DR InterPro; IPR002405; -;
 DR Pfam; PF00019; TGF-beta; 1.
 DR Pfam; PF00688; TGF-beta-propeptide; 1.
 DR PRINTS; PR00669; INHIBIN.
 DR PROSITE; PS00250; TGF_BETA; 1.
 DR SMART; SM00204; TGF; 1.
 KW Glycoprotein. 1
 FT NON_TER 1 1
 FT NON_TER 324 324
 SQ SEQUENCE 324 AA; 37206 MW; 0B8A7CB111375007 CRC64;

Query Match 26.0%; Score 165; DB 13; Length 324;
 Best Local Similarity 34.0%; Pred. No. 9.4e-11;
 Matches 35; Conservative 24; Mismatches 32; Indels 12; Gaps 5;
 QY 9 RNLENCVVRPLIYDFRODLGW-KWHEPKGYANFCGCPY-LRS--ADTHSTVLGL 64
 DB 226 KNLKARCARKALHVFVK-DMGDDWIIAPLEYEHCEGLCFPLRSHLEPTNHAIVQTL 284
 QY 65 YNTLNPASASCCVPPQDLPLTILYVGRTPKEQLSNVVK 107
 DB 285 MNSMDPESTPTCCVPTLSPISILF-----IDSANNVVK 320

RESULT 99
 Q90388
 ID Q90388 PRELIMINARY; PRT; 102 AA.
 AC Q90388;
 DT 01-NOV-1996 (Tremblrel. 01, Created)
 DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
 DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
 DE ACTIVIN BETA-B-1 SURUNIT (FRAGMENT).
 OS Carassius auratus (Goldfish).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
 OC Cypriniformes; Cyprinidae; Cyprininae; Carassius.
 OX NCBI_TaxID=7957;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=BLOOD;
 RX MEDLINE=93290666; PubMed=8512569;
 RA Ge W., Gallin W.J., Strobeck C., Peter R.E.;
 RT "Cloning and sequencing of goldfish activin subunit genes: strong
 RT structural conservation during vertebrate evolution."
 RL Biochem. Biophys. Res. Commun. 193:711-717(1993).
 CC -!- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
 DR EMBL; L15340; AAA49160.1; -;
 DR HSSP; P18075; LBMP.
 DR InterPro; IPR001839; -;
 DR Pfam; PF00019; TGF-beta; 1.

DR PROSITE; PS00250; TGF_BETA; 1.
 DR SMART; SM00204; TGF; 1.
 KW Glycoprotein.
 FT NON_TER 1 1
 FT NON_TER 102 102
 SQ SEQUENCE 102 AA; 11358 MW; 222222E54A828A7C CRC64;
 Query Match 25.9%; Score 164; DB 13; Length 102;
 Best Local Similarity 38.8%; Pred. No. 3.7e-11;
 Matches 33; Conservative 16; Mismatches 26; Indels 10; Gaps 6;
 QY 15 CCVRPLIYDFRODLGW-KWHEPKGYANFCGCPY-YLR----SADTHSTVLGLYNT- 67
 DB 6 CCRQOQFVDFRL-ICWINDWIIAPAGYGYGCGSPAYMAGVPGSASFHTAVVQYRMR 64
 QY 68 -LNPEASASCCVPPQDLPLTILY 91
 DB 65 GISP-GSVNSCCIPTKLSTMSMLYF 88

RESULT 100
 P79707
 ID P79707 PRELIMINARY; PRT; 83 AA.
 AC P79707;
 DT 01-MAY-1997 (Tremblrel. 03, Created)
 DT 01-MAY-1997 (Tremblrel. 03, Last sequence update)
 DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
 DE VG-1 (FRAGMENT).
 OS Cynops pyrrhogaster (Japanese common newt).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Caudata; Salamandroidea; Salamandridae; Cynops.
 OX NCBI_TaxID=8330;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=EMBRYO;
 RA Suzuki A.S., Tabata T., Sakaguchi K., Takabatake T., Takeshima K.,
 RA Kaneda T.;
 RT "Serial expression of the genes in a mesodermalizing ectoderms of
 RT early Cynops gastrula."
 RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
 CC -!- SIMILARITY: TO TRANSFORMING GROWTH FACTOR (TGF) BETA FAMILY.
 DR EMBL; D89444; BAA13959.1; -;
 DR HSSP; P18075; LBMP.
 DR InterPro; IPR001839; -;
 DR Pfam; PF00019; TGF-beta; 1.
 DR PROSITE; PS00250; TGF_BETA; 1.
 DR SMART; SM00204; TGF; 1.
 KW Glycoprotein. 1
 FT NON_TER 1 1
 FT NON_TER 83 83
 SQ SEQUENCE 83 AA; 9530 MW; 1538F56763FC4A67 CRC64;

Query Match 25.6%; Score 162; DB 13; Length 83;
 Best Local Similarity 43.3%; Pred. No. 5e-11;
 Matches 29; Conservative 13; Mismatches 21; Indels 4; Gaps 2;
 QY 29 GWK-WHEPKGYANFCGCPYLRSA---DTHTSTVLGLYNTLNPEASASCCVPPQDL 84
 DB 1 GWQWVIAPOGYMANYCHGCPYPLTEILNGTNAILOTLVHSMPEPTPPCCVPRLS 60
 QY 85 PLTILY 91
 DB 61 PISMLY 67

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